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(54) Title: METHODS OF DIAGNOSIS OF LUNG CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF LUNG CANCER

(57) Abstract: Described herein are methods and compositions that can be used for diagnosis and treatment of lung cancer and similar pathologies. Also described herein are methods that can be used to identify modulators of lung cancer and similar pathologies.



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METHODS OF DIAGNOSIS OF LUNG CANCER, COMPOSITIONS AND METHODS  
OF SCREENING FOR MODULATORS OF LUNG CANCER

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CROSS-REFERENCES TO RELATED APPLICATIONS

This application is related to USSN 60/284,770, filed April 18, 2001; USSN 60/290,492, filed May 10, 2001; USSN 60/334,370, filed November 29, 2001; USSN 60/339,245, filed November 9, 2001; USSN 60/350,666, filed November 13, 2001; and  
10 USSN 60/xxx,xxx, filed April 12, 2002 (Docket OMNI-002P); each of which is incorporated herein by reference in its entirety.

FIELD OF THE INVENTION

The invention relates to the identification of nucleic acid and protein expression  
15 profiles and nucleic acids, products, and antibodies thereto that are involved in lung cancer; and to the use of such expression profiles and compositions in diagnosis and therapy of lung cancer. The invention further relates to methods for identifying and using agents and/or targets that inhibit lung cancer or related conditions.

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BACKGROUND OF THE INVENTION

Lung cancer is the second most commonly occurring cancer in the United States and is the leading cause of cancer-related death. It is estimated that there are over 160,000 new cases of lung cancer in the United States every year. Of those who are diagnosed with lung cancer, 86 percent will die within five years. Lung cancer is the most common visceral  
25 cancer in men and accounts for nearly one third of all cancer deaths in both men and women. In fact, lung cancer accounts for 7% of all deaths, due to any cause, in both men and women.

Smoking is the primary cause of lung cancer, with more than 80% of lung cancers resulting from smoking. About 400 to 500 separate gaseous substances are present in the smoke of a non-filter cigarette. The most noteworthy substances include nitrogen oxides,  
30 hydrogen cyanide, formaldehyde, benzene, and toluene. The particles present in cigarette smoke contain at least 3,500 individual compounds such as nicotine, tobacco alkaloids (nornicotine, anatabine, anabasine), polycyclic aromatic hydrocarbons (e.g., benzo(a)pyrene, B(a)P), naphthalenes, aromatic amines, phenols, and tobacco-specific nitrosamines.



Tobacco-specific nitrosamines are formed during tobacco curing and processing, and are suspected of causing lung cancer in humans. In rodent studies, regardless of the where or how it is applied, the tobacco-specific nitrosamine known as NNK produces lung adenomas and lung adenocarcinomas. The tobacco-specific nitrosamine known as NNAL also produces lung adenocarcinomas in rodents.

Many of the chemicals found in cigarette smoke also affect the nonsmoker inhaling "secondhand" or sidestream smoke. Indeed, the smoke inhaled by non-smokers has a chemical composition similar to the smoke inhaled by smokers, but, importantly, the concentrations of the carcinogenic tobacco-specific nitrosamines are present in higher concentrations in second hand smoke. For this and other reasons, "passive smoking" is an important cause of lung cancer, causing as many as 3,000 lung cancer deaths in nonsmokers each year.

In addition to smoking, other factors thought to be causes of lung cancer include on-the-job exposure to carcinogens such as asbestos and uranium, exposure to chemical hazards such as radon, polycyclic aromatic hydrocarbons, chromium, nickel, and inorganic arsenic, genetic factors, and diet.

Histological classification of various lung cancers define the types of cancer that begin in the lung. See, e.g., Travis, et al. (1999) Histological Typing of Lung and Pleural Tumours (International Histological Classification of Tumours, No 1. Four major cell types make up more than 88% of all primary lung neoplasms. These are: squamous or epidermoid carcinoma, small cell (also called oat cell) carcinoma, adenocarcinoma, and large cell (also called large cell anaplastic) carcinoma. The remainder include undifferentiated carcinomas, carcinoids, bronchial gland tumors, and other rarer types. The various cell types have different natural histories and responses to therapy, and, thus, a correct histologic diagnosis is the first step of effective treatment.

Small cell lung cancer (SCLC) accounts for 18-25% of all lung cancers, and occurs less frequently than non-small cell lung cancers, and generally spread to distant organs more rapidly than non-small cell lung cancer. In general, at the time of presentation small cell lung cancers have already spread beyond the bounds where surgery and curative intent can be undertaken. However, if identified early enough, these cancers are often responsive to chemotherapy and thoracic radiation treatment.

Non-small cell lung cancers (NSCLC) are the more frequently occurring form of lung cancer. They comprise squamous cell carcinoma, adenocarcinoma, and large cell carcinoma



and account for more than 75% of all lung cancers. Non-small cell tumors that are localized at the time of presentation can sometimes be cured with surgery and/or radiotherapy, but usually are not identified until significant metastasis has occurred, which are typically not very responsive to surgical, chemotherapy, or radiation treatment..

5           The screening of asymptomatic persons at high risk for lung cancer has often proven ineffective. In general, only 5 to 15 percent of lung cancer patients have their disease detected while they are asymptomatic. Of course, early detection and treatment are critical factors in the fight against lung cancer. The average survival rate is 49% for those whose cancer is detected early, before the cancer has spread from the lung. Lung cancer often  
10 spreads outside of the lung, and it may have spread to the bones or brain by the time it is diagnosed. While the prognosis may be better for lung cancers that are detected early, because of the lack ofv effective curative treatments, early detection does not necessarily alter the total death rate from lung cancer.

          Thus, methods for diagnosis and prognosis of lung cancer and effective treatment of  
15 lung cancer would be desirable. Accordingly, provided herein are methods that can be used in diagnosis and prognosis of lung cancer. Further provided are methods that can be used to screen candidate therapeutic agents for the ability to modulate, e.g., treat, lung cancer. Additionally, provided herein are molecular targets and compositions for therapeutic intervention in lung disease and other metastatic cancers.

## SUMMARY OF THE INVENTION

20           The present invention provides nucleotide sequences of genes that are up- and down-regulated in lung cancer cells. Such genes are useful for diagnostic purposes, and also as targets for screening for therapeutic compounds that modulate lung cancer, such as  
25 antibodies. The methods of detecting nucleic acids of the invention or their encoded proteins can be used for a number of purposes. Examples include early detection of lung cancers, monitoring and early detection of relapse following treatment of lung cancers, monitoring response to therapy of lung cancers, determining prognosis of lung cancers, directing therapy of lung cancers, selecting patients for postoperative chemotherapy or radiation therapy,  
30 selecting therapy, determining tumor prognosis, treatment, or response to treatment, and early detection of precancerous lesions of the lung. Examples of benign or precancerous lesions include: atelectasis, emphysema, brochitis, chronic obstructive pulmonary disease, fibrosis, hypersensitivity pneumonitis (HP), interstitial pulmonary fibrosis (IPF), asthma, and



bronchiectasis. Other aspects of the invention will become apparent to the skilled artisan by the following description of the invention.

In one aspect, the present invention provides a method of detecting a lung cancer-associated transcript in a cell from a patient, the method comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16. Alternatively, the sample may be contacted with a specific binding reagent, e.g., antibody.

In one embodiment, the polynucleotide selectively hybridizes to a sequence at least 95% identical to a sequence as shown in Tables 1A-16. In another embodiment, the polynucleotide comprises a sequence as shown in Tables 1A-16.

In one embodiment, the biological sample is a tissue sample, or a body fluid. In another embodiment, the biological sample comprises isolated nucleic acids, e.g., mRNA.

In one embodiment, the polynucleotide is labeled, e.g., with a fluorescent label. In one embodiment, the polynucleotide is immobilized on a solid surface. In one embodiment, the patient is undergoing a therapeutic regimen to treat lung cancer. In another embodiment, the patient is suspected of having lung cancer. In one embodiment, the patient is a primate, e.g., a human.

In one embodiment, the method further comprises the step of amplifying nucleic acids before the step of contacting the biological sample with the polynucleotide.

In another aspect, the present invention provides a method of monitoring the efficacy of a therapeutic treatment of lung cancer, the method comprising the steps of: (i) providing a biological sample from a patient undergoing the therapeutic treatment; and (ii) determining the level of a lung cancer-associated transcript in the biological sample by contacting the biological sample with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16, thereby monitoring the efficacy of the therapy. Or the sample may be evaluated for protein, e.g., contacting the sample with an antibody.

In one embodiment, the method further comprises the step of: (iii) comparing the level of the lung cancer-associated transcript to a level of the lung cancer-associated transcript in a biological sample from the patient prior to, or earlier in, the therapeutic treatment. Or the sample may be evaluated for comparison of protein.

In another aspect, the present invention provides a method of monitoring the efficacy of a therapeutic treatment of lung cancer, the method comprising the steps of: (i) providing a



biological sample from a patient undergoing the therapeutic treatment; and (ii) determining the level of a lung cancer-associated antibody in the biological sample by contacting the biological sample with a polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16, wherein the polypeptide specifically binds to the lung cancer-associated antibody, thereby monitoring the efficacy of the therapy.

In one embodiment, the method further comprises the step of: (iii) comparing the level of the lung cancer-associated antibody to a level of the lung cancer-associated antibody in a biological sample from the patient prior to, or earlier in, the therapeutic treatment.

In another aspect, the present invention provides a method of monitoring the efficacy of a therapeutic treatment of lung cancer, the method comprising the steps of: (i) providing a biological sample from a patient undergoing the therapeutic treatment; and (ii) determining the level of a lung cancer-associated polypeptide in the biological sample by contacting the biological sample with an antibody, wherein the antibody specifically binds to a polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16, thereby monitoring the efficacy of the therapy.

In one embodiment, the method further comprises the step of: (iii) comparing the level of the lung cancer-associated polypeptide to a level of the lung cancer-associated polypeptide in a biological sample from the patient prior to, or earlier in, the therapeutic treatment. In one aspect, the present invention provides an isolated nucleic acid molecule consisting of a polynucleotide sequence as shown in Tables 1A-16. In one embodiment, an expression vector or cell comprises the isolated nucleic acid. In one aspect, the present invention provides an isolated polypeptide which is encoded by a nucleic acid molecule having polynucleotide sequence as shown in Tables 1A-16.

In another aspect, the present invention provides an antibody that specifically binds to an isolated polypeptide which is encoded by a nucleic acid molecule having polynucleotide sequence as shown in Tables 1A-16. In one embodiment, the antibody is conjugated to an effector component, e.g., a fluorescent label, a radioisotope or a cytotoxic chemical. In one embodiment, the antibody is an antibody fragment. In another embodiment, the antibody is humanized.

In one aspect, the present invention provides a method of detecting lung cancer in a patient, the method comprising contacting a biological sample from the patient with an antibody or protein as described herein.



In another aspect, the present invention provides a method of detecting antibodies specific to a lung cancer gene in a patient, the method comprising contacting a biological sample from the patient with a polypeptide encoded by a nucleic acid comprises a sequence from Tables 1A-16.

5 In another aspect, the present invention provides a method for identifying a compound that modulates a lung cancer-associated polypeptide, the method comprising the steps of: (i) contacting the compound with a lung cancer-associated polypeptide, the polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16; and (ii) determining the functional effect of the  
10 compound upon the polypeptide.

In one embodiment, the functional effect is a physical effect, an enzymatic effect, or a chemical effect. In one embodiment, the polypeptide is expressed in a eukaryotic host cell or cell membrane. In another embodiment, the polypeptide is recombinant. In one  
15 embodiment, the functional effect is determined by measuring ligand binding to the polypeptide.

In another aspect, the present invention provides a method of inhibiting proliferation or another critical process of a lung cancer-associated cell to treat lung cancer in a patient, the method comprising the step of administering to the subject a therapeutically effective amount of a compound identified as described herein. In one embodiment, the compound is an  
20 antibody.

In another aspect, the present invention provides a drug screening assay comprising the steps of: (i) administering a test compound to a mammal having lung cancer or a cell isolated therefrom; (ii) comparing the level of gene expression of a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables  
25 1A-16 in a treated cell or mammal with the level of gene expression of the polynucleotide in a control cell or mammal, wherein a test compound that modulates the level of expression of the polynucleotide is a candidate for the treatment of lung cancer.

In one embodiment, the control is a mammal with lung cancer or a cell therefrom that has not been treated with the test compound. In another embodiment, the control is a normal  
30 cell or mammal, or a non-malignant lung disease.

In another aspect, the present invention provides a method for treating a mammal having lung cancer comprising administering a compound identified by the assay described herein.



In another aspect, the present invention provides a pharmaceutical composition for treating a mammal having lung cancer, the composition comprising a compound identified by the assay described herein and a physiologically acceptable excipient.

## DETAILED DESCRIPTION OF THE INVENTION

In accordance with the objects outlined above, the present invention provides novel methods for diagnosis and treatment of lung disease or cancer, as well as methods for screening for compositions which modulate lung cancer. "Treatment, monitoring, detection or modulation of lung disease or cancer" includes treatment, monitoring, detection, or modulation of lung disease in those patients who have lung disease (whether malignant or non-malignant, e.g., emphysema, bronchitis, or fibrosis) as well as patients with lung cancers in which gene expression from a gene in Tables 1A-16 is increased or decreased, indicating that the subject is more likely to have disease. In particular, while these targets are identified primarily from lung cancer samples, these same targets are likely to be similarly found in analyses of other medical conditions. These other conditions may result from similar pathological processes which affect similar tissues, e.g., lung cancer, small cell lung carcinoma (oat cell carcinoma), non-small cell carcinomas (e.g., squamous cell carcinoma, adenocarcinoma, large cell lung carcinoma, carcinoid, granulomatous), fibrosis (idiopathic pulmonary fibrosis (IPF), hypersensitivity pneumonitis (HP), interstitial pneumonitis, nonspecific idiopathic pneumonitis (NSIP)), chronic obstructive pulmonary disease (COPD, e.g., emphysema, chronic bronchitis), asthma, bronchiectasis, and esophageal cancer. See, e.g., the NCI webpage and USSN 60/347,349 and USSN 60/xxx,xxx (docket LFBR-001-1P, filed March 29, 2002), each of which is incorporated herein by reference. The treatment may be of lung cancer or related condition itself, or treatment of metastasis.

In particular, identification of markers selectively expressed on these cancers allows for use of that expression in diagnostic, prognostic, or therapeutic methods. As such, the invention defines various compositions, e.g., nucleic acids, polypeptides, antibodies, and small molecule agonists/antagonists, which will be useful to selectively identify those markers. For example, therapeutic methods may take the form of protein therapeutics which use the marker expression for selective localization or modulation of function (for those markers which have a causative disease effect), for vaccines, identification of binding partners, or antagonism, e.g., using antisense or RNAi. The markers may be useful for molecular characterization of subsets of lung diseases, which subsets may actually require



very different treatments. Moreover, the markers may also be important in related diseases to the specific cancers, e.g., which affect similar tissues in non-malignant diseases, or have similar mechanisms of induction/maintenance. Metastatic processes or characteristics may also be targeted. Diagnostic and prognostic uses are made available, e.g., to subset related but distinct diseases, or to determine treatment strategy. The detection methods may be based upon nucleic acid, e.g., PCR or hybridization techniques, or protein, e.g., ELISA, imaging, IHC, etc. The diagnosis may be qualitative or quantitative, and may detect increases or decreases in expression levels.

Tables 1A-16 provide unigene cluster identification numbers for the nucleotide sequence of genes that exhibit increased or decreased expression in lung cancer samples. The tables also provide an exemplar accession number that provides a nucleotide sequence that is part of the unigene cluster. In Table 1A, genes marked as “target 1” or “target 2” are particularly useful as therapeutic targets. Genes marked as “target 3” are particularly useful as diagnostic markers. Genes marked as “chron” are upregulated in chronically diseased lung (e.g., emphysema, bronchitis, fibrosis) relative to lung tumors and normal tissue. In certain analyses, the ratio for the “chron” category was determined using the 70th percentile of chronically diseased lung samples divided by the 90th percentile of normal lung samples. The ratio for the targets was determined using the 70th percentile of lung tumor samples divided by the 90th percentile of normal lung samples.

## Definitions

The term “lung cancer protein” or “lung cancer polynucleotide” or “lung cancer-associated transcript” refers to nucleic acid and polypeptide polymorphic variants, alleles, mutants, and interspecies homologs that: (1) have a nucleotide sequence that has greater than about 60% nucleotide sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% or greater nucleotide sequence identity, preferably over a region of at least about 25, 50, 100, 200, 500, 1000, or more nucleotides, to a nucleotide sequence of or associated with a unigene cluster of Tables 1A-16; (2) bind to antibodies, e.g., polyclonal antibodies, raised against an immunogen comprising an amino acid sequence encoded by a nucleotide sequence of or associated with a unigene cluster of Tables 1A-16, and conservatively modified variants thereof; (3) specifically hybridize under stringent hybridization conditions to a nucleic acid sequence, or the complement thereof of Tables 1A-16 and conservatively modified variants thereof; or (4)



have an amino acid sequence that has greater than about 60% amino acid sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% or greater amino sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more amino acid, to an amino acid sequence encoded by a nucleotide sequence of or associated with a unigene cluster of Tables 1A-16. A polynucleotide or polypeptide sequence is typically from a mammal including, but not limited to, primate, e.g., human; rodent, e.g., rat, mouse, hamster; cow, pig, horse, sheep, or other mammal. A "lung cancer polypeptide" and a "lung cancer polynucleotide," include both naturally occurring or recombinant forms.

A "full length" lung cancer protein or nucleic acid refers to a lung cancer polypeptide or polynucleotide sequence, or a variant thereof, that contains the elements normally contained in one or more naturally occurring, wild type lung cancer polynucleotide or polypeptide sequences. The "full length" may be prior to, or after, various stages of post-translational processing or splicing, including alternative splicing.

"Biological sample" as used herein is a sample of biological tissue or fluid that contains nucleic acids or polypeptides, e.g., of a lung cancer protein, polynucleotide, or transcript. Such samples include, but are not limited to, tissue isolated from primates, e.g., humans, or rodents, e.g., mice, and rats. Biological samples may also include sections of tissues such as biopsy and autopsy samples, frozen sections taken for histologic purposes, archival materials, blood, plasma, serum, sputum, stool, tears, mucus, hair, skin, etc. Biological samples also include explants and primary and/or transformed cell cultures derived from patient tissues. A biological sample is typically obtained from a eukaryotic organism, most preferably a mammal such as a primate, e.g., chimpanzee or human; cow; dog; cat; a rodent, e.g., guinea pig, rat, mouse; rabbit; or other mammal; or a bird; reptile; fish. Livestock and domestic animals are of interest.

"Providing a biological sample" means to obtain a biological sample for use in methods described in this invention. Most often, this will be done by removing a sample of cells from an animal, but can also be accomplished by using previously isolated cells (e.g., isolated by another person, at another time, and/or for another purpose), or by performing the methods of the invention in vivo. Archival tissues or materials, having treatment or outcome history, will be particularly useful.

The terms "identical" or percent "identity," in the context of two or more nucleic acids or polypeptide sequences, refer to two or more sequences or subsequences that are the



same or have a specified percentage of amino acid residues or nucleotides that are the same (e.g., about 60% identity, preferably 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or higher identity over a specified region, when compared and aligned for maximum correspondence over a comparison window or designated region) as

5 measured using, e.g., a BLAST or BLAST 2.0 sequence comparison algorithms with default parameters described below, or by manual alignment and visual inspection (see, e.g., NCBI web site <http://www.ncbi.nlm.nih.gov/BLAST/> or the like). Such sequences are then said to be “substantially identical.” This definition also refers to, or may be applied to, the complement of a test sequence. The definition also includes sequences that have deletions and/or insertions, substitutions, and naturally occurring, e.g., polymorphic or allelic variants, 10 and man-made variants. As described below, the preferred algorithms can account for gaps and the like. Preferably, identity exists over a region that is at least about 25 amino acids or nucleotides in length, or more preferably over a region that is 50-100 amino acids or nucleotides in length.

15 For sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. Preferably, default program parameters can be used, or alternative parameters can be designated. The sequence 20 comparison algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters.

A “comparison window”, as used herein, includes reference to a segment of contiguous positions selected from the group consisting typically of from 20 to 600, usually about 50 to about 200, more usually about 100 to about 150 in which a sequence may be 25 compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequences for comparison are well-known in the art. Optimal alignment of sequences for comparison can be conducted, e.g., by the local homology algorithm of Smith and Waterman (1981) Adv. Appl. Math. 2:482, by the homology alignment algorithm of Needleman and Wunsch (1970) J. Mol. Biol. 48:443, by the search for similarity method of Pearson and Lipman (1988) Proc. Nat’l. Acad. Sci. USA 85:2444, by computerized implementations of these algorithms (GAP, BESTFIT, 30 FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer



Group, 575 Science Dr., Madison, WI), or by manual alignment and visual inspection (see, e.g., Ausubel, et al. (eds. 1995 and supplements) Current Protocols in Molecular Biology.

Preferred examples of algorithms that are suitable for determining percent sequence identity and sequence similarity include the BLAST and BLAST 2.0 algorithms, which are described in Altschul, et al. (1977) Nuc. Acids Res. 25:3389-3402 and Altschul, et al. (1990) J. Mol. Biol. 215:403-410. BLAST and BLAST 2.0 are used, with the parameters described herein, to determine percent sequence identity for the nucleic acids and proteins of the invention. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov/>). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul, et al., *supra*). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, e.g., for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, M=5, N=-4 and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength of 3, and expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff and Henikoff (1989) Proc. Natl. Acad. Sci. USA 89:10915) alignments (B) of 50, expectation (E) of 10, M=5, N=-4, and a comparison of both strands.

The BLAST algorithm also performs a statistical analysis of the similarity between two sequences (see, e.g., Karlin and Altschul (1993) Proc. Nat'l. Acad. Sci. USA 90:5873-5787). One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between



two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.2, more preferably less than about 0.01, and most preferably less than about 0.001. Log values may be negative large numbers, e.g., 5, 10, 20, 30, 40, 40, 70, 90, 110, 150, 170, etc.

An indication that two nucleic acid sequences are substantially identical is that the polypeptide encoded by the first nucleic acid is immunologically cross reactive with the antibodies raised against the polypeptide encoded by the second nucleic acid. Thus, a polypeptide is typically substantially identical to a second polypeptide, e.g., where the two peptides differ only by conservative substitutions. Another indication that two nucleic acid sequences are substantially identical is that the two molecules or their complements hybridize to each other under stringent conditions. Yet another indication that two nucleic acid sequences are substantially identical is that the same primers can be used to amplify the sequences.

A "host cell" is a naturally occurring cell or a transformed cell that contains an expression vector and supports the replication or expression of the expression vector. Host cells may be cultured cells, explants, cells *in vivo*, and the like. Host cells may be prokaryotic cells such as *E. coli*, or eukaryotic cells such as yeast, insect, amphibian, or mammalian cells such as CHO, HeLa, and the like (see, e.g., the American Type Culture Collection catalog or web site, [www.atcc.org](http://www.atcc.org)).

The terms "isolated," "purified," or "biologically pure" refer to material that is substantially or essentially free from components that normally accompany it as found in its native state. Purity and homogeneity are typically determined using analytical chemistry techniques such as polyacrylamide gel electrophoresis or high performance liquid chromatography. A protein or nucleic acid that is the predominant species present in a preparation is substantially purified. In particular, an isolated nucleic acid is separated from some open reading frames that naturally flank the gene and encode proteins other than protein encoded by the gene. The term "purified" in some embodiments denotes that a nucleic acid or protein gives rise to essentially one band in an electrophoretic gel. Preferably, it means that the nucleic acid or protein is at least about 85% pure, more preferably at least 95% pure, and most preferably at least 99% pure. "Purify" or "purification" in other embodiments means removing at least one contaminant or component from the composition to be purified.



In this sense, purification does not require that the purified compound be homogeneous, e.g., 100% pure.

The terms “polypeptide,” “peptide” and “protein” are used interchangeably herein to refer to a polymer of amino acid residues. The terms apply to amino acid polymers in which one or more amino acid residue is an artificial chemical mimetic of a corresponding naturally occurring amino acid, as well as to naturally occurring amino acid polymers, those containing modified residues, and non-naturally occurring amino acid polymer.

The term “amino acid” refers to naturally occurring and synthetic amino acids, as well as amino acid analogs and amino acid mimetics that function similarly to the naturally occurring amino acids. Naturally occurring amino acids are those encoded by the genetic code, as well as those amino acids that are later modified, e.g., hydroxyproline,  $\gamma$ -carboxyglutamate, and O-phosphoserine. Amino acid analogs refer to compounds that have the same basic chemical structure as a naturally occurring amino acid, e.g., an  $\alpha$  carbon that is bound to a hydrogen, a carboxyl group, an amino group, and an R group, e.g., homoserine, norleucine, methionine sulfoxide, methionine methyl sulfonium. Such analogs may have modified R groups (e.g., norleucine) or modified peptide backbones, but retain some basic chemical structure as a naturally occurring amino acid. Amino acid mimetics refer to chemical compounds that have a structure that is different from the general chemical structure of an amino acid, but that function similarly to another amino acid.

Amino acids may be referred to herein by either their commonly known three letter symbols or by the one-letter symbols recommended by the IUPAC-IUB Biochemical Nomenclature Commission. Nucleotides, likewise, may be referred to by their commonly accepted single-letter codes.

“Conservatively modified variants” applies to both amino acid and nucleic acid sequences. With respect to particular nucleic acid sequences, conservatively modified variants refers to those nucleic acids which encode identical or essentially identical amino acid sequences, or where the nucleic acid does not encode an amino acid sequence, to essentially identical or associated, e.g., naturally contiguous, sequences. Because of the degeneracy of the genetic code, a large number of functionally identical nucleic acids encode most proteins. For instance, the codons GCA, GCC, GCG, and GCU each encode the amino acid alanine. Thus, at each position where an alanine is specified by a codon, the codon can be altered to another of the corresponding codons described without altering the encoded polypeptide. Such nucleic acid variations are “silent variations,” which are one species of



conservatively modified variations. Every nucleic acid sequence herein which encodes a polypeptide also describes silent variations of the nucleic acid. In certain contexts each codon in a nucleic acid (except AUG, which is ordinarily the only codon for methionine, and TGG, which is ordinarily the only codon for tryptophan) can be modified to yield a functionally similar molecule. Accordingly, a silent variation of a nucleic acid which encodes a polypeptide is implicit in a described sequence with respect to the expression product, but not necessarily with respect to actual probe sequences.

As to amino acid sequences, one of skill will recognize that individual substitutions, deletions or additions to a nucleic acid, peptide, polypeptide, or protein sequence which alters, adds or deletes a single amino acid or a small percentage of amino acids in the encoded sequence is a "conservatively modified variant" where the alteration results in the substitution of an amino acid with a chemically similar amino acid. Conservative substitution tables providing functionally similar amino acids are well known in the art. Such conservatively modified variants are in addition to and do not exclude polymorphic variants, interspecies homologs, and alleles of the invention. Typically conservative substitutions include for one another: 1) Alanine (A), Glycine (G); 2) Aspartic acid (D), Glutamic acid (E); 3) Asparagine (N), Glutamine (Q); 4) Arginine (R), Lysine (K); 5) Isoleucine (I), Leucine (L), Methionine (M), Valine (V); 6) Phenylalanine (F), Tyrosine (Y), Tryptophan (W); 7) Serine (S), Threonine (T); and 8) Cysteine (C), Methionine (M) (see, e.g., Creighton, Proteins (1984)).

Macromolecular structures such as polypeptide structures can be described in terms of various levels of organization. For a general discussion of this organization, see, e.g., Alberts, et al. (1994) Molecular Biology of the Cell (3<sup>rd</sup> ed.) and Cantor and Schimmel (1980) Biophysical Chemistry Part I: The Conformation of Biological Macromolecules. "Primary structure" refers to the amino acid sequence of a particular peptide. "Secondary structure" refers to locally ordered, three dimensional structures within a polypeptide. These structures are commonly known as domains. Domains are portions of a polypeptide that often form a compact unit of the polypeptide and are typically 25 to approximately 500 amino acids long. Typical domains are made up of sections of lesser organization such as stretches of  $\beta$ -sheet and  $\alpha$ -helices. "Tertiary structure" refers to the complete three dimensional structure of a polypeptide monomer. "Quaternary structure" refers to the three dimensional structure formed, usually by the noncovalent association of independent tertiary units. Anisotropic terms are also known as energy terms.



“Nucleic acid” or “oligonucleotide” or “polynucleotide” or grammatical equivalents

used herein means at least two nucleotides covalently linked together. Oligonucleotides are typically from about 5, 6, 7, 8, 9, 10, 12, 15, 25, 30, 40, 50 or more nucleotides in length, up to about 100 nucleotides in length. Nucleic acids and polynucleotides are a polymers of any length, including longer lengths, e.g., 200, 300, 500, 1000, 2000, 3000, 5000, 7000, 10,000, etc. A nucleic acid of the present invention will generally contain phosphodiester bonds, although in some cases, nucleic acid analogs are included that may have at least one different linkage, e.g., phosphoramidate, phosphorothioate, phosphorodithioate, or O-methylphosphoroamidite linkages (see Eckstein (1992) Oligonucleotides and Analogues: A Practical Approach Oxford University Press); and peptide nucleic acid backbones and linkages. Other analog nucleic acids include those with positive backbones; non-ionic backbones, and non-ribose backbones, including those described in U.S. Patent Nos. 5,235,033 and 5,034,506, and Chapters 6 and 7, in Sanghui and Cook, eds. Carbohydrate Modifications in Antisense Research, ASC Symposium Series 580. Nucleic acids containing one or more carbocyclic sugars are also included within one definition of nucleic acids. Modifications of the ribose-phosphate backbone may be done for a variety of reasons, e.g., to increase the stability and half-life of such molecules in physiological environments or as probes on a biochip. Mixtures of naturally occurring nucleic acids and analogs can be made; alternatively, mixtures of different nucleic acid analogs, and mixtures of naturally occurring nucleic acids and analogs may be made.

Particularly preferred are peptide nucleic acids (PNA) which includes peptide nucleic acid analogs. These backbones are substantially non-ionic under neutral conditions, in contrast to the highly charged phosphodiester backbone of naturally occurring nucleic acids. This results in two advantages. First, the PNA backbone exhibits improved hybridization kinetics. PNAs have larger changes in the melting temperature ( $T_m$ ) for mismatched versus perfectly matched basepairs. DNA and RNA typically exhibit a 2-4° C drop in  $T_m$  for an internal mismatch. With the non-ionic PNA backbone, the drop is closer to 7-9° C. Similarly, due to their non-ionic nature, hybridization of the bases attached to these backbones is relatively insensitive to salt concentration. In addition, PNAs are not degraded by cellular enzymes, and thus can be more stable.

The nucleic acids may be single stranded or double stranded, as specified, or contain portions of both double stranded or single stranded sequence. As will be appreciated by those in the art, the depiction of a single strand also defines the sequence of the complementary



strand; thus the sequences described herein also provide the complement of the sequence.

The nucleic acid may be DNA, both genomic and cDNA, RNA, or a hybrid, where the nucleic acid may contain combinations of deoxyribo- and ribo-nucleotides, and combinations of bases, including uracil, adenine, thymine, cytosine, guanine, inosine, xanthine

5 hypoxanthine, isocytosine, isoguanine, etc. "Transcript" typically refers to a naturally occurring RNA, e.g., a pre-mRNA, hnRNA, or mRNA. As used herein, the term "nucleoside" includes nucleotides and nucleoside and nucleotide analogs, and modified nucleosides such as amino modified nucleosides. In addition, "nucleoside" includes non-naturally occurring analog structures. Thus, e.g., the individual units of a peptide nucleic  
10 acid, each containing a base, are referred to herein as a nucleoside.

A "label" or a "detectable moiety" is a composition detectable by spectroscopic, photochemical, biochemical, immunochemical, physiological, chemical, or other physical means. For example, useful labels include  $^{32}\text{P}$ , fluorescent dyes, electron-dense reagents, enzymes (e.g., as commonly used in an ELISA), biotin, digoxigenin, or haptens and proteins  
15 or other entities which can be made detectable, e.g., by incorporating a radiolabel into the peptide or used to detect antibodies specifically reactive with the peptide. The labels may be incorporated into the cancer nucleic acids, proteins, and antibodies. Many methods known in the art for conjugating the antibody to the label may be employed, including those methods described by Hunter, et al. (1962) Nature 144:945; David, et al. (1974) Biochemistry  
20 13:1014-1021; Pain, et al. (1981) J. Immunol. Meth., 40:219-230; and Nygren (1982) J. Histochem. and Cytochem. 30:407-412.

An "effector" or "effector moiety" or "effector component" is a molecule that is bound (or linked, or conjugated), either covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds, to an antibody.  
25 The "effector" can be a variety of molecules including, e.g., detection moieties including radioactive compounds, fluorescent compounds, an enzyme or substrate, tags such as epitope tags, a toxin; activatable moieties, a chemotherapeutic agent; a lipase; an antibiotic; or a radioisotope emitting "hard" e.g., beta radiation.

A "labeled nucleic acid probe or oligonucleotide" is one that is bound, either  
30 covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds to a label such that the presence of the probe may be detected by detecting the presence of the label bound to the probe. Alternatively, method



using high affinity interactions may achieve the same results where one of a pair of binding partners binds to the other, e.g., biotin, streptavidin.

As used herein a “nucleic acid probe or oligonucleotide” is a nucleic acid capable of binding to a target nucleic acid of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing, e.g., through hydrogen bond formation. As used herein, a probe may include natural (i.e., A, G, C, or T) or modified bases (7-deazaguanosine, inosine, etc.). In addition, the bases in a probe may be joined by a linkage other than a phosphodiester bond, preferably one that does not functionally interfere with hybridization. Thus, e.g., probes may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages. Probes may bind target sequences lacking complete complementarity with the probe sequence depending upon the stringency of the hybridization conditions. The probes are preferably directly labeled, e.g., with isotopes, chromophores, lumiphores, chromogens, or indirectly labeled, e.g., with biotin to which a streptavidin complex may later bind. By assaying for the presence or absence of the probe, one can detect the presence or absence of the select sequence or subsequence. Diagnosis or prognosis may be based at the genomic level, or at the level of RNA or protein expression.

The term “recombinant” when used with reference, e.g., to a cell, or nucleic acid, protein, or vector, indicates that the cell, nucleic acid, protein or vector, has been modified by the introduction of a heterologous nucleic acid or protein or the alteration of a native nucleic acid or protein, or that the cell is derived from a cell so modified. Thus, e.g., recombinant cells express genes that are not found within the native (non-recombinant) form of the cell or express native genes that are otherwise abnormally expressed, under expressed or not expressed at all. By the term “recombinant nucleic acid” herein is meant nucleic acid, originally formed *in vitro*, in general, by the manipulation of nucleic acid, e.g., using polymerases and endonucleases, in a form not normally found in nature. In this manner, operably linkage of different sequences is achieved. Thus an isolated nucleic acid, in a linear form, or an expression vector formed *in vitro* by ligating DNA molecules that are not normally joined, are both considered recombinant for the purposes of this invention. It is understood that once a recombinant nucleic acid is made and reintroduced into a host cell or organism, it will replicate non-recombinantly, i.e., using the *in vivo* cellular machinery of the host cell rather than *in vitro* manipulations; however, such nucleic acids, once produced recombinantly, although subsequently replicated non-recombinantly, are still considered



recombinant for the purposes of the invention. Similarly, a “recombinant protein” is a protein made using recombinant techniques, i.e., through the expression of a recombinant nucleic acid as depicted above.

The term “heterologous” when used with reference to portions of a nucleic acid indicates that the nucleic acid comprises two or more subsequences that are not normally found in the same relationship to each other in nature. For instance, the nucleic acid is typically recombinantly produced, having two or more sequences, e.g., from unrelated genes arranged to make a new functional nucleic acid, e.g., a promoter from one source and a coding region from another source. Similarly, a heterologous protein will often refer to two or more subsequences that are not found in the same relationship to each other in nature (e.g., a fusion protein).

A “promoter” is typically an array of nucleic acid control sequences that direct transcription of a nucleic acid. As used herein, a promoter includes necessary nucleic acid sequences near the start site of transcription, such as, in the case of a polymerase II type promoter, a TATA element. A promoter also optionally includes distal enhancer or repressor elements, which can be located as much as several thousand base pairs from the start site of transcription. A “constitutive” promoter is a promoter that is active under most environmental and developmental conditions. An “inducible” promoter is a promoter that is active under environmental or developmental regulation. The term “operably linked” refers to a functional linkage between a nucleic acid expression control sequence (such as a promoter, or array of transcription factor binding sites) and a second nucleic acid sequence, e.g., wherein the expression control sequence directs transcription of the nucleic acid corresponding to the second sequence.

An “expression vector” is a nucleic acid construct, generated recombinantly or synthetically, with a series of specified nucleic acid elements that permit transcription of a particular nucleic acid in a host cell. The expression vector can be part of a plasmid, virus, or nucleic acid fragment. Typically, the expression vector includes a nucleic acid to be transcribed in operable linkage to a promoter.

The phrase “selectively (or specifically) hybridizes to” refers to the binding, duplexing, or hybridizing of a molecule selectively to a particular nucleotide sequence under stringent hybridization conditions when that sequence is present in a complex mixture (e.g., total cellular or library DNA or RNA).



The phrase “stringent hybridization conditions” refers to conditions under which a

probe will hybridize to its target subsequence, typically in a complex mixture of nucleic acids, but to essentially no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at

5 higher temperatures. An extensive guide to the hybridization of nucleic acids is found in “Overview of principles of hybridization and the strategy of nucleic acid assays” in Tijssen (1993) Techniques in Biochemistry and Molecular Biology--Hybridization with Nucleic

Probes (vol. 24) Elsevier. Generally, stringent conditions are selected to be about 5-10° C

lower than the thermal melting point ( $T_m$ ) for the specific sequence at a defined ionic strength

10 pH. The  $T_m$  is the temperature (under defined ionic strength, pH, and nucleic concentration)

at which 50% of the probes complementary to the target hybridize to the target sequence at

equilibrium (as the target sequences are present in excess, at  $T_m$ , 50% of the probes are

occupied at equilibrium). Stringent conditions will be those in which the salt concentration is

less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion concentration (or

15 other salts) at pH 7.0 to 8.3 and the temperature is at least about 30° C for short probes (e.g.,

10 to 50 nucleotides) and at least about 60° C for long probes (e.g., greater than 50

nucleotides). Stringent conditions may also be achieved with the addition of destabilizing

agents such as formamide. For selective or specific hybridization, a positive signal is

typically at least two times background, preferably 10 times background hybridization.

20 Exemplary stringent hybridization conditions are often: 50% formamide, 5x SSC, and 1%

SDS, incubating at 42° C, or, 5x SSC, 1% SDS, incubating at 65° C, with wash in 0.2x SSC,

and 0.1% SDS at 65° C. For PCR, a temperature of about 36° C is typical for low stringency

amplification, although annealing temperatures may vary between about 32° C and 48° C

depending on primer length. For high stringency PCR amplification, a temperature of about

25 62° C is typical, although high stringency annealing temperatures can range from about 50° C

to about 65° C, depending on the primer length and specificity. Typical cycle conditions for

both high and low stringency amplifications include a denaturation phase of 90° C - 95° C for

0.5 - 2 min., an annealing phase lasting 0.5 - 2 min., and an extension phase of about 72° C

for 1 - 2 min. Protocols and guidelines for low and high stringency amplification reactions

30 are provided, e.g., in Innis, et al.(1990) PCR Protocols, A Guide to Methods and

Applications.

Nucleic acids that do not hybridize to each other under stringent conditions are still substantially identical if the polypeptides which they encode are substantially identical. This



occurs, e.g., when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code. In such cases, the nucleic acids typically hybridize under moderately stringent hybridization conditions. Exemplary “moderately stringent hybridization conditions” include a hybridization in a buffer of 40% formamide, 1 M NaCl, 1% SDS at 37° C, and a wash in 1X SSC at 45° C. A positive hybridization is at least twice background. Alternative hybridization and wash conditions can be utilized to provide conditions of similar stringency. Additional guidelines for determining hybridization parameters are provided in numerous reference, e.g., Ausubel, et al. (ed.) Current Protocols in Molecular Biology Lippincott.

The phrase “functional effects” in the context of assays for testing compounds that modulate activity of a lung cancer protein includes the determination of a parameter that is indirectly or directly under the influence of the lung cancer protein or nucleic acid, e.g., a physiological, enzymatic, functional, physical, or chemical effect, such as the ability to decrease lung cancer. It includes ligand binding activity; cell viability, cell growth on soft agar; anchorage dependence; contact inhibition and density limitation of growth; cellular proliferation; cellular transformation; growth factor or serum dependence; tumor specific marker levels; invasiveness into Matrigel; tumor growth and metastasis *in vivo*; mRNA and protein expression in cells undergoing metastasis, and other characteristics of lung cancer cells. “Functional effects” include *in vitro*, *in vivo*, and *ex vivo* activities.

By “determining the functional effect” is meant assaying for a compound that increases or decreases a parameter that is indirectly or directly under the influence of a lung cancer protein sequence, e.g., physiological, functional, enzymatic, physical, or chemical effects. Such functional effects can be measured by many means known to those skilled in the art, e.g., changes in spectroscopic characteristics (e.g., fluorescence, absorbance, refractive index), hydrodynamic (e.g., shape), chromatographic, or solubility properties for the protein, measuring inducible markers or transcriptional activation of the lung cancer protein; measuring binding activity or binding assays, e.g., binding to antibodies or other ligands, and measuring cellular proliferation. Determination of the functional effect of a compound on lung cancer can also be performed using lung cancer assays known to those of skill in the art such as an *in vitro* assays, e.g., cell growth on soft agar; anchorage dependence; contact inhibition and density limitation of growth; cellular proliferation; cellular transformation; growth factor or serum dependence; tumor specific marker levels; invasiveness into Matrigel; tumor growth and metastasis *in vivo*; mRNA and protein



expression in cells undergoing metastasis, and other characteristics of lung cancer cells. The functional effects can be evaluated by many means known to those skilled in the art, e.g., microscopy for quantitative or qualitative measures of alterations in morphological features, measurement of changes in RNA or protein levels for lung cancer-associated sequences, measurement of RNA stability, identification of downstream or reporter gene expression (CAT, luciferase,  $\beta$ -gal, GFP, and the like), e.g., via chemiluminescence, fluorescence, colorimetric reactions, antibody binding, inducible markers, and ligand binding assays.

“Inhibitors”, “activators”, and “modulators” of lung cancer polynucleotide and polypeptide sequences are used to refer to activating, inhibitory, or modulating molecules or compounds identified using *in vitro* and *in vivo* assays of lung cancer polynucleotide and polypeptide sequences. Inhibitors are compounds that, e.g., bind to, partially or totally block activity, decrease, prevent, delay activation, inactivate, desensitize, or down regulate the activity or expression of lung cancer proteins, e.g., antagonists. Antisense or inhibitory nucleic acids may seem to inhibit expression and subsequent function of the protein.

“Activators” are compounds that increase, open, activate, facilitate, enhance activation, sensitize, agonize, or up regulate lung cancer protein activity. Inhibitors, activators, or modulators also include genetically modified versions of lung cancer proteins, e.g., versions with altered activity, as well as naturally occurring and synthetic ligands, antagonists, agonists, antibodies, small chemical molecules and the like. Such assays for inhibitors and activators include, e.g., expressing the lung cancer protein *in vitro*, in cells, or cell membranes, applying putative modulator compounds, and then determining the functional effects on activity, as described above. Activators and inhibitors of lung cancer can also be identified by incubating lung cancer cells with the test compound and determining increases or decreases in the expression of 1 or more lung cancer proteins, e.g., 1, 2, 3, 4, 5, 10, 15, 20, 25, 30, 40, 50 or more lung cancer proteins, such as lung cancer proteins encoded by the sequences set out in Tables 1A-16.

Samples or assays comprising lung cancer proteins that are treated with a potential activator, inhibitor, or modulator are compared to control samples without the inhibitor, activator, or modulator to examine the extent of inhibition. Control samples (untreated with inhibitors) are assigned a relative protein activity value of 100%. Inhibition of a polypeptide is achieved when the activity value relative to the control is about 80%, preferably 50%, more preferably 25-0%. Activation of a lung cancer polypeptide is achieved when the activity value relative to the control (untreated with activators) is 110%, more preferably 150%, more



preferably 200-500% (i.e., two to five fold higher relative to the control), more preferably 1000-3000% higher.

The phrase “changes in cell growth” refers to any change in cell growth and proliferation characteristics *in vitro* or *in vivo*, such as cell viability, formation of foci, anchorage independence, semi-solid or soft agar growth, changes in contact inhibition and density limitation of growth, loss of growth factor or serum requirements, changes in cell morphology, gaining or losing immortalization, gaining or losing tumor specific markers, ability to form or suppress tumors when injected into suitable animal hosts, and/or immortalization of the cell. See, e.g., Freshney (1994) Culture of Animal Cells a Manual of Basic Technique pp. 231-241 (3<sup>rd</sup> ed.).

“Tumor cell” refers to precancerous, cancerous, and normal cells in a tumor.

“Cancer cells,” “transformed” cells, or “transformation” in tissue culture, refers to spontaneous or induced phenotypic changes that do not necessarily involve the uptake of new genetic material. Although transformation can arise from infection with a transforming virus and incorporation of new genomic DNA, or uptake of exogenous DNA, it can also arise spontaneously or following exposure to a carcinogen, thereby mutating an endogenous gene. Transformation is associated with phenotypic changes, such as immortalization of cells, aberrant growth control, nonmorphological changes, and/or malignancy (see, Freshney (1994) Culture of Animal Cells a Manual of Basic Technique (3<sup>rd</sup> ed.)).

“Antibody” refers to a polypeptide comprising a framework region from an immunoglobulin gene or fragments thereof that specifically binds and recognizes an antigen. The recognized immunoglobulin genes include the kappa, lambda, alpha, gamma, delta, epsilon, and mu constant region genes, as well as the myriad immunoglobulin variable region genes. Light chains are classified as either kappa or lambda. Heavy chains are classified as gamma, mu, alpha, delta, or epsilon, which in turn define the immunoglobulin classes, IgG, IgM, IgA, IgD, and IgE, respectively. Typically, the antigen-binding region of an antibody or its functional equivalent will be most critical in specificity and affinity of binding. See Paul, Fundamental Immunology.

An exemplary immunoglobulin (antibody) structural unit comprises a tetramer. Each tetramer is composed of two identical pairs of polypeptide chains, each pair having one “light” (about 25 kD) and one “heavy” chain (about 50-70 kD). The N-terminus of each chain defines a variable region of about 100 to 110 or more amino acids primarily responsible



for antigen recognition. The terms variable light chain ( $V_L$ ) and variable heavy chain ( $V_H$ ) refer to these light and heavy chains respectively.

Antibodies exist, e.g., as intact immunoglobulins or as a number of well-characterized fragments produced by digestion with various peptidases. Thus, e.g., pepsin digests an antibody below the disulfide linkages in the hinge region to produce  $F(ab)'_2$ , a dimer of Fab which itself is a light chain joined to  $V_H-C_{H1}$  by a disulfide bond. The  $F(ab)'_2$  may be reduced under mild conditions to break the disulfide linkage in the hinge region, thereby converting the  $F(ab)'_2$  dimer into an Fab' monomer. The Fab' monomer is essentially Fab with part of the hinge region (see Paul (ed. 1999) Fundamental Immunology (4th ed.). While various antibody fragments are defined in terms of the digestion of an intact antibody, one of skill will appreciate that such fragments may be synthesized *de novo* either chemically or by using recombinant DNA methodology. Thus, the term antibody, as used herein, also includes antibody fragments either produced by the modification of whole antibodies, or those synthesized *de novo* using recombinant DNA methodologies (e.g., single chain Fv) or those identified using phage display libraries (see, e.g., McCafferty, et al. (1990) Nature 348:552-554).

For preparation of antibodies, e.g., recombinant, monoclonal, or polyclonal antibodies, many technique known in the art can be used (see, e.g., Kohler and Milstein (1975) Nature 256:495-497; Kozbor, et al. (1983) Immunology Today 4:72; Cole, et al. (1985), pp. 77-96 in Monoclonal Antibodies and Cancer Therapy; Coligan (1991 and supplements) Current Protocols in Immunology; Harlow and Lane (1988) Antibodies, A Laboratory Manual; and Goding (1986) Monoclonal Antibodies: Principles and Practice (2d ed.)). Techniques for the production of single chain antibodies (U.S. Patent 4,946,778) can be adapted to produce antibodies to polypeptides of this invention. Also, transgenic mice, or other organisms such as other mammals, may be used to express humanized antibodies. Alternatively, phage display technology can be used to identify antibodies and heteromeric Fab fragments that specifically bind to selected antigens (see, e.g., McCafferty, et al. (1990) Nature 348:552-554; Marks, et al. (1992) Biotechnology 10:779-783).

A "chimeric antibody" is an antibody molecule in which, e.g., (a) the constant region, or a portion thereof, is altered, replaced, or exchanged so that the antigen binding site (variable region) is linked to a constant region of a different or altered class, effector function, and/or species, or an entirely different molecule which confers new properties to the chimeric antibody, e.g., an enzyme, toxin, hormone, growth factor, drug, etc.; or (b) the



variable region, or a portion thereof, is altered, replaced, or exchanged with a variable region having a different or altered antigen specificity.

### Identification of lung cancer-associated sequences

5           In one aspect, the expression levels of genes are determined in different patient samples for which diagnosis information is desired, to provide expression profiles. An expression profile of a particular sample is essentially a “fingerprint” of the state of the sample; while two states may have any particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is  
10       characteristic of the state of the cell. That is, normal tissue may be distinguished from cancerous or metastatic cancerous tissue, or metastatic cancerous tissue can be compared with tissue from surviving cancer patients. By comparing expression profiles of tissue in known different lung cancer states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained.  
15       Molecular profiling may distinguish subtypes of a currently collective disease designation, e.g., different forms of lung cancer (chronic disease, adenocarcinoma, etc.)

          The identification of sequences that are differentially expressed in lung cancer versus non-lung cancer tissue allows the use of this information in a number of ways. For example, a particular treatment regime may be evaluated: does a chemotherapeutic drug act to down-  
20       regulate lung cancer, and thus tumor growth or recurrence, in a particular patient. Alternatively, a treatment step may induce other markers which may be used as targets to destroy tumor cells. Similarly, diagnosis and treatment outcomes may be done or confirmed by comparing patient samples with the known expression profiles. Malignant disease may be compared to non-malignant conditions. Metastatic tissue can also be analyzed to determine  
25       the stage of lung cancer in the tissue, or origin of primary tumor, e.g., metastasis from a remote primary site. Furthermore, these gene expression profiles (or individual genes) allow screening of drug candidates with an eye to mimicking or altering a particular expression profile; e.g., screening can be done for drugs that suppress the lung cancer expression profile. This may be done by making biochips comprising sets of the important lung cancer genes,  
30       which can then be used in these screens. PCR methods may be applied with selected primer pairs, and analysis may be of RNA or of genomic sequences. These methods can also be done on the protein basis; that is, protein expression levels of the lung cancer proteins can be evaluated for diagnostic purposes or to screen candidate agents. In addition, the lung cancer



nucleic acid sequences can be administered for gene therapy purposes, including the administration of antisense nucleic acids, or the lung cancer proteins (including antibodies and other modulators thereof) administered as therapeutic drugs or as protein or DNA vaccines.

5           Thus the present invention provides nucleic acid and protein sequences that are differentially expressed in lung cancer relative to normal tissues and/or non-malignant lung disease, or in different types of lung disease, herein termed "lung cancer sequences." As outlined below, lung cancer sequences include those that are up-regulated (i.e., expressed at a higher level) in lung cancer, as well as those that are down-regulated (i.e., expressed at a lower level). In a preferred embodiment, the lung cancer sequences are from humans; however, as will be appreciated by those in the art, lung cancer sequences from other organisms may be useful in animal models of disease and drug evaluation; thus, other lung cancer sequences are provided, from vertebrates, including mammals, including rodents (rats, mice, hamsters, guinea pigs, etc.), primates, farm animals (including sheep, goats, pigs, cows, horses, etc.) and pets (dogs, cats, etc.). Lung cancer sequences from other organisms may be obtained using the techniques outlined below.

          Lung cancer sequences can include both nucleic acid and amino acid sequences. As will be appreciated by those in the art and is more fully outlined below, lung cancer nucleic acid sequences are useful in a variety of applications, including diagnostic applications, which will detect naturally occurring nucleic acids, as well as screening applications; e.g., biochips comprising nucleic acid probes or PCR microtiter plates with selected probes to the lung cancer sequences can be generated.

          A lung cancer sequence can be initially identified by substantial nucleic acid and/or amino acid sequence homology to the lung cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, e.g., using homology programs or hybridization conditions.

          For identifying lung cancer-associated sequences, the lung cancer screen typically includes comparing genes identified in different tissues, e.g., normal and cancerous tissues, cancer and non-malignant conditions, non-malignant conditions and normal tissues, or tumor tissue samples from patients who have metastatic disease vs. non metastatic tissue. Other suitable tissue comparisons include comparing lung cancer samples with metastatic cancer samples from other cancers, such as, breast, other gastrointestinal cancers, prostate, ovarian,



etc. Samples of, non metastatic disease tissue and tissue undergoing metastasis are applied to biochips comprising nucleic acid probes. The samples are first microdissected, if applicable, and treated as is known in the art for the preparation of mRNA. Suitable biochips are commercially available, e.g., from Affymetrix, Santa Clara, CA. Gene expression profiles as described herein are generated and the data analyzed.

In one embodiment, the genes showing changes in expression as between normal and disease states are compared to genes expressed in other normal tissues, preferably normal lung, but also including, and not limited to colon, heart, brain, liver, breast, kidney, muscle, prostate, small intestine, large intestine, spleen, bone, and/or placenta. In a preferred embodiment, those genes identified during the lung cancer screen that are expressed in significant amounts in other tissues (e.g., essential organs) are removed from the profile, although in some embodiments, this is not necessary (e.g., where organs may be dispensable at a later stage of life). That is, when screening for drugs, it is usually preferable that the target expression be disease specific, to minimize possible side effects on other organs.

In a preferred embodiment, lung cancer sequences are those that are up-regulated in lung cancer; that is, the expression of these genes is higher in cancerous tissue than in normal lung or other tissue. "Up-regulation" as used herein means, when the ratio is presented as a number greater than one, that the ratio is greater than one, preferably 1.5 or greater, more preferably 2.0 or greater. Another embodiment is directed to sequences up-regulated in non-malignant conditions relative to normal. Unigene cluster identification numbers and accession numbers herein are for the GenBank sequence database and the sequences of the accession numbers are hereby expressly incorporated by reference. GenBank is known in the art, see, e.g., Benson, DA, et al (1998) *Nucleic Acids Research* 26:1-7 and <http://www.ncbi.nlm.nih.gov/>. Sequences are also available in other databases, e.g., European Molecular Biology Laboratory (EMBL) and DNA Database of Japan (DDBJ). Another embodiment is directed to sequences up-regulated in non-malignant conditions relative to normal. In some situations, the sequences may be derived from assembly of available sequences or be predicted from genomic DNA using exon prediction algorithms, such as FGENESH (Salamov and Solovyev (2000) *Genome Res.* 10:516-522). In other situations, sequences have been derived from cloning and sequencing of isolated nucleic acids.

In another preferred embodiment, lung cancer sequences are those that are down-regulated in the lung cancer; that is, the expression of these genes is lower in cancerous tissue



or normal lung or other tissue. "Down-regulation" as used herein means, when the ratio is presented as a number greater than one, that the ratio is greater than one, preferably 1.5 or greater, more preferably 2.0 or greater, or, when the ratio is presented as a number less than one, that the ratio is less than one, preferably 0.5 or less, more preferably 0.25 or less.

5

### Informatics

The ability to identify genes that are over or under expressed in lung cancer can additionally provide high-resolution, high-sensitivity datasets which can be used in the areas of diagnostics, therapeutics, drug development, pharmacogenetics, protein structure, biosensor development, and other related areas. For example, the expression profiles can be used in diagnostic or prognostic evaluation of patients with lung cancer. Or as another example, subcellular toxicological information can be generated to better direct drug structure and activity correlation (see Anderson (1998) Pharmaceutical Proteomics: Targets, Mechanism, and Function, paper presented at the IBC Proteomics conference, Coronado, CA (June 11-12, 1998)). Subcellular toxicological information can also be utilized in a biological sensor device to predict the likely toxicological effect of chemical exposures and likely tolerable exposure thresholds (see U.S. Patent No. 5,811,231). Similar advantages accrue from datasets relevant to other biomolecules and bioactive agents (e.g., nucleic acids, saccharides, lipids, drugs, and the like).

Thus, in another embodiment, the present invention provides a database that includes at least one set of assay data. The data contained in the database is acquired, e.g., using array analysis either singly or in a library format. The database can be in a form in which data can be maintained and transmitted, but is preferably an electronic database. The electronic database of the invention can be maintained on any electronic device allowing for the storage of and access to the database, such as a personal computer, but is preferably distributed on a wide area network, such as the World Wide Web.

The focus of the present section on databases that include peptide sequence data is for clarity of illustration only. It will be apparent to those of skill in the art that similar databases can be assembled for assay data acquired using an assay of the invention.

The compositions and methods for identifying and/or quantitating the relative and/or absolute abundance of a variety of molecular and macromolecular species from a biological sample representing lung cancer, i.e., the identification of lung cancer-associated sequences described herein, provide an abundance of information, which can be correlated with



pathological conditions, predisposition to disease, drug testing, therapeutic monitoring, gene-disease causal linkages, identification of correlates of immunity and physiological status, among others. Although the data generated from the assays of the invention is suited for manual review and analysis, in a preferred embodiment, data processing using high-speed computers is utilized.

An array of methods for indexing and retrieving biomolecular information is known in the art. For example, U.S. Patents 6,023,659 and 5,966,712 disclose a relational database system for storing biomolecular sequence information in a manner that allows sequences to be catalogued and searched according to one or more protein function hierarchies. U.S. Patent 5,953,727 discloses a relational database having sequence records containing information in a format that allows a collection of partial-length DNA sequences to be catalogued and searched according to association with one or more sequencing projects for obtaining full-length sequences from the collection of partial length sequences. U.S. Patent 5,706,498 discloses a gene database retrieval system for making a retrieval of a gene sequence similar to a sequence data item in a gene database based on the degree of similarity between a key sequence and a target sequence. U.S. Patent 5,538,897 discloses a method using mass spectroscopy fragmentation patterns of peptides to identify amino acid sequences in computer databases by comparison of predicted mass spectra with experimentally-derived mass spectra using a closeness-of-fit measure. U.S. Patent 5,926,818 discloses a multi-dimensional database comprising a functionality for multi-dimensional data analysis described as on-line analytical processing (OLAP), which entails the consolidation of projected and actual data according to more than one consolidation path or dimension. U.S. Patent 5,295,261 reports a hybrid database structure in which the fields of each database record are divided into two classes, navigational and informational data, with navigational fields stored in a hierarchical topological map which can be viewed as a tree structure or as the merger of two or more such tree structures.

See also Mount, et al. (2001) *Bioinformatics*; Durbin, et al. (eds., 1999) *Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids* (; Baxeavanis and Oeullette (eds., 1998) *Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins*); Rashidi and Buehler (1999) *Bioinformatics: Basic Applications in Biological Science and Medicine*; Setubal, et al. (eds 1997) *Introduction to Computational Molecular Biology*; Misener and Krawetz (eds, 2000) *Bioinformatics: Methods and Protocols*; Higgins and Taylor (eds., 2000) *Bioinformatics: Sequence, Structure, and Databanks: A Practical*



Approach; Brown (2001) Bioinformatics: A Biologist's Guide to Biocomputing and the Internet; Han and Kamber (2000) Data Mining: Concepts and Techniques (2000); and Waterman (1995) Introduction to Computational Biology: Maps, Sequences, and Genomes.

The present invention provides a computer database comprising a computer and software for storing in computer-retrievable form assay data records cross-tabulated, e.g., with data specifying the source of the target-containing sample from which each sequence specificity record was obtained.

In an exemplary embodiment, at least one of the sources of target-containing sample is from a control tissue sample known to be free of pathological disorders. In a variation, at least one of the sources is a known pathological tissue specimen, e.g., a neoplastic lesion or another tissue specimen to be analyzed for lung cancer. In another variation, the assay records cross-tabulate one or more of the following parameters for each target species in a sample: (1) a unique identification code, which can include, e.g., a target molecular structure and/or characteristic separation coordinate (e.g., electrophoretic coordinates); (2) sample source; and (3) absolute and/or relative quantity of the target species present in the sample.

The invention also provides for the storage and retrieval of a collection of target data in a computer data storage apparatus, which can include magnetic disks, optical disks, magneto-optical disks, DRAM, SRAM, SGRAM, SDRAM, RDRAM, DDR RAM, magnetic bubble memory devices, and other data storage devices, including CPU registers and on-CPU data storage arrays. Typically, the target data records are stored as a bit pattern in an array of magnetic domains on a magnetizable medium or as an array of charge states or transistor gate states, such as an array of cells in a DRAM device (e.g., each cell comprised of a transistor and a charge storage area, which may be on the transistor). In one embodiment, the invention provides such storage devices, and computer systems built therewith, comprising a bit pattern encoding a protein expression fingerprint record comprising unique identifiers for at least 10 target data records cross-tabulated with target source.

When the target is a peptide or nucleic acid, the invention preferably provides a method for identifying related peptide or nucleic acid sequences, comprising performing a computerized comparison between a peptide or nucleic acid sequence assay record stored in or retrieved from a computer storage device or database and at least one other sequence. The comparison can include a sequence analysis or comparison algorithm or computer program embodiment thereof (e.g., FASTA, TFASTA, GAP, BESTFIT) and/or the comparison may



be of the relative amount of a peptide or nucleic acid sequence in a pool of sequences determined from a polypeptide or nucleic acid sample of a specimen.

The invention also preferably provides a magnetic disk, such as an IBM-compatible (DOS, Windows, Windows95/98/2000, Windows NT, OS/2) or other format (e.g., Linux, SunOS, Solaris, AIX, SCO Unix, VMS, MV, Macintosh, etc.) floppy diskette or hard (fixed, Winchester) disk drive, comprising a bit pattern encoding data from an assay of the invention in a file format suitable for retrieval and processing in a computerized sequence analysis, comparison, or relative quantitation method.

The invention also provides a network, comprising a plurality of computing devices linked via a data link, such as an Ethernet cable (coax or 10BaseT), telephone line, ISDN line, wireless network, optical fiber, or other suitable signal transmission medium, whereby at least one network device (e.g., computer, disk array, etc.) comprises a pattern of magnetic domains (e.g., magnetic disk) and/or charge domains (e.g., an array of DRAM cells) composing a bit pattern encoding data acquired from an assay of the invention.

The invention also provides a method for transmitting assay data that includes generating an electronic signal on an electronic communications device, such as a modem, ISDN terminal adapter, DSL, cable modem, ATM switch, or the like, wherein the signal includes (in native or encrypted format) a bit pattern encoding data from an assay or a database comprising a plurality of assay results obtained by the method of the invention.

In a preferred embodiment, the invention provides a computer system for comparing a query target to a database containing an array of data structures, such as an assay result obtained by the method of the invention, and ranking database targets based on the degree of identity and gap weight to the target data. A central processor is preferably initialized to load and execute the computer program for alignment and/or comparison of the assay results. Data for a query target is entered into the central processor via an I/O device. Execution of the computer program results in the central processor retrieving the assay data from the data file, which comprises a binary description of an assay result.

The target data or record and the computer program can be transferred to secondary memory, which is typically random access memory (e.g., DRAM, SRAM, SGRAM, or SDRAM). Targets are ranked according to the degree of correspondence between a selected assay characteristic (e.g., binding to a selected affinity moiety) and the same characteristic of the query target and results are output via an I/O device. For example, a central processor can be a conventional computer (e.g., Intel Pentium, PowerPC, Alpha, PA-8000, SPARC,



MIPS 4400, MIPS 10000, VAX, etc.); a program can be a commercial or public domain molecular biology software package (e.g., UWGCG Sequence Analysis Software, Darwin); a data file can be an optical or magnetic disk, a data server, a memory device (e.g., DRAM, SRAM, SGRAM, SDRAM, EPROM, bubble memory, flash memory, etc.); an I/O device can be a terminal comprising a video display and a keyboard, a modem, an ISDN terminal adapter, an Ethernet port, a punched card reader, a magnetic strip reader, or other suitable I/O device.

The invention also preferably provides the use of a computer system, such as that described above, which comprises: (1) a computer; (2) a stored bit pattern encoding a collection of peptide sequence specificity records obtained by the methods of the invention, which may be stored in the computer; (3) a comparison target, such as a query target; and (4) a program for alignment and comparison, typically with rank-ordering of comparison results on the basis of computed similarity values.

#### **Characteristics of lung cancer-associated proteins**

Lung cancer proteins of the present invention may be classified as secreted proteins, transmembrane proteins or intracellular proteins. In one embodiment, the lung cancer protein is an intracellular protein. Intracellular proteins may be found in the cytoplasm and/or in the nucleus. Intracellular proteins are involved in all aspects of cellular function and replication (including, e.g., signaling pathways); aberrant expression of such proteins often results in unregulated or dysregulated cellular processes (see, e.g., Alberts (ed. 1994) Molecular Biology of the Cell (3d ed.)). For example, many intracellular proteins have enzymatic activity such as protein kinase activity, protein phosphatase activity, protease activity, nucleotide cyclase activity, polymerase activity and the like. Intracellular proteins also serve as docking proteins that are involved in organizing complexes of proteins, or targeting proteins to various subcellular localizations, and are involved in maintaining the structural integrity of organelles.

An increasingly appreciated concept in characterizing proteins is the presence in the proteins of one or more structural motifs for which defined functions have been attributed. In addition to the highly conserved sequences found in the enzymatic domain of proteins, highly conserved sequences have been identified in proteins that are involved in protein-protein interaction. For example, Src-homology-2 (SH2) domains bind tyrosine-phosphorylated targets in a sequence dependent manner. PTB domains, which are distinct from SH2



domains, also bind tyrosine phosphorylated targets. SH3 domains bind to proline-rich targets. In addition, PH domains, tetratricopeptide repeats and WD domains to name only a few, have been shown to mediate protein-protein interactions. Some of these may also be involved in binding to phospholipids or other second messengers. As will be appreciated by one of ordinary skill in the art, these motifs can be identified on the basis of amino acid sequence; thus, an analysis of the sequence of proteins may provide insight into both the enzymatic potential of the molecule and/or molecules with which the protein may associate. One useful database is Pfam (protein families), which is a large collection of multiple sequence alignments and hidden Markov models covering many common protein domains. Versions are available via the internet from Washington University in St. Louis, the Sanger Center in England, and the Karolinska Institute in Sweden (see, e.g., Bateman, et al (2000) *Nuc. Acids Res.* 28:263-266; Sonnhammer, et al. (1997) *Proteins* 28:405-420; Bateman, et al. (1999) *Nuc. Acids Res.* 27:260-262; and Sonnhammer, et al. (1998) *Nuc. Acids Res.* 26:320-322).

In another embodiment, the lung cancer sequences are transmembrane proteins. Transmembrane proteins are molecules that span a phospholipid bilayer of a cell. They may have an intracellular domain, an extracellular domain, or both. The intracellular domains of such proteins may have a number of functions including those already described for intracellular proteins. For example, the intracellular domain may have enzymatic activity and/or may serve as a binding site for additional proteins. Frequently the intracellular domain of transmembrane proteins serves both roles. For example certain receptor tyrosine kinases have both protein kinase activity and SH2 domains. In addition, autophosphorylation of tyrosines on the receptor molecule itself, creates binding sites for additional SH2 domain containing proteins.

Transmembrane proteins may contain from one to many transmembrane domains. For example, receptor tyrosine kinases, certain cytokine receptors, receptor guanylyl cyclases and receptor serine/threonine protein kinases contain a single transmembrane domain. However, various other proteins including channels, pumps, and adenylyl cyclases contain numerous transmembrane domains. Many important cell surface receptors such as G protein coupled receptors (GPCRs) are classified as "seven transmembrane domain" proteins, as they contain 7 membrane spanning regions. Characteristics of transmembrane domains include approximately 17 consecutive hydrophobic amino acids that may be followed by charged amino acids. Therefore, upon analysis of the amino acid sequence of a particular protein, the



localization and number of transmembrane domains within the protein may be predicted (see, e.g., PSORT web site <http://psort.nibb.ac.jp/>).

The extracellular domains of transmembrane proteins are diverse; however, conserved motifs are found repeatedly among various extracellular domains. Conserved structure and/or functions have been ascribed to different extracellular motifs. Many extracellular domains are involved in binding to other molecules. In one aspect, extracellular domains are found on receptors. Factors that bind the receptor domain include circulating ligands, which may be peptides, proteins, or small molecules such as adenosine and the like. For example, growth factors such as EGF, FGF, and PDGF are circulating growth factors that bind to their cognate receptors to initiate a variety of cellular responses. Other factors include cytokines, mitogenic factors, hormones, neurotrophic factors and the like. Extracellular domains also bind to cell-associated molecules. In this respect, they may mediate cell-cell interactions. Cell-associated ligands can be tethered to the cell, e.g., via a glycosylphosphatidylinositol (GPI) anchor, or may themselves be transmembrane proteins. Extracellular domains may also associate with the extracellular matrix and contribute to the maintenance of the cell structure.

Lung cancer proteins that are transmembrane are particularly preferred in the present invention as they are readily accessible targets for extracellular immunotherapeutics, as are described herein. In addition, as outlined below, transmembrane proteins can be also useful in imaging modalities. Antibodies may be used to label such readily accessible proteins *in situ* or in histological analysis. Alternatively, antibodies can also label intracellular proteins, in which case analytical samples are typically permeabilized to provide access to intracellular proteins. In addition, some membrane proteins can be processed to release a soluble protein, or to expose a residual fragment. Released soluble proteins may be useful diagnostic markers, processed residual protein fragments may be useful lung markers of disease.

It will also be appreciated by those in the art that a transmembrane protein can be made soluble by removing transmembrane sequences, e.g., through recombinant methods. Furthermore, transmembrane proteins that have been made soluble can be made to be secreted through recombinant means by adding an appropriate signal sequence.

In another embodiment, the lung cancer proteins are secreted proteins; the secretion of which can be either constitutive or regulated. These proteins may have a signal peptide or signal sequence that targets the molecule to the secretory pathway. Secreted proteins are involved in numerous physiological events; e.g., if circulating, they often serve to transmit



signals to various other cell types. The secreted protein may function in an autocrine manner (acting on the cell that secreted the factor), a paracrine manner (acting on cells in close proximity to the cell that secreted the factor), an endocrine manner (acting on cells at a distance, e.g., secretion into the blood stream), or exocrine (secretion, e.g., through a duct or to adjacent epithelial surface as sweat glands, sebaceous glands, pancreatic ducts, lacrimal glands, mammary glands, wax producing glands of the ear, etc.). Thus secreted molecules often find use in modulating or altering numerous aspects of physiology. Lung cancer proteins that are secreted proteins are particularly preferred in the present invention as they serve as good targets for diagnostic markers, e.g., for blood, plasma, serum, or stool tests. Those which are enzymes may be antibody or small molecule targets. Others may be useful as vaccine targets, e.g., via CTL mechanisms.

### Use of lung cancer nucleic acids

As described above, lung cancer sequence is initially identified by substantial nucleic acid and/or amino acid sequence homology or linkage to the lung cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, using either homology programs or hybridization conditions. Typically, linked sequences on a mRNA are found on the same molecule.

The lung cancer nucleic acid sequences of the invention, e.g., the sequences in Tables 1A-16, can be fragments of larger genes, i.e., they are nucleic acid segments. "Genes" in this context includes coding regions, non-coding regions, and mixtures of coding and non-coding regions. Accordingly, as will be appreciated by those in the art, using the sequences provided herein, extended sequences, in either direction, of the lung cancer genes can be obtained, using techniques well known in the art for cloning either longer sequences or the full length sequences; see Ausubel, et al., *supra*. Much can be done by informatics and many sequences can be clustered to include multiple sequences corresponding to a single gene, e.g., systems such as UniGene (see, <http://www.ncbi.nlm.nih.gov/UniGene/>).

Once a lung cancer nucleic acid is identified, it can be cloned and, if necessary, its constituent parts recombined to form the entire lung cancer nucleic acid coding regions or the entire mRNA sequence. Once isolated from its natural source, e.g., contained within a plasmid or other vector or excised therefrom as a linear nucleic acid segment, the recombinant lung cancer nucleic acid can be further-used as a probe to identify and isolate



other lung cancer nucleic acids, e.g., extended coding regions. It can also be used as a “precursor” nucleic acid to make modified or variant lung cancer nucleic acids and proteins.

The lung cancer nucleic acids of the present invention are used in several ways. In a first embodiment, nucleic acid probes to the lung cancer nucleic acids are made and attached to biochips to be used in screening and diagnostic methods, as outlined below, or for administration, e.g., for gene therapy, RNAi, vaccine, and/or antisense applications. Alternatively, the lung cancer nucleic acids that include coding regions of lung cancer proteins can be put into expression vectors for the expression of lung cancer proteins, again for screening purposes or for administration to a patient.

In a preferred embodiment, nucleic acid probes to lung cancer nucleic acids (both the nucleic acid sequences outlined in the figures and/or the complements thereof) are made. The nucleic acid probes attached to the biochip are designed to be substantially complementary to the lung cancer nucleic acids, i.e., the target sequence (either the target sequence of the sample or to other probe sequences, e.g., in sandwich assays), such that hybridization of the target sequence and the probes of the present invention occurs. As outlined below, this complementarity need not be perfect; there may be any number of base pair mismatches which will interfere with hybridization between the target sequence and the single stranded nucleic acids of the present invention. However, if the number of mutations is so great that no hybridization can occur under even the least stringent of hybridization conditions, the sequence is not a complementary target sequence. Thus, by “substantially complementary” herein is meant that the probes are sufficiently complementary to the target sequences to hybridize under appropriate reaction conditions, particularly high stringency conditions, as outlined herein.

A nucleic acid probe is generally single stranded but can be partially single and partially double stranded. The strandedness of the probe is dictated by the structure, composition, and properties of the target sequence. In general, the nucleic acid probes range from about 8 to about 100 bases long, with from about 10 to about 80 bases being preferred, and from about 30 to about 50 bases being particularly preferred. That is, generally complements of ORFs or whole genes are not used. In some embodiments, nucleic acids of lengths up to hundreds of bases can be used.

In a preferred embodiment, more than one probe per sequence is used, with either overlapping probes or probes to different sections of the target being used. That is, two, three, four or more probes, with three being preferred, are used to build in a redundancy for a



particular target. The probes can be overlapping (i.e., have some sequence in common), or separate. In some cases, PCR primers may be used to amplify signal for higher sensitivity.

As will be appreciated by those in the art, nucleic acids can be attached or immobilized to a solid support in a wide variety of ways. By “immobilized” and grammatical equivalents herein is meant the association or binding between the nucleic acid probe and the solid support is sufficient to be stable under the conditions of binding, washing, analysis, and removal as outlined below. The binding can typically be covalent or non-covalent. By “non-covalent binding” and grammatical equivalents herein is typically meant one or more of electrostatic, hydrophilic, and hydrophobic interactions. Included in non-covalent binding is the covalent attachment of a molecule, such as, streptavidin to the support and the non-covalent binding of the biotinylated probe to the streptavidin. By “covalent binding” and grammatical equivalents herein is meant that the two moieties, the solid support and the probe, are attached by at least one bond, including sigma bonds, pi bonds and coordination bonds. Covalent bonds can be formed directly between the probe and the solid support or can be formed by a cross linker or by inclusion of a specific reactive group on either the solid support or the probe or both molecules. Immobilization may also involve a combination of covalent and non-covalent interactions.

In general, the probes are attached to a biochip in a wide variety of ways, as will be appreciated by those in the art. As described herein, the nucleic acids can either be synthesized first, with subsequent attachment to the biochip, or can be directly synthesized on the biochip.

The biochip comprises a suitable solid substrate. By “substrate” or “solid support” or other grammatical equivalents herein is meant a material that can be modified for the attachment or association of the nucleic acid probes and is amenable to at least one detection method. Often the substrate may contain discrete individual sites appropriate for individual partitioning and identification. As will be appreciated by those in the art, the number of possible substrates are very large, and include, but are not limited to, glass and modified or functionalized glass, plastics (including acrylics, polystyrene and copolymers of styrene and other materials, polypropylene, polyethylene, polybutylene, polyurethanes, Teflon, etc.), polysaccharides, nylon or nitrocellulose, resins, silica or silica-based materials including silicon and modified silicon, carbon, metals, inorganic glasses, plastics, etc. In general, the substrates allow optical detection and do not appreciably fluoresce. A preferred substrate is described in US application entitled Reusable Low Fluorescent Plastic Biochip, U.S.



Application Serial No. 09/270,214, filed March 15, 1999, herein incorporated by reference in its entirety.

Generally the substrate is planar, although as will be appreciated by those in the art, other configurations of substrates may be used as well. For example, the probes may be placed on the inside surface of a tube, for flow-through sample analysis to minimize sample volume. Similarly, the substrate may be flexible, such as a flexible foam, including closed cell foams made of particular plastics.

In a preferred embodiment, the surface of the biochip and the probe may be derivatized with chemical functional groups for subsequent attachment of the two. Thus, e.g., the biochip is derivatized with a chemical functional group including, but not limited to, amino groups, carboxy groups, oxo groups and thiol groups, with amino groups being particularly preferred. Using these functional groups, the probes can be attached using functional groups on the probes. For example, nucleic acids containing amino groups can be attached to surfaces comprising amino groups, e.g., using linkers as are known in the art; e.g., homo-or hetero-bifunctional linkers as are well known (see 1994 Pierce Chemical Company catalog, technical section on cross-linkers, pages 155-200). In addition, in some cases, additional linkers, such as alkyl groups (including substituted and heteroalkyl groups) may be used.

In this embodiment, oligonucleotides are synthesized, and then attached to the surface of the solid support. Either the 5' or 3' terminus may be attached to the solid support, or attachment may be via linkage to an internal nucleoside.

In another embodiment, the immobilization to the solid support may be very strong, yet non-covalent. For example, biotinylated oligonucleotides can be made, which bind to surfaces covalently coated with streptavidin, resulting in attachment.

Alternatively, the oligonucleotides may be synthesized on the surface, as is known in the art. For example, photoactivation techniques utilizing photopolymerization compounds and techniques are used. In a preferred embodiment, the nucleic acids can be synthesized *in situ*, using known photolithographic techniques, such as those described in WO 95/25116; WO 95/35505; U.S. Patent Nos. 5,700,637 and 5,445,934; and references cited within, all of which are expressly incorporated by reference; these methods of attachment form the basis of the Affymetrix GeneChip™ technology.

Often, amplification-based assays are performed to measure the expression level of lung cancer-associated sequences. These assays are typically performed in conjunction with



reverse transcription. In such assays, a lung cancer-associated nucleic acid sequence acts as a template in an amplification reaction (e.g., Polymerase Chain Reaction, or PCR). In a quantitative amplification, the amount of amplification product will be proportional to the amount of template in the original sample. Comparison to appropriate controls provides a measure of the amount of lung cancer-associated RNA. Methods of quantitative amplification are well known to those of skill in the art. Detailed protocols for quantitative PCR are provided, e.g., in Innis, et al. (1990) PCR Protocols, A Guide to Methods and Applications.

In some embodiments, a TaqMan based assay is used to measure expression.

TaqMan based assays use a fluorogenic oligonucleotide probe that contains a 5' fluorescent dye and a 3' quenching agent. The probe hybridizes to a PCR product, but cannot itself be extended due to a blocking agent at the 3' end. When the PCR product is amplified in subsequent cycles, the 5' nuclease activity of the polymerase, e.g., AmpliTaq, results in the cleavage of the TaqMan probe. This cleavage separates the 5' fluorescent dye and the 3' quenching agent, thereby resulting in an increase in fluorescence as a function of amplification (see, e.g., literature provided by Perkin-Elmer, e.g., [www2.perkin-elmer.com](http://www2.perkin-elmer.com)).

Other suitable amplification methods include, but are not limited to, ligase chain reaction (LCR) (see Wu and Wallace (1989) Genomics 4:560, Landegren, et al. (1988) Science 241:1077, and Barringer, et al. (1990) Gene 89:117), transcription amplification (Kwoh, et al. (1989) Proc. Natl. Acad. Sci. USA 86:1173), self-sustained sequence replication (Guatelli, et al. (1990) Proc. Nat. Acad. Sci. USA 87:1874), dot PCR, and linker adapter PCR, etc.

### **Expression of lung cancer proteins from nucleic acids**

In a preferred embodiment, lung cancer nucleic acids, e.g., encoding lung cancer proteins, are used to make a variety of expression vectors to express lung cancer proteins which can then be used in screening assays, as described below. Expression vectors and recombinant DNA technology are well known to those of skill in the art (see, e.g., Ausubel, *supra*, and Fernandez and Hoeffler (eds 1999) Gene Expression Systems) and are used to express proteins. The expression vectors may be either self-replicating extrachromosomal vectors or vectors which integrate into a host genome. Generally, these expression vectors include transcriptional and translational regulatory nucleic acid operably linked to the nucleic acid encoding the lung cancer protein. The term "control sequences" refers to DNA



sequences used for the expression of an operably linked coding sequence in a particular host organism. Control sequences that are suitable for prokaryotes, e.g., include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

5 Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding  
10 sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is typically accomplished by ligation at convenient restriction sites. If such sites do not exist, synthetic oligonucleotide adaptors or linkers are used in  
15 accordance with conventional practice. Transcriptional and translational regulatory nucleic acid will generally be appropriate to the host cell used to express the lung cancer protein. Numerous types of appropriate expression vectors, and suitable regulatory sequences are known in the art for a variety of host cells.

In general, transcriptional and translational regulatory sequences may include, but are  
20 not limited to, promoter sequences, ribosomal binding sites, transcriptional start and stop sequences, translational start and stop sequences, and enhancer or activator sequences. In a preferred embodiment, the regulatory sequences include a promoter and transcriptional start and stop sequences.

Promoter sequences may be either constitutive or inducible promoters. The promoters  
25 may be either naturally occurring promoters or hybrid promoters. Hybrid promoters, which combine elements of more than one promoter, are also known in the art, and are useful in the present invention.

In addition, an expression vector may comprise additional elements. For example, the expression vector may have two replication systems, thus allowing it to be maintained in two  
30 organisms, e.g., in mammalian or insect cells for expression and in a prokaryotic host for cloning and amplification. Furthermore, for integrating expression vectors, the expression vector often contains at least one sequence homologous to the host cell genome, and preferably two homologous sequences which flank the expression construct. The integrating



vector may be directed to a specific locus in the host cell by selecting the appropriate homologous sequence for inclusion in the vector. Constructs for integrating vectors are well known in the art (e.g., Fernandez and Hoeffler, *supra*).

In addition, in a preferred embodiment, the expression vector contains a selectable  
5 marker gene to allow the selection of transformed host cells. Selection genes are well known in the art and will vary with the host cell used.

The lung cancer proteins of the present invention are usually produced by culturing a host cell transformed with an expression vector containing nucleic acid encoding a lung cancer protein, under the appropriate conditions to induce or cause expression of the lung  
10 cancer protein. Conditions appropriate for lung cancer protein expression will vary with the choice of the expression vector and the host cell, and will be easily ascertained by one skilled in the art through routine experimentation or optimization. For example, the use of constitutive promoters in the expression vector will require optimizing the growth and proliferation of the host cell, while the use of an inducible promoter requires the appropriate  
15 growth conditions for induction. In addition, in some embodiments, the timing of the harvest is important. For example, the baculoviral systems used in insect cell expression are lytic viruses, and thus harvest time selection can be crucial for product yield.

Appropriate host cells include yeast, bacteria, archaeobacteria, fungi, and insect and animal cells, including mammalian cells. Of particular interest are *Saccharomyces cerevisiae*  
20 and other yeasts, *E. coli*, *Bacillus subtilis*, Sf9 cells, C129 cells, 293 cells, *Neurospora*, BHK, CHO, COS, HeLa cells, HUVEC (human umbilical vein endothelial cells), THP1 cells (a macrophage cell line) and various other human cells and cell lines.

In a preferred embodiment, the lung cancer proteins are expressed in mammalian cells. Mammalian expression systems are also known in the art, and include retroviral and  
25 adenoviral systems. Of particular use as mammalian promoters are the promoters from mammalian viral genes, since the viral genes are often highly expressed and have a broad host range. Examples include the SV40 early promoter, mouse mammary tumor virus LTR promoter, adenovirus major late promoter, herpes simplex virus promoter, and the CMV promoter (see, e.g., Fernandez and Hoeffler, *supra*). Typically, transcription termination and  
30 polyadenylation sequences recognized by mammalian cells are regulatory regions located 3' to the translation stop codon and thus, together with the promoter elements, flank the coding sequence. Examples of transcription terminator and polyadenylation signals include those derived from SV40.



The methods of introducing exogenous nucleic acid into mammalian hosts, as well as other hosts, is well known in the art, and will vary with the host cell used. Techniques include dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, viral infection, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei.

In a preferred embodiment, lung cancer proteins are expressed in bacterial systems. Promoters from bacteriophage may also be used and are known in the art. In addition, synthetic promoters and hybrid promoters are also useful; e.g., the tac promoter is a hybrid of the trp and lac promoter sequences. Furthermore, a bacterial promoter can include naturally occurring promoters of non-bacterial origin that have the ability to bind bacterial RNA polymerase and initiate transcription. In addition to a functioning promoter sequence, an efficient ribosome binding site is desirable. The expression vector may also include a signal peptide sequence that provides for secretion of the lung cancer protein in bacteria. The protein is either secreted into the growth media (gram-positive bacteria) or into the periplasmic space, located between the inner and outer membrane of the cell (gram-negative bacteria). The bacterial expression vector may also include a selectable marker gene to allow for the selection of bacterial strains that have been transformed. Suitable selection genes include genes which render the bacteria resistant to drugs such as ampicillin, chloramphenicol, erythromycin, kanamycin, neomycin and tetracycline. Selectable markers also include biosynthetic genes, such as those in the histidine, tryptophan and leucine biosynthetic pathways. These components are assembled into expression vectors. Expression vectors for bacteria are well known in the art, and include vectors for *Bacillus subtilis*, *E. coli*, *Streptococcus cremoris*, and *Streptococcus lividans*, among others (e.g., Fernandez and Hoeffler, *supra*). The bacterial expression vectors are transformed into bacterial host cells using techniques well known in the art, such as calcium chloride treatment, electroporation, and others.

In one embodiment, lung cancer proteins are produced in insect cells. Expression vectors for the transformation of insect cells, and in particular, baculovirus-based expression vectors, are well known in the art.

In a preferred embodiment, lung cancer protein is produced in yeast cells. Yeast expression systems are well known in the art, and include expression vectors for *Saccharomyces cerevisiae*, *Candida albicans* and *C. maltosa*, *Hansenula polymorpha*,



*Kluyveromyces fragilis* and *K. lactis*, *Pichia guilliermondii*, and *P. pastoris*, *Schizosaccharomyces pombe*, and *Yarrowia lipolytica*.

The lung cancer protein may also be made as a fusion protein, using techniques well known in the art. Thus, e.g., for the creation of monoclonal antibodies, if the desired epitope is small, the lung cancer protein may be fused to a carrier protein to form an immunogen. Alternatively, the lung cancer protein may be made as a fusion protein to increase expression for affinity purification purposes, or for other reasons. For example, when the lung cancer protein is a lung cancer peptide, the nucleic acid encoding the peptide may be linked to other nucleic acid for expression purposes.

In a preferred embodiment, the lung cancer protein is purified or isolated after expression. Lung cancer proteins may be isolated or purified in a variety of appropriate ways. Standard purification methods include electrophoretic, molecular, immunological and chromatographic techniques, including ion exchange, hydrophobic, affinity, and reverse-phase HPLC chromatography, and chromatofocusing. For example, the lung cancer protein may be purified using a standard anti-lung cancer protein antibody column. Ultrafiltration and diafiltration techniques, in conjunction with protein concentration, are also useful. For general guidance in suitable purification techniques, see Scopes (1982) Protein Purification. The degree of purification necessary will vary depending on the use of the lung cancer protein. In some instances no purification will be necessary.

Once expressed and purified if necessary, the lung cancer proteins and nucleic acids are useful in a number of applications. They may be used as immunoselection reagents, as vaccine reagents, as screening agents, therapeutic entities, for production of antibodies, as transcription or translation inhibitors, etc.

## **Variants of lung cancer proteins**

In one embodiment, the lung cancer proteins are derivative or variant lung cancer proteins as compared to the wild-type sequence. That is, as outlined more fully below, the derivative lung cancer peptide will often contain at least one amino acid substitution, deletion or insertion, with amino acid substitutions being particularly preferred. The amino acid substitution, insertion or deletion may occur at a particular residue within the lung cancer peptide.

Also included within one embodiment of lung cancer proteins of the present invention are amino acid sequence variants. These variants typically fall into one or more of three



classes: substitutional, insertional or deletional variants. These variants ordinarily are prepared by site specific mutagenesis of nucleotides in the DNA encoding the lung cancer protein, using cassette or PCR mutagenesis or other techniques, to produce DNA encoding the variant, and thereafter expressing the DNA in recombinant cell culture as outlined above.

5 However, variant lung cancer protein fragments having up to about 100-150 residues may be prepared by *in vitro* synthesis. Amino acid sequence variants are characterized by the predetermined nature of the variation, a feature that sets them apart from naturally occurring allelic or interspecies variation of the lung cancer protein amino acid sequence. The variants typically exhibit a similar qualitative biological activity as the naturally occurring analogue,

10 although variants can also be selected which have modified characteristics as will be more fully outlined below.

While the site or region for introducing an amino acid sequence variation is often predetermined, the mutation per se need not be predetermined. For example, in order to optimize the performance of a mutation at a given site, random mutagenesis may be

15 conducted at the target codon or region and the expressed lung cancer variants screened for the optimal combination of desired activity. Techniques exist for making substitution mutations at predetermined sites in DNA having a known sequence, e.g., M13 primer mutagenesis and PCR mutagenesis. Screening of mutants is often done using assays of lung cancer protein activities.

20 Amino acid substitutions are typically of single residues; insertions usually will be on the order of from about 1 to 20 amino acids, although considerably larger insertions may be occasionally tolerated. Deletions generally range from about 1 to about 20 residues, although in some cases deletions may be much larger.

Substitutions, deletions, insertions or any combination thereof may be used to arrive

25 at a final derivative. Generally these changes are done on a few amino acids to minimize the alteration of the molecule. Larger changes may be tolerated in certain circumstances. When small alterations in the characteristics of a lung cancer protein are desired, substitutions are generally made in accordance with the amino acid substitution chart provided in the definition section.

30 Variants typically exhibit essentially the same qualitative biological activity and will elicit the same immune response as a naturally-occurring analog, although variants also are selected to modify the characteristics of lung cancer proteins as needed. Alternatively, the



variant may be designed or reorganized such that a biological activity of the lung cancer protein is altered. For example, glycosylation sites may be added, altered, or removed.

Covalent modifications of lung cancer polypeptides are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of a lung cancer polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N-or C-terminal residues of a lung cancer polypeptide. Derivatization with bifunctional agents is useful, for instance, for crosslinking lung cancer polypeptides to a water-insoluble support matrix or surface for use in a method for purifying anti-lung cancer polypeptide antibodies or screening assays, as is more fully described below. Commonly used crosslinking agents include, e.g., 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, e.g., esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-((p-azidophenyl)dithio)propioimide.

Other modifications include deamidation of glutaminyl and asparaginyl residues to the corresponding glutamyl and aspartyl residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of serinyl, threonyl or tyrosyl residues, methylation of the  $\gamma$ -amino groups of lysine, arginine, and histidine side chains (Creighton (1983) Proteins: Structure and Molecular Properties, pp. 79-86), acetylation of the N-terminal amine, and amidation of any C-terminal carboxyl group.

Another type of covalent modification of the lung cancer polypeptide encompassed by this invention is an altered native glycosylation pattern of the polypeptide. "Altering the native glycosylation pattern" is intended herein to mean adding to or deleting one or more carbohydrate moieties of a native sequence lung cancer polypeptide. Glycosylation patterns can be altered in many ways. For example the use of different cell types to express lung cancer-associated sequences can result in different glycosylation patterns.

Addition of glycosylation sites to lung cancer polypeptides may also be accomplished by altering the amino acid sequence thereof. The alteration may be made, e.g., by the addition of, or substitution by, one or more serine or threonine residues to the native sequence lung cancer polypeptide (for O-linked glycosylation sites). The lung cancer amino acid sequence may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding the lung cancer polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.



Another means of increasing the number of carbohydrate moieties on the lung cancer polypeptide is by chemical or enzymatic coupling of glycosides to the polypeptide. Such methods are described in the art, e.g., in WO 87/05330, and in Aplin and Wriston (1981) CRC Crit. Rev. Biochem., pp. 259-306.

Removal of carbohydrate moieties present on the lung cancer polypeptide may be accomplished chemically or enzymatically or by mutational substitution of codons encoding for amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are known in the art and described, for instance, by Hakimuddin, et al. (1987) Arch. Biochem. Biophys., 259:52 and by Edge, et al. (1981) Anal. Biochem., 118:131.

Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo-and exo-glycosidases as described by Thotakura, et al. (1987) Meth. Enzymol., 138:350.

Another type of covalent modification of lung cancer comprises linking the lung cancer polypeptide to one of a variety of nonproteinaceous polymers, e.g., polyethylene glycol, polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192, or 4,179,337.

Lung cancer polypeptides of the present invention may also be modified in a way to form chimeric molecules comprising a lung cancer polypeptide fused to another, heterologous polypeptide or amino acid sequence. In one embodiment, such a chimeric molecule comprises a fusion of a lung cancer polypeptide with a tag polypeptide which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino-or carboxyl-terminus of the lung cancer polypeptide. The presence of such epitope-tagged forms of a lung cancer polypeptide can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the lung cancer polypeptide to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. In an alternative embodiment, the chimeric molecule may comprise a fusion of a lung cancer polypeptide with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the chimeric molecule, such a fusion could be to the Fc region of an IgG molecule.

Various tag polypeptides and their respective antibodies are well known and examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; HIS6 and metal chelation tags, the flu HA tag polypeptide and its antibody 12CA5 (Field, et al. (1988) Mol. Cell. Biol. 8:2159-2165); the c-myc tag and the 8F9, 3C7, 6E10, G4, B7 and 9E10 antibodies



thereto (Evan, et al. (1985) Molecular and Cellular Biology 5:3610-3616); and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody (Paborsky, et al. (1990) Protein Engineering 3(6):547-553). Other tag polypeptides include the Flag-peptide (Hopp, et al. (1988) BioTechnology 6:1204-1210); the KT3 epitope peptide (Martin, et al. (1992) Science 255:192-194); tubulin epitope peptide (Skinner, et al. (1991) J. Biol. Chem. 266:15163-15166); and the T7 gene 10 protein peptide tag (Lutz-Freyermuth, et al. (1990) Proc. Nat'l Acad. Sci. USA 87:6393-6397).

Also included are other lung cancer proteins of the lung cancer family, and lung cancer proteins from other organisms, which are cloned and expressed as outlined below.

Thus, probe or degenerate polymerase chain reaction (PCR) primer sequences may be used to find other related lung cancer proteins from primates or other organisms. As will be appreciated by those in the art, particularly useful probe and/or PCR primer sequences include unique areas of the lung cancer nucleic acid sequence. As is generally known in the art, preferred PCR primers are from about 15 to about 35 nucleotides in length, with from about 20 to about 30 being preferred, and may contain inosine as needed. PCR reaction conditions are well known in the art (e.g., Innis, PCR Protocols, *supra*).

### **Antibodies to lung cancer proteins**

In a preferred embodiment, when a lung cancer protein is to be used to generate antibodies, e.g., for immunotherapy or immunodiagnosis, the lung cancer protein should share at least one epitope or determinant with the full length protein. By "epitope" or "determinant" herein is typically meant a portion of a protein which will generate and/or bind an antibody or T-cell receptor in the context of MHC. Thus, in most instances, antibodies made to a smaller lung cancer protein will be able to bind to the full-length protein, particularly linear epitopes. In a preferred embodiment, the epitope is unique; that is, antibodies generated to a unique epitope show little or no cross-reactivity.

Methods of preparing polyclonal antibodies are well known (e.g., Coligan, *supra*; and Harlow and Lane, *supra*). Polyclonal antibodies can be raised in a mammal, e.g., by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may include a protein encoded by a nucleic acid of Tables 1A-16 or fragment thereof or a fusion protein thereof. It may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal



being immunized. Immunogenic proteins include, e.g., keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Adjuvants include, e.g., Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). The immunization protocol may be selected by one skilled in the art.

The antibodies may, alternatively, be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler and Milstein (1975) Nature 256:495. In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes may be immunized *in vitro*. The immunizing agent will typically include a polypeptide encoded by a nucleic acid of the tables, or fragment thereof, or a fusion protein thereof. Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (Goding (1986) Monoclonal Antibodies: Principles and Practice, pp. 59-103). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovin, or primate origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

In one embodiment, the antibodies are bispecific antibodies. Bispecific antibodies are typically monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens or that have binding specificities for two epitopes on the same antigen. In one embodiment, one of the binding specificities is for a protein encoded by a nucleic acid of the tables or a fragment thereof, the other one is for any other antigen, and preferably for a cell-surface protein or receptor or receptor subunit, preferably one that is tumor specific. Alternatively, tetramer-type technology may create multivalent reagents.



In a preferred embodiment, the antibodies to lung cancer protein are capable of reducing or eliminating a biological function of a lung cancer protein, in a naked form or conjugated to an effector moiety. That is, the addition of anti-lung cancer protein antibodies (either polyclonal or preferably monoclonal) to lung cancer tissue (or cells containing lung cancer) may reduce or eliminate the lung cancer. Generally, at least a 25% decrease in activity, growth, size or the like is preferred, with at least about 50% being particularly preferred and about a 95-100% decrease being especially preferred.

In a preferred embodiment the antibodies to the lung cancer proteins are humanized antibodies (e.g., Xenex Biosciences, Medarex, Inc., Abgenix, Inc., Protein Design Labs, Inc.) Humanized forms of non-human (e.g., murine) antibodies are chimeric molecules of immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')<sub>2</sub> or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues from a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity and capacity. In some instances, Fv framework residues of a human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, a humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework (FR) regions are those of a human immunoglobulin consensus sequence. A humanized antibody optimally also will typically comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin (Jones, et al. (1986) Nature 321:522-525; Riechmann, et al. (1988) Nature 332:323-329; and Presta (1992) Curr. Op. Struct. Biol. 2:593-596). Humanization can be performed following the method of Winter and co-workers (Jones, et al. (1986) Nature 321:522-525; Riechmann, et al. (1988) Nature 332:323-327; Verhoeven, et al. (1988) Science 239:1534-1536), by substituting rodent CDRs or CDR sequences for corresponding sequences of a human antibody. Accordingly, such humanized antibodies are chimeric antibodies (U.S. Patent No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted by corresponding sequence from a non-human species.



Human-like antibodies can also be produced using various techniques known in the art, including phage display libraries (Hoogenboom and Winter (1991) J. Mol. Biol. 227:381; Marks, et al. (1991) J. Mol. Biol. 222:581). The techniques of Cole, et al. and Boerner, et al. are also available for the preparation of human monoclonal antibodies (Cole, et al. (1985) Monoclonal Antibodies and Cancer Therapy, p. 77 and Boerner, et al. (1991) J. Immunol. 147(1):86-95). Similarly, human antibodies can be made by introducing human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in nearly all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, e.g., in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in the following scientific publications: Marks, et al. (1992) Bio/Technology 10:779-783; Lonberg, et al. (1994) Nature 368:856-859; Morrison (1994) Nature 368:812-13; Fishwild, et al. (1996) Nature Biotechnology 14:845-51; Neuberger (1996) Nature Biotechnology 14:826; and Lonberg and Huszar (1995) Intern. Rev. Immunol. 13:65-93.

By immunotherapy is meant treatment of lung cancer with an antibody raised against a lung cancer proteins. As used herein, immunotherapy can be passive or active. Passive immunotherapy as defined herein is the passive transfer of antibody to a recipient (patient). Active immunization is the induction of antibody and/or T-cell responses in a recipient (patient). Induction of an immune response is the result of providing the recipient with an antigen to which antibodies are raised. The antigen may be provided by injecting a polypeptide against which antibodies are desired to be raised into a recipient, or contacting the recipient with a nucleic acid capable of expressing the antigen and under conditions for expression of the antigen, leading to an immune response.

In a preferred embodiment the lung cancer proteins against which antibodies are raised are secreted proteins as described above. Without being bound by theory, antibodies used for treatment, may bind and prevent the secreted protein from binding to its receptor, thereby inactivating the secreted lung cancer protein.

In another preferred embodiment, the lung cancer protein to which antibodies are raised is a transmembrane protein. Without being bound by theory, antibodies used for treatment may bind the extracellular domain of the lung cancer protein and prevent it from binding to other proteins, such as circulating ligands or cell-associated molecules. The



antibody may cause down-regulation of the transmembrane lung cancer protein. The antibody may be a competitive, non-competitive or uncompetitive inhibitor of protein binding to the extracellular domain of the lung cancer protein. The antibody may be an antagonist of the lung cancer protein or may prevent activation of a transmembrane lung cancer protein, or  
5 may induce or suppress a particular cellular pathway. In some embodiments, when the antibody prevents the binding of other molecules to the lung cancer protein, the antibody prevents growth of the cell. The antibody may also be used to target or sensitize the cell to cytotoxic agents, including, but not limited to TNF- $\alpha$ , TNF- $\beta$ , IL-1, INF- $\gamma$ , and IL-2, or chemotherapeutic agents including 5FU, vinblastine, actinomycin D, cisplatin, methotrexate,  
10 and the like. In some instances the antibody may belong to a sub-type that activates serum complement when complexed with the transmembrane protein thereby mediating cytotoxicity or antigen-dependent cytotoxicity (ADCC). Thus, lung cancer may be treated by administering to a patient antibodies directed against the transmembrane lung cancer protein. Antibody-labeling may activate a co-toxin, localize a toxin payload, or otherwise provide  
15 means to locally ablate cells.

In another preferred embodiment, the antibody is conjugated to an effector moiety. The effector moiety can be various molecules, including labeling moieties such as radioactive labels or fluorescent labels, or can be a therapeutic moiety. In one aspect the therapeutic moiety is a small molecule that modulates the activity of a lung cancer protein. In another  
20 aspect the therapeutic moiety may modulate an activity of molecules associated with or in close proximity to a lung cancer protein. The therapeutic moiety may inhibit enzymatic or signaling activity such as protease or collagenase activity associated with lung cancer.

In a preferred embodiment, the therapeutic moiety can also be a cytotoxic agent. In this method, targeting the cytotoxic agent to lung cancer tissue or cells results in a reduction  
25 in the number of afflicted cells, thereby reducing symptoms associated with lung cancer. Cytotoxic agents are numerous and varied and include, but are not limited to, cytotoxic drugs or toxins or active fragments of such toxins. Suitable toxins and their corresponding fragments include diphtheria A chain, exotoxin A chain, ricin A chain, abrin A chain, curcin, crotin, phenomycin, enomycin, saporin, auristatin, and the like. Cytotoxic agents also include  
30 radiochemicals made by conjugating radioisotopes to antibodies raised against lung cancer proteins, or binding of a radionuclide to a chelating agent that has been covalently attached to the antibody. Targeting the therapeutic moiety to transmembrane lung cancer proteins not only serves to increase the local concentration of therapeutic moiety in the lung cancer



afflicted area, but also serves to reduce deleterious side effects that may be associated with the untargeted therapeutic moiety.

In another preferred embodiment, the lung cancer protein against which the antibodies are raised is an intracellular protein. In this case, the antibody may be conjugated to a protein or other entity which facilitates entry into the cell. In one case, the antibody enters the cell by endocytosis. In another embodiment, a nucleic acid encoding the antibody is administered to the individual or cell. Moreover, wherein the lung cancer protein can be targeted within a cell, i.e., the nucleus, an antibody theretomay contain a signal for that target localization, i.e., a nuclear localization signal.

The lung cancer antibodies of the invention specifically bind to lung cancer proteins. By “specifically bind” herein is meant that the antibodies bind to the protein with a  $K_d$  of at least about 0.1 mM, more usually at least about 1  $\mu$ M, preferably at least about 0.1  $\mu$ M or better, and most preferably, 0.01  $\mu$ M or better. Selectivity of binding to the specific target and not to related other sequences is also important.

#### **Detection of lung cancer sequence for diagnostic and therapeutic applications**

In one aspect, the RNA expression levels of genes are determined for different cellular states in the lung cancer phenotype. Expression levels of genes in normal tissue (e.g., not undergoing lung cancer), in lung cancer tissue (and in some cases, for varying severities of lung cancer that relate to prognosis, as outlined below), or in non-malignant disease are evaluated to provide expression profiles. A gene expression profile of a particular cell state or point of development is essentially a “fingerprint” of the state of the cell. While two states may have a particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is reflective of the state of the cell. By comparing expression profiles of cells in different states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. Then, diagnosis may be performed or confirmed to determine whether a tissue sample has the gene expression profile of normal or cancerous tissue. This will provide for molecular diagnosis of related conditions.

“Differential expression,” or grammatical equivalents as used herein, refers to qualitative or quantitative differences in the temporal and/or cellular gene expression patterns within and among cells and tissue. Thus, a differentially expressed gene can qualitatively have its expression altered, including an activation or inactivation, in, e.g.,



normal versus lung cancer tissue. Genes may be turned on or turned off in a particular state, relative to another state thus permitting comparison of two or more states. A qualitatively regulated gene will exhibit an expression pattern within a state or cell type which is

detectable by standard techniques. Some genes will be expressed in one state or cell type, but

not in both. Alternatively, the difference in expression may be quantitative, e.g., in that expression is increased or decreased; i.e., gene expression is either upregulated, resulting in an increased amount of transcript, or downregulated, resulting in a decreased amount of transcript. The degree to which expression differs need only be large enough to quantify via standard characterization techniques as outlined below, such as by use of Affymetrix

GeneChip™ expression arrays, Lockhart (1996) Nature Biotechnology 14:1675-1680, hereby expressly incorporated by reference. Other techniques include, but are not limited to, quantitative reverse transcriptase PCR, northern analysis and RNase protection. As outlined above, preferably the change in expression (i.e., upregulation or downregulation) is typically at least about 50%, more preferably at least about 100%, more preferably at least about 150%, more preferably at least about 200%, with from 300 to at least 1000% being especially preferred.

Evaluation may be at the gene transcript or the protein level. The amount of gene expression may be monitored using nucleic acid probes to the RNA or DNA equivalent of the gene transcript, and the quantification of gene expression levels, or, alternatively, the final gene product itself (protein) can be monitored, e.g., with antibodies to the lung cancer protein and standard immunoassays (ELISAs, etc.) or other techniques, including mass spectroscopy assays, 2D gel electrophoresis assays, etc. Proteins corresponding to lung cancer genes, e.g., those identified as being important in a lung cancer or disease phenotype, can be evaluated in a lung cancer diagnostic test. In a preferred embodiment, gene expression monitoring is performed simultaneously on a number of genes.

The lung cancer nucleic acid probes may be attached to biochips as outlined herein for the detection and quantification of lung cancer sequences in a particular cell. The assays are further described below in the example. PCR techniques can be used to provide greater sensitivity. Multiple protein expression monitoring can be performed as well. Similarly, these assays may be performed on an individual basis as well.

In a preferred embodiment nucleic acids encoding the lung cancer protein are detected. Although DNA or RNA encoding the lung cancer protein may be detected, of particular interest are methods wherein an mRNA encoding a lung cancer protein is detected.



Probes to detect mRNA can be a nucleotide/deoxynucleotide probe that is complementary to and hybridizes with the mRNA and includes, but is not limited to, oligonucleotides, cDNA or RNA. Probes also should contain a detectable label, as defined herein. In one method the mRNA is detected after immobilizing the nucleic acid to be examined on a solid support such as nylon membranes and hybridizing the probe with the sample. Following washing to remove the non-specifically bound probe, the label is detected. In another method detection of the mRNA is performed *in situ*. In this method permeabilized cells or tissue samples are contacted with a detectably labeled nucleic acid probe for sufficient time to allow the probe to hybridize with the target mRNA. Following washing to remove the non-specifically bound probe, the label is detected. For example a digoxigenin labeled riboprobe (RNA probe) that is complementary to the mRNA encoding a lung cancer protein is detected by binding the digoxigenin with an anti-digoxigenin secondary antibody and developed with nitro blue tetrazolium and 5-bromo-4-chloro-3-indoyl phosphate.

In a preferred embodiment, various proteins from the three classes of proteins as described herein (secreted, transmembrane or intracellular proteins) are used in diagnostic assays. The lung cancer proteins, antibodies, nucleic acids, modified proteins and cells containing lung cancer sequences are used in diagnostic assays. This can be performed on an individual gene or corresponding polypeptide level. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes and/or corresponding polypeptides.

As described and defined herein, lung cancer proteins, including intracellular, transmembrane, or secreted proteins, find use as markers of lung cancer, e.g., for prognostic or diagnostic purposes. Detection of these proteins in putative lung cancer tissue allows for detection, prognosis, or diagnosis of lung cancer or similar disease, and perhaps for selection of therapeutic strategy. In one embodiment, antibodies are used to detect lung cancer proteins. A preferred method separates proteins from a sample by electrophoresis on a gel (typically a denaturing and reducing protein gel, but may be another type of gel, including isoelectric focusing gels and the like). Following separation of proteins, the lung cancer protein is detected, e.g., by immunoblotting with antibodies raised against the lung cancer protein. Methods of immunoblotting are well known to those of ordinary skill in the art.

In another preferred method, antibodies to the lung cancer protein find use in *in situ* imaging techniques, e.g., in histology (e.g., Asai (ed. 1993) Methods in Cell Biology:



Antibodies in Cell Biology, volume 37. In this method cells are contacted with from one to many antibodies to the lung cancer protein(s). Following washing to remove non-specific antibody binding, the presence of the antibody or antibodies is detected. In one embodiment the antibody is detected by incubating with a secondary antibody that contains a detectable label, e.g., multicolor fluorescence or confocal imaging. In another method the primary antibody to the lung cancer protein(s) contains a detectable label, e.g., an enzyme marker that can act on a substrate. In another preferred embodiment each one of multiple primary antibodies contains a distinct and detectable label. This method finds particular use in simultaneous screening for a plurality of lung cancer proteins. Many other histological imaging techniques are also provided by the invention.

In a preferred embodiment the label is detected in a fluorometer which has the ability to detect and distinguish emissions of different wavelengths. In addition, a fluorescence activated cell sorter (FACS) can be used in the method.

In another preferred embodiment, antibodies find use in diagnosing lung cancer from blood, serum, plasma, stool, and other samples. Such samples, therefore, are useful as samples to be probed or tested for the presence of lung cancer proteins. Antibodies can be used to detect a lung cancer protein by previously described immunoassay techniques including ELISA, immunoblotting (western blotting), immunoprecipitation, BIAcore technology and the like. Conversely, the presence of antibodies may indicate an immune response against an endogenous lung cancer protein or vaccine.

In a preferred embodiment, *in situ* hybridization of labeled lung cancer nucleic acid probes to tissue arrays is done. For example, arrays of tissue samples, including lung cancer tissue and/or normal tissue, are made. *In situ* hybridization (see, e.g., Ausubel, *supra*) is then performed. When comparing the fingerprints between an individual and a standard, the skilled artisan can make a diagnosis, a prognosis, or a prediction based on the findings. It is further understood that the genes which indicate the diagnosis may differ from those which indicate the prognosis and molecular profiling of the condition of the cells may lead to distinctions between responsive or refractory conditions or may be predictive of outcomes.

In a preferred embodiment, the lung cancer proteins, antibodies, nucleic acids, modified proteins and cells containing lung cancer sequences are used in prognosis assays. As above, gene expression profiles can be generated that correlate to lung cancer, clinical, pathological, or other information, in terms of long term prognosis. Again, this may be done on either a protein or gene level, with the use of genes being preferred. Single or multiple



genes may be useful in various combinations. As above, lung cancer probes may be attached to biochips for the detection and quantification of lung cancer sequences in a tissue or patient. The assays proceed as outlined above for diagnosis. PCR method may provide more sensitive and accurate quantification.

5

### Assays for therapeutic compounds

In a preferred embodiment, the proteins, nucleic acids, and antibodies as described herein are used in drug screening assays. The lung cancer proteins, antibodies, nucleic acids, modified proteins and cells containing lung cancer sequences are used in drug screening  
10 assays or by evaluating the effect of drug candidates on a “gene expression profile” or expression profile of polypeptides. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent (e.g., Zlokarnik, et al. (1998) Science 279:84-8; Heid (1996) Genome Res. 6:986-94.

15 In a preferred embodiment, the lung cancer proteins, antibodies, nucleic acids, modified proteins and cells containing the native or modified lung cancer proteins are used in screening assays. That is, the present invention provides novel methods for screening for compositions which modulate the lung cancer phenotype or an identified physiological function of a lung cancer protein. As above, this can be done on an individual gene level or  
20 by evaluating the effect of drug candidates on a “gene expression profile”. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent, see Zlokarnik, *supra*.

Having identified differentially expressed genes herein, a variety of assays may be  
25 performed. In a preferred embodiment, assays may be run on an individual gene or protein level. That is, having identified a particular gene with altered regulation in lung cancer, test compounds can be screened for the ability to modulate gene expression or for binding to the lung cancer protein. “Modulation” thus includes an increase or a decrease in gene expression. The preferred amount of modulation will depend on the original change of the  
30 gene expression in normal versus tissue undergoing lung cancer, with changes of at least 10%, preferably 50%, more preferably 100-300%, and in some embodiments 300-1000% or greater. Thus, if a gene exhibits a 4-fold increase in lung cancer tissue compared to normal tissue, a decrease of about four-fold is often desired; similarly, a 10-fold decrease in lung



cancer tissue compared to normal tissue often provides a target value of a 10-fold increase in expression to be induced by the test compound.

The amount of gene expression may be monitored using nucleic acid probes and the quantification of gene expression levels, or, alternatively, the gene product itself can be monitored, e.g., through the use of antibodies to the lung cancer protein and standard immunoassays. Proteomics and separation techniques may also allow quantification of expression.

In a preferred embodiment, gene or protein expression monitoring of a number of entities, i.e., an expression profile, is monitored simultaneously. Such profiles will typically involve a plurality of those entities described herein.

In this embodiment, the lung cancer nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of lung cancer sequences in a particular cell. Alternatively, PCR may be used. Thus, a series, e.g., of microtiter plate, may be used with dispensed primers in desired wells. A PCR reaction can then be performed and analyzed for each well.

Expression monitoring can be performed to identify compounds that modify the expression of one or more lung cancer-associated sequences, e.g., a polynucleotide sequence set out in the tables. Generally, in a preferred embodiment, a test compound is added to the cells prior to analysis. Moreover, screens are also provided to identify agents that modulate lung cancer, modulate lung cancer proteins, bind to a lung cancer protein, or interfere with the binding of a lung cancer protein and an antibody, substrate, or other binding partner.

The term "test compound" or "drug candidate" or "modulator" or grammatical equivalents as used herein describes a molecule, e.g., protein, oligopeptide, small organic molecule, polysaccharide, polynucleotide, etc., to be tested for the capacity to directly or indirectly alter the lung cancer phenotype or the expression of a lung cancer sequence, e.g., a nucleic acid or protein sequence. In preferred embodiments, modulators alter expression profiles of nucleic acids or proteins provided herein. In one embodiment, the modulator suppresses a lung cancer phenotype, e.g., to a normal or non-malignant tissue fingerprint. In another embodiment, a modulator induces a lung cancer phenotype. Generally, a plurality of assay mixtures are run in parallel with different agent concentrations to obtain a differential response to the various concentrations. Typically, one of these concentrations serves as a negative control, i.e., at zero concentration or below the level of detection.



In one aspect, a modulator will neutralize the effect of a lung cancer protein. By “neutralize” is meant that activity of a protein and the consequent effect on the cell is inhibited or blocked.

In certain embodiments, combinatorial libraries of potential modulators will be screened for an ability to bind to a lung cancer polypeptide or to modulate activity. Conventionally, new chemical entities with useful properties are generated by identifying a chemical compound (called a “lead compound”) with some desirable property or activity, e.g., inhibiting activity, creating variants of the lead compound, and evaluating the property and activity of those variant compounds. Often, high throughput screening (HTS) methods are employed for such an analysis.

In one preferred embodiment, high throughput screening methods involve providing a library containing a large number of potential therapeutic compounds (candidate compounds). Such “combinatorial chemical libraries” are then screened in one or more assays to identify those library members (particular chemical species or subclasses) that display a desired characteristic activity. The compounds thus identified can serve as conventional “lead compounds” or can themselves be used as potential or actual therapeutics.

A combinatorial chemical library is a collection of diverse chemical compounds generated by either chemical synthesis or biological synthesis by combining a number of chemical “building blocks” such as reagents. For example, a linear combinatorial chemical library, such as a polypeptide (e.g., mutein) library, is formed by combining a set of chemical building blocks called amino acids in every possible way for a given compound length (i.e., the number of amino acids in a polypeptide compound). Millions of chemical compounds can be synthesized through such combinatorial mixing of chemical building blocks (Gallop, et al. (1994) J. Med. Chem. 37(9):1233-1251).

Preparation and screening of combinatorial chemical libraries is well known to those of skill in the art. Such combinatorial chemical libraries include, but are not limited to, peptide libraries (see, e.g., U.S. Patent No. 5,010,175, Furka (1991) Pept. Prot. Res. 37:487-493, Houghton, et al. (1991) Nature, 354:84-88), peptoids (PCT Publication No WO 91/19735), encoded peptides (PCT Publication WO 93/20242), random bio-oligomers (PCT Publication WO 92/00091), benzodiazepines (U.S. Pat. No. 5,288,514), diversomers such as hydantoins, benzodiazepines and dipeptides (Hobbs, et al. (1993) Proc. Nat. Acad. Sci. USA 90:6909-6913), vinylogous polypeptides (Hagihara, et al. (1992) J. Amer. Chem. Soc. 114:6568), nonpeptidal peptidomimetics with a Beta-D-Glucose scaffolding (Hirschmann, et



al. (1992) J. Amer. Chem. Soc. 114:9217-9218), analogous organic syntheses of small compound libraries (Chen, et al. (1994) J. Amer. Chem. Soc. 116:2661), oligocarbamates (Cho, et al. (1993) Science 261:1303), and/or peptidyl phosphonates (Campbell, et al. (1994) J. Org. Chem. 59:658). See, generally, Gordon, et al. (1994) J. Med. Chem. 37:1385, nucleic acid libraries (see, e.g., Stratagene, Corp.), peptide nucleic acid libraries (see, e.g., U.S. Patent 5,539,083), antibody libraries (see, e.g., Vaughn, et al. (1996) Nature Biotechnology 14(3):309-314, and PCT/US96/10287), carbohydrate libraries (see, e.g., Liang, et al. (1996) Science 274:1520-1522, and U.S. Patent No. 5,593,853), and small organic molecule libraries (see, e.g., benzodiazepines, Baum (1993) C&EN, Jan 18, page 33; isoprenoids, U.S. Patent No. 5,569,588; thiazolidinones and metathiazanones, U.S. Patent No. 5,549,974; pyrrolidines, U.S. Patent Nos. 5,525,735 and 5,519,134; morpholino compounds, U.S. Patent No. 5,506,337; benzodiazepines, U.S. Patent No. 5,288,514; and the like).

Devices for the preparation of combinatorial libraries are commercially available (see, e.g., 357 MPS, 390 MPS, Advanced Chem Tech, Louisville KY, Symphony, Rainin, Woburn, MA, 433A Applied Biosystems, Foster City, CA, 9050 Plus, Millipore, Bedford, MA).

A number of well known robotic systems have also been developed for solution phase chemistries. These systems include automated workstations like the automated synthesis apparatus developed by Takeda Chemical Industries, LTD. (Osaka, Japan) and many robotic systems utilizing robotic arms (Zymate II, Zymark Corporation, Hopkinton, Mass.; Orca, Hewlett-Packard, Palo Alto, Calif.), which mimic the manual synthetic operations performed by a chemist. The above devices, with appropriate modification, are suitable for use with the present invention. In addition, numerous combinatorial libraries are themselves commercially available (see, e.g., ComGenex, Princeton, N.J., Asinex, Moscow, Ru, Tripos, Inc., St. Louis, MO, ChemStar, Ltd, Moscow, RU, 3D Pharmaceuticals, Exton, PA, Martek Biosciences, Columbia, MD, etc.).

The assays to identify modulators are amenable to high throughput screening. Preferred assays thus detect modulation of lung cancer gene transcription, polypeptide expression, and polypeptide activity.

High throughput assays for evaluating the presence, absence, quantification, or other properties of particular nucleic acids or protein products are well known to those of skill in the art. Similarly, binding assays and reporter gene assays are similarly well known. Thus, e.g., U.S. Patent No. 5,559,410 discloses high throughput screening methods for proteins,



U.S. Patent No. 5,585,639 discloses high throughput screening methods for nucleic acid binding (i.e., in arrays), while U.S. Patent Nos. 5,576,220 and 5,541,061 disclose high throughput methods of screening for ligand/antibody binding.

In addition, high throughput screening systems are commercially available (see, e.g.,  
5 Zymark Corp., Hopkinton, MA; Air Technical Industries, Mentor, OH; Beckman Instruments, Inc. Fullerton, CA; Precision Systems, Inc., Natick, MA, etc.). These systems typically automate procedures, including sample and reagent pipetting, liquid dispensing, timed incubations, and final readings of the microplate in detector(s) appropriate for the assay. These configurable systems provide high throughput and rapid start up as well as a  
10 high degree of flexibility and customization. The manufacturers of such systems provide detailed protocols for various high throughput systems. Thus, e.g., Zymark Corp. provides technical bulletins describing screening systems for detecting the modulation of gene transcription, ligand binding, and the like.

In one embodiment, modulators are proteins, often naturally occurring proteins or  
15 fragments of naturally occurring proteins. Thus, e.g., cellular extracts containing proteins, or random or directed digests of proteinaceous cellular extracts, may be used. In this way libraries of proteins may be made for screening in the methods of the invention. Particularly preferred in this embodiment are libraries of bacterial, fungal, viral, and mammalian proteins, with the latter being preferred, and human proteins being especially preferred. Particularly  
20 useful test compound will be directed to the class of proteins to which the target belongs, e.g., substrates for enzymes or ligands and receptors.

In a preferred embodiment, modulators are peptides of from about 5 to about 30 amino acids, with from about 5 to about 20 amino acids being preferred, and from about 7 to about 15 being particularly preferred. The peptides may be digests of naturally occurring  
25 proteins, random peptides, or "biased" random peptides. By "randomized" or grammatical equivalents herein is meant that the nucleic acid or peptide consists of essentially random sequences of nucleotides and amino acids, respectively. Since these random peptides (or nucleic acids, discussed below) are often chemically synthesized, they may incorporate a nucleotide or amino acid at any position. The synthetic process can be designed to generate  
30 randomized proteins or nucleic acids, to allow the formation of all or most of the possible combinations over the length of the sequence, thus forming a library of randomized candidate bioactive proteinaceous agents.



In one embodiment, the library is fully randomized, with no sequence preferences or constants at any position. In a preferred embodiment, the library is biased. That is, some positions within the sequence are either held constant, or are selected from a limited number of possibilities. In a preferred embodiment, the nucleotides or amino acid residues are randomized within a defined class, e.g., of hydrophobic amino acids, hydrophilic residues, 5 sterically biased (either small or large) residues, towards the creation of nucleic acid binding domains, the creation of cysteines, for cross-linking, prolines for SH-3 domains, serines, threonines, tyrosines or histidines for phosphorylation sites, etc.

Modulators of lung cancer can also be nucleic acids, as defined above.

10 As described above generally for proteins, nucleic acid modulating agents may be naturally occurring nucleic acids, random nucleic acids, or "biased" random nucleic acids. Digests of procaryotic or eucaryotic genomes may be used as is outlined above for proteins.

In a preferred embodiment, the candidate compounds are organic chemical moieties, a wide variety of which are available in the literature.

15 After a candidate agent has been added and the cells allowed to incubate for some period of time, the sample containing a target sequence is analyzed. If required, the target sequence is prepared using known techniques. For example, the sample may be treated to lyse the cells, using known lysis buffers, electroporation, etc., with purification and/or amplification such as PCR performed as appropriate. For example, an *in vitro* transcription 20 with labels covalently attached to the nucleotides is performed. Generally, the nucleic acids are labeled with biotin-FITC or PE, or with cy3 or cy5.

In a preferred embodiment, the target sequence is labeled with, e.g., a fluorescent, a chemiluminescent, a chemical, or a radioactive signal, to provide a means of detecting the target sequence's specific binding to a probe. The label also can be an enzyme, such as, 25 alkaline phosphatase or horseradish peroxidase, which when provided with an appropriate substrate produces a product that can be detected. Alternatively, the label can be a labeled compound or small molecule, such as an enzyme inhibitor, that binds but is not catalyzed or altered by the enzyme. The label also can be a moiety or compound, such as, an epitope tag or biotin which specifically binds to streptavidin. For the example of biotin, the streptavidin 30 is labeled as described above, thereby, providing a detectable signal for the bound target sequence. Unbound labeled streptavidin is typically removed prior to analysis.

Nucleic acid assays can be direct hybridization assays or can comprise "sandwich assays", which include the use of multiple probes, as is generally outlined in U.S. Patent Nos.



5,681,702, 5,597,909, 5,545,730, 5,594,117, 5,591,584, 5,571,670, 5,580,731, 5,571,670, 5,591,584, 5,624,802, 5,635,352, 5,594,118, 5,359,100, 5,124,246 and 5,681,697, all of which are hereby incorporated by reference. In this embodiment, in general, the target nucleic acid is prepared as outlined above, and then added to the biochip comprising a plurality of nucleic acid probes, under conditions that allow the formation of a hybridization complex.

A variety of hybridization conditions may be used in the present invention, including high, moderate and low stringency conditions as outlined above. The assays are generally run under stringency conditions which allow formation of the label probe hybridization complex only in the presence of target. Stringency can be controlled by altering a step parameter that is a thermodynamic variable, including, but not limited to, temperature, formamide concentration, salt concentration, chaotropic salt concentration, pH, organic solvent concentration, etc.

These parameters may also be used to control non-specific binding, as is generally outlined in U.S. Patent No. 5,681,697. Thus it may be desirable to perform certain steps at higher stringency conditions to reduce non-specific binding.

The reactions outlined herein may be accomplished in a variety of ways. Components of the reaction may be added simultaneously, or sequentially, in different orders, with preferred embodiments outlined below. In addition, the reaction may include a variety of other reagents. These include salts, buffers, neutral proteins, e.g., albumin, detergents, etc. which may be used to facilitate optimal hybridization and detection, and/or reduce non-specific or background interactions. Reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may also be used as appropriate, depending on the sample preparation methods and purity of the target.

The assay data are analyzed to determine the expression levels, and changes in expression levels as between states, of individual genes, forming a gene expression profile.

Screens are performed to identify modulators of the lung cancer phenotype. In one embodiment, screening is performed to identify modulators that can induce or suppress a particular expression profile, thus preferably generating the associated phenotype. In another embodiment, e.g., for diagnostic applications, having identified differentially expressed genes important in a particular state, screens can be performed to identify modulators that alter expression of individual genes. In another embodiment, screening is performed to identify modulators that alter a biological function of the expression product of a differentially expressed gene. Again, having identified the importance of a gene in a particular state,



screens are performed to identify agents that bind and/or modulate the biological activity of the gene product, or evaluate genetic polymorphisms.

Genes can be screened for those that are induced in response to a candidate agent. After identifying a modulator based upon its ability to suppress a lung cancer expression pattern leading to a normal expression pattern, or to modulate a single lung cancer gene expression profile so as to mimic the expression of the gene from normal tissue, a screen as described above can be performed to identify genes that are specifically modulated in response to the agent. Comparing expression profiles between normal tissue and agent treated lung cancer tissue reveals genes that are not expressed in normal tissue or lung cancer tissue, but are expressed in agent treated tissue. These agent-specific sequences can be identified and used by methods described herein for lung cancer genes or proteins. In particular these sequences and the proteins they encode find use in marking or identifying agent treated cells. In addition, antibodies can be raised against the agent induced proteins and used to target novel therapeutics to the treated lung cancer tissue sample.

Thus, in one embodiment, a test compound is administered to a population of lung cancer cells, that have an associated lung cancer expression profile. By “administration” or “contacting” herein is meant that the candidate agent is added to the cells in such a manner as to allow the agent to act upon the cell, whether by uptake and intracellular action, or by action at the cell surface. In some embodiments, nucleic acid encoding a proteinaceous candidate agent (i.e., a peptide) may be put into a viral construct such as an adenoviral or retroviral construct, and added to the cell, such that expression of the peptide agent is accomplished, e.g., PCT US97/01019. Regulatable gene therapy systems can also be used.

Once a test compound has been administered to the cells, the cells can be washed if desired and are allowed to incubate under preferably physiological conditions for some period of time. The cells are then harvested and a new gene expression profile is generated, as outlined herein.

Thus, e.g., lung cancer or non-malignant tissue may be screened for agents that modulate, e.g., induce or suppress a lung cancer phenotype. A change in at least one gene, preferably many, of the expression profile indicates that the agent has an effect on lung cancer activity. By defining such a signature for the lung cancer phenotype, screens for new drugs that alter the phenotype can be devised. With this approach, the drug target need not be known and need not be represented in the original expression screening platform, nor does the level of transcript for the target protein need to change.



Measure of lung cancer polypeptide activity, or of lung cancer or the lung cancer phenotype can be performed using a variety of assays. For example, the effects of the test compounds upon the function of the metastatic polypeptides can be measured by examining parameters described above. A suitable physiological change that affects activity can be used to assess the influence of a test compound on the polypeptides of this invention. When the functional consequences are determined using intact cells or animals, one can also measure a variety of effects such as, in the case of lung cancer associated with tumors, tumor growth, tumor metastasis, neovascularization, hormone release, transcriptional changes to both known and uncharacterized genetic markers (e.g., northern blots), changes in cell metabolism such as cell growth or pH changes, and changes in intracellular second messengers such as cGMP. In the assays of the invention, mammalian lung cancer polypeptide is typically used, e.g., mouse, preferably human.

Assays to identify compounds with modulating activity can be performed *in vitro*. For example, a lung cancer polypeptide is first contacted with a potential modulator and incubated for a suitable amount of time, e.g., from 0.5 to 48 hours. In one embodiment, the lung cancer polypeptide levels are determined *in vitro* by measuring the level of protein or mRNA. The level of protein is typically measured using immunoassays such as western blotting, ELISA and the like with an antibody that selectively binds to the lung cancer polypeptide or a fragment thereof. For measurement of mRNA, amplification, e.g., using PCR, LCR, or hybridization assays, e.g., northern hybridization, RNase protection, dot blotting, are preferred. The level of protein or mRNA is typically detected using directly or indirectly labeled detection agents, e.g., fluorescently or radioactively labeled nucleic acids, radioactively or enzymatically labeled antibodies, and the like, as described herein.

Alternatively, a reporter gene system can be devised using a lung cancer protein promoter operably linked to a reporter gene such as luciferase, green fluorescent protein, CAT, or  $\beta$ -gal. The reporter construct is typically transfected into a cell. After treatment with a potential modulator, the amount of reporter gene transcription, translation, or activity is measured according to standard techniques known to those of skill in the art.

In a preferred embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of the expression of the gene or the gene product itself can be done. The gene products of differentially expressed



genes are sometimes referred to herein as “lung cancer proteins.” The lung cancer protein may be a fragment, or alternatively, be the full length protein to a fragment shown herein.

In one embodiment, screening for modulators of expression of specific genes is performed. Typically, the expression of only one or a few genes are evaluated. In another  
5 embodiment, screens are designed to first find compounds that bind to differentially expressed proteins. These compounds are then evaluated for the ability to modulate differentially expressed activity. Moreover, once initial candidate compounds are identified, variants can be further screened to better evaluate structure activity relationships.

In a preferred embodiment, binding assays are done. In general, purified or isolated  
10 gene product is used; that is, the gene products of one or more differentially expressed nucleic acids are made. For example, antibodies are generated to the protein gene products, and standard immunoassays are run to determine the amount of protein present. Alternatively, cells comprising the lung cancer proteins can be used in the assays.

Thus, in a preferred embodiment, the methods comprise combining a lung cancer  
15 protein and a candidate compound, and determining the binding of the compound to the lung cancer protein. Preferred embodiments utilize the human lung cancer protein, although other mammalian proteins may also be used, e.g., for the development of animal models of human disease. In some embodiments, as outlined herein, variant or derivative lung cancer proteins may be used.

Generally, in a preferred embodiment of the methods herein, the lung cancer protein  
20 or the candidate agent is non-diffusably bound to an insoluble support, preferably having isolated sample receiving areas (e.g., a microtiter plate, an array, etc.). The insoluble supports may be made of a composition to which the compositions can be bound, is readily separated from soluble material, and is otherwise compatible with the overall method of  
25 screening. The surface of such supports may be solid or porous and of a convenient shape. Examples of suitable insoluble supports include microtiter plates, arrays, membranes and beads. These are typically made of glass, plastic (e.g., polystyrene), polysaccharides, nylon or nitrocellulose, teflon™, etc. Microtiter plates and arrays are especially convenient because a large number of assays can be carried out simultaneously, using small amounts of reagents  
30 and samples. The particular manner of binding of the composition is typically not crucial so long as it is compatible with the reagents and overall methods of the invention, maintains the activity of the composition, and is nondiffusable. Preferred methods of binding include the use of antibodies (which do not sterically block either the ligand binding site or activation



sequence when the protein is bound to the support), direct binding to “sticky” or ionic supports, chemical crosslinking, the synthesis of the protein or agent on the surface, etc. Following binding of the protein or agent, excess unbound material is removed by washing. The sample receiving areas may then be blocked through incubation with bovine serum albumin (BSA), casein or other innocuous protein or other moiety.

In a preferred embodiment, the lung cancer protein is bound to the support, and a test compound is added to the assay. Alternatively, the candidate agent is bound to the support and the lung cancer protein is added. Novel binding agents include specific antibodies, non-natural binding agents identified in screens of chemical libraries, peptide analogs, etc. Of particular interest are screening assays for agents that have a low toxicity for human cells. A wide variety of assays may be used for this purpose, including labeled *in vitro* protein-protein binding assays, electrophoretic mobility shift assays, immunoassays for protein binding, functional assays (phosphorylation assays, etc.) and the like.

The determination of the binding of the test modulating compound to the lung cancer protein may be done in a number of ways. In a preferred embodiment, the compound is labeled, and binding determined directly, e.g., by attaching all or a portion of the lung cancer protein to a solid support, adding a labeled candidate agent (e.g., a fluorescent label), washing off excess reagent, and determining whether the label is present on the solid support. Various blocking and washing steps may be utilized as appropriate.

In some embodiments, only one of the components is labeled, e.g., the proteins (or proteinaceous candidate compounds) can be labeled. Alternatively, more than one component can be labeled with different labels, e.g.,  $^{125}\text{I}$  for the proteins and a fluorophor for the compound. Proximity reagents, e.g., quenching or energy transfer reagents are also useful.

In one embodiment, the binding of the test compound is determined by competitive binding assay. The competitor may be a binding moiety known to bind to the target molecule (i.e., a lung cancer protein), such as an antibody, peptide, binding partner, ligand, etc. Under certain circumstances, there may be competitive binding between the compound and the binding moiety, with the binding moiety displacing the compound. In one embodiment, the test compound is labeled. Either the compound, or the competitor, or both, is added first to the protein for a time sufficient to allow binding, if present. Incubations may be performed at a temperature which facilitates optimal activity, typically between 4 and 40° C. Incubation periods are typically optimized, e.g., to facilitate rapid high throughput screening. Typically



between 0.1 and 1 hour will be sufficient. Excess reagent is generally removed or washed away. The second component is then added, and the presence or absence of the labeled component is followed, to indicate binding.

In a preferred embodiment, the competitor is added first, followed by a test compound. Displacement of the competitor is an indication that the test compound is binding to the lung cancer protein and thus is capable of binding to, and potentially modulating, the activity of the lung cancer protein. In this embodiment, either component can be labeled. Thus, e.g., if the competitor is labeled, the presence of label in the wash solution indicates displacement by the agent. Alternatively, if the test compound is labeled, the presence of the label on the support indicates displacement.

In an alternative embodiment, the test compound is added first, with incubation and washing, followed by the competitor. The absence of binding by the competitor may indicate that the test compound is bound to the lung cancer protein with a higher affinity. Thus, if the test compound is labeled, the presence of the label on the support, coupled with a lack of competitor binding, may indicate that the test compound is capable of binding to the lung cancer protein.

In a preferred embodiment, the methods comprise differential screening to identify agents that are capable of modulating the activity of the lung cancer proteins. In one embodiment, the methods comprise combining a lung cancer protein and a competitor in a first sample. A second sample comprises a test compound, a lung cancer protein, and a competitor. The binding of the competitor is determined for both samples, and a change, or difference in binding between the two samples indicates the presence of an agent capable of binding to the lung cancer protein and potentially modulating its activity. That is, if the binding of the competitor is different in the second sample relative to the first sample, the agent is capable of binding to the lung cancer protein.

Alternatively, differential screening is used to identify drug candidates that bind to the native lung cancer protein, but cannot bind to modified lung cancer proteins. The structure of the lung cancer protein may be modeled, and used in rational drug design to synthesize agents that interact with that site. Drug candidates that affect the activity of a lung cancer protein are also identified by screening drugs for the ability to either enhance or reduce the activity of the protein.

Positive controls and negative controls may be used in the assays. Preferably control and test samples are performed in at least triplicate to obtain statistically significant results.



Incubation of all samples is for a time sufficient for the binding of the agent to the protein. Following incubation, samples are washed free of non-specifically bound material and the amount of bound, generally labeled agent determined. For example, where a radiolabel is employed, the samples may be counted in a scintillation counter to determine the amount of bound compound.

A variety of other reagents may be included in the screening assays. These include reagents like salts, neutral proteins, e.g., albumin, detergents, etc. which may be used to facilitate optimal protein-protein binding and/or reduce non-specific or background interactions. Also reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may be used. The mixture of components may be added in an order that provides for the requisite binding.

In a preferred embodiment, the invention provides methods for screening for a compound capable of modulating the activity of a lung cancer protein. The methods comprise adding a test compound, as defined above, to a cell comprising lung cancer proteins. Preferred cell types include almost any cell. The cells contain a recombinant nucleic acid that encodes a lung cancer protein. In a preferred embodiment, a library of candidate agents are tested on a plurality of cells.

In one aspect, the assays are evaluated in the presence or absence or previous or subsequent exposure of physiological signals, e.g., hormones, antibodies, peptides, antigens, cytokines, growth factors, action potentials, pharmacological agents including chemotherapeutics, radiation, carcinogenics, or other cells (e.g., cell-cell contacts). In another example, the determinations are determined at different stages of the cell cycle process.

In this way, compounds that modulate lung cancer agents are identified. Compounds with pharmacological activity are able to enhance or interfere with the activity of the lung cancer protein. Once identified, similar structures are evaluated to identify critical structural feature of the compound.

In one embodiment, a method of inhibiting lung cancer cell division is provided. The method comprises administration of a lung cancer inhibitor. In another embodiment, a method of inhibiting lung cancer is provided. The method may comprise administration of a lung cancer inhibitor. In a further embodiment, methods of treating cells or individuals with lung cancer are provided, e.g., comprising administration of a lung cancer inhibitor.

In one embodiment, a lung cancer inhibitor is an antibody as discussed above. In another embodiment, the lung cancer inhibitor is an antisense molecule.



A variety of cell growth, proliferation, viability, and metastasis assays are known to those of skill in the art, as described below.

*Soft agar growth or colony formation in suspension*

5 Normal cells require a solid substrate to attach and grow. When the cells are transformed, they lose this phenotype and grow detached from the substrate. For example, transformed cells can grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft agar. The transformed cells, when transfected with tumor suppressor genes, regenerate normal phenotype and require a solid substrate to attach and grow. Soft agar growth or colony formation in suspension assays can be used to identify modulators of lung cancer sequences, which when expressed in host cells, inhibit abnormal cellular proliferation and transformation. A therapeutic compound would reduce or eliminate the host cells' ability to grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft.

10 Techniques for soft agar growth or colony formation in suspension assays are described in Freshney (1994) Culture of Animal Cells a Manual of Basic Technique (3<sup>rd</sup> ed.), herein incorporated by reference. See also, the methods section of Garkavtsev, et al. (1996), *supra*, herein incorporated by reference.

20 *Contact inhibition and density limitation of growth*

Normal cells typically grow in a flat and organized pattern in a petri dish until they touch other cells. When the cells touch one another, they are contact inhibited and stop growing. When cells are transformed, however, the cells are not contact inhibited and continue to grow to high densities in disorganized foci. Thus, the transformed cells grow to a higher saturation density than normal cells. This can be detected morphologically by the formation of a disoriented monolayer of cells or rounded cells in foci within the regular pattern of normal surrounding cells. Alternatively, labeling index with (<sup>3</sup>H)-thymidine at saturation density can be used to measure density limitation of growth. See Freshney (1994), *supra*. The transformed cells, when transfected with tumor suppressor genes, regenerate a normal phenotype and become contact inhibited and would grow to a lower density.

30 In this assay, labeling index with (<sup>3</sup>H)-thymidine at saturation density is a preferred method of measuring density limitation of growth. Transformed host cells are transfected with a lung cancer-associated sequence and are grown for 24 hours at saturation density in



non-limiting medium conditions. The percentage of cells labeling with (<sup>3</sup>H)-thymidine is determined autoradiographically. See, Freshney (1994), *supra*.

*Growth factor or serum dependence*

5 Transformed cells typically have a lower serum dependence than their normal counterparts (see, e.g., Temin (1966) J. Natl. Cancer Inst. 37:167-175; Eagle, et al. (1970) J. Exp. Med. 131:836-879); Freshney, *supra*. This is in part due to release of various growth factors by the transformed cells. Growth factor or serum dependence of transformed host cells can be compared with that of control.

10 *Tumor specific markers levels*

Tumor cells release an increased amount of certain factors (hereinafter "tumor specific markers") than their normal counterparts. For example, plasminogen activator (PA) is released from human glioma at a higher level than from normal brain cells (see, e.g.,  
15 Gullino, "Angiogenesis, tumor vascularization, and potential interference with tumor growth" in Mihich (ed. 1985) Biological Responses in Cancer, pp. 178-184). Similarly, Tumor angiogenesis factor (TAF) is released at a higher level in tumor cells than their normal counterparts. See, e.g., Folkman (1992) "Angiogenesis and Cancer" in Sem Cancer Biol.

Various techniques which measure the release of these factors are described in  
20 Freshney (1994), *supra*. Also, see, Unkeless, et al. (1974) J. Biol. Chem. 249:4295-4305; Strickland and Beers (1976) J. Biol. Chem. 251:5694-5702; Whur, et al. (1980) Br. J. Cancer 42:305-312; Gullino, "Angiogenesis, tumor vascularization, and potential interference with tumor growth" in Mihich (ed. 1985) Biological Responses in Cancer, pp. 178-184; Freshney Anticancer Res. 5:111-130 (1985).

25 *Invasiveness into Matrigel*

The degree of invasiveness into Matrigel or some other extracellular matrix constituent can be used as an assay to identify compounds that modulate lung cancer-associated sequences. Tumor cells exhibit a good correlation between malignancy and  
30 invasiveness of cells into Matrigel or some other extracellular matrix constituent. In this assay, tumorigenic cells are typically used as host cells. Expression of a tumor suppressor gene in these host cells would decrease invasiveness of the host cells.



Techniques described in Freshney (1994), *supra*, can be used. Briefly, the level of invasion of host cells can be measured by using filters coated with Matrigel or some other extracellular matrix constituent. Penetration into the gel, or through to the distal side of the filter, is rated as invasiveness, and rated histologically by number of cells and distance moved, or by prelabeling the cells with  $^{125}\text{I}$  and counting the radioactivity on the distal side of the filter or bottom of the dish. See, e.g., Freshney (1984), *supra*.

#### *Tumor growth in vivo*

Effects of lung cancer-associated sequences on cell growth can be tested in transgenic or immune-suppressed mice. Knock-out transgenic mice can be made, in which the lung cancer gene is disrupted or in which a lung cancer gene is inserted. Knock-out transgenic mice can be made by insertion of a marker gene or other heterologous gene into the endogenous lung cancer gene site in the mouse genome via homologous recombination. Such mice can also be made by substituting the endogenous lung cancer gene with a mutated version of the lung cancer gene, or by mutating the endogenous lung cancer gene, e.g., by exposure to carcinogens.

A DNA construct is introduced into the nuclei of embryonic stem cells. Cells containing the newly engineered genetic lesion are injected into a host mouse embryo, which is re-implanted into a recipient female. Some of these embryos develop into chimeric mice that possess germ cells partially derived from the mutant cell line. Therefore, by breeding the chimeric mice it is possible to obtain a new line of mice containing the introduced genetic lesion (see, e.g., Capecchi, et al. (1989) Science 244:1288). Chimeric targeted mice can be derived according to Hogan, et al. (1988) Manipulating the Mouse Embryo: A Laboratory Manual, Cold Spring Harbor Laboratory and Robertson (ed. 1987) Teratocarcinomas and Embryonic Stem Cells: A Practical Approach, IRL Press, Washington, D.C.

Alternatively, various immune-suppressed or immune-deficient host animals can be used. For example, genetically athymic “nude” mouse (see, e.g., Giovanella, et al. (1974) J. Natl. Cancer Inst. 52:921), a SCID mouse, a thymectomized mouse, or an irradiated mouse (see, e.g., Bradley, et al. (1978) Br. J. Cancer 38:263; Selby, et al. (1980) Br. J. Cancer 41:52) can be used as a host. Transplantable tumor cells (typically about  $10^6$  cells) injected into isogenic hosts will produce invasive tumors in a high proportions of cases, while normal cells of similar origin will not. In hosts which developed invasive tumors, cells expressing a lung cancer-associated sequences are injected subcutaneously. After a suitable length of time,



preferably 4-8 weeks, tumor growth is measured (e.g., by volume or by its two largest dimensions) and compared to the control. Tumors that have statistically significant reduction (using, e.g., Student's T test) are said to have inhibited growth.

## 5 Polynucleotide modulators of lung cancer

### *Antisense and RNAi Polynucleotides*

In certain embodiments, the activity of a lung cancer-associated protein is downregulated, or entirely inhibited, by the use of antisense or an inhibitory polynucleotide, i.e., a nucleic acid complementary to, and which can preferably hybridize specifically to, a  
10 coding mRNA nucleic acid sequence, e.g., a lung cancer protein mRNA, or a subsequence thereof. Binding of the antisense polynucleotide to the mRNA reduces the translation and/or stability of the mRNA.

In the context of this invention, antisense polynucleotides can comprise naturally-occurring nucleotides, or synthetic species formed from naturally-occurring subunits or their  
15 close homologs. Antisense polynucleotides may also have altered sugar moieties or inter-sugar linkages. Exemplary among these are the phosphorothioate and other sulfur containing species which are known for use in the art. Analogs are comprehended by this invention so long as they function effectively to hybridize with the lung cancer protein mRNA. See, e.g., Isis Pharmaceuticals, Carlsbad, CA; Sequitor, Inc., Natick, MA.

20 Such antisense polynucleotides can readily be synthesized using recombinant means, or can be synthesized *in vitro*. Equipment for such synthesis is sold by several vendors, including Applied Biosystems. The preparation of other oligonucleotides such as phosphorothioates and alkylated derivatives is also well known to those of skill in the art.

Antisense molecules as used herein include antisense or sense oligonucleotides.  
25 Sense oligonucleotides can, e.g., be employed to block transcription by binding to the antisense strand. The antisense and sense oligonucleotide comprise a single-stranded nucleic acid sequence (either RNA or DNA) capable of binding to target mRNA (sense) or DNA (antisense) sequences for lung cancer molecules. A preferred antisense molecule is for a lung cancer sequence in the tables, or for a ligand or activator thereof. Antisense or sense  
30 oligonucleotides, according to the present invention, comprise a fragment generally at least about 14 nucleotides, preferably from about 14 to 30 nucleotides. The ability to derive an antisense or a sense oligonucleotide, based upon a cDNA sequence encoding a given protein



is described in, e.g., Stein and Cohen (1988) Cancer Res. 48:2659 and van der Krol, et al. (1988) BioTechniques 6:958).

RNA interference is a mechanism to suppress gene expression in a sequence specific manner. See, e.g., Brumelkamp, et al. (2002) Scienceexpress (21March2002); Sharp (1999) Genes Dev. 13:139-141; and Cathew (2001) Curr. Op. Cell Biol. 13:244-248. In mammalian cells, short, e.g., 21 nt, double stranded small interfering RNAs (siRNA) have been shown to be effective at inducing an RNAi response. See, e.g., Elbashir, et al. (2001) Nature 411:494-498. The mechanism may be used to downregulate expression levels of identified genes, e.g., treatment of or validation of relevance to disease.

### *Ribozymes*

In addition to antisense polynucleotides, ribozymes can be used to target and inhibit transcription of lung cancer-associated nucleotide sequences. A ribozyme is an RNA molecule that catalytically cleaves other RNA molecules. Different kinds of ribozymes have been described, including group I ribozymes, hammerhead ribozymes, hairpin ribozymes, RNase P, and axhead ribozymes (see, e.g., Castanotto, et al. (1994) Adv. in Pharmacology 25: 289-317 for a general review of the properties of different ribozymes).

The general features of hairpin ribozymes are described, e.g., in Hampel, et al. (1990) Nucl. Acids Res. 18:299-304; European Patent Publication No. 0 360 257; U.S. Patent No. 5,254,678. Methods of preparing are well known to those of skill in the art (see, e.g., WO 94/26877; Ojwang, et al. (1993) Proc. Natl. Acad. Sci. USA 90:6340-6344; Yamada, et al. (1994) Human Gene Therapy 1:39-45; Leavitt, et al. (1995) Proc. Natl. Acad. Sci. USA 92:699-703; Leavitt, et al. (19994) Human Gene Therapy 5:1151-120; and Yamada, et al. (1994) Virology 205: 121-126).

Polynucleotide modulators of lung cancer may be introduced into a cell containing the target nucleotide sequence by formation of a conjugate with a ligand binding molecule, as described in WO 91/04753. Suitable ligand binding molecules include, but are not limited to, cell surface receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. Preferably, conjugation of the ligand binding molecule does not substantially interfere with the ability of the ligand binding molecule to bind to its corresponding molecule or receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell. Alternatively, a polynucleotide modulator of lung cancer may be introduced into a cell containing the target nucleic acid sequence, e.g., by



formation of an polynucleotide-lipid complex, as described in WO 90/10448. It is understood that the use of antisense molecules or knock out and knock in models may also be used in screening assays as discussed above, in addition to methods of treatment.

Thus, in one embodiment, methods of modulating lung cancer in cells or organisms are provided. In one embodiment, the methods comprise administering to a cell an anti-lung cancer antibody that reduces or eliminates the biological activity of an endogenous lung cancer protein. Alternatively, the methods comprise administering to a cell or organism a recombinant nucleic acid encoding a lung cancer protein. This may be accomplished in any number of ways. In a preferred embodiment, e.g., when the lung cancer sequence is down-regulated in lung cancer, such state may be reversed by increasing the amount of lung cancer gene product in the cell. This can be accomplished, e.g., by overexpressing the endogenous lung cancer gene or administering a gene encoding the lung cancer sequence, using known gene-therapy techniques. In a preferred embodiment, the gene therapy techniques include the incorporation of the exogenous gene using enhanced homologous recombination (EHR), e.g., as described in PCT/US93/03868, hereby incorporated by reference in its entirety. Alternatively, e.g., when the lung cancer sequence is up-regulated in lung cancer, the activity of the endogenous lung cancer gene is decreased, e.g., by the administration of a lung cancer antisense or RNAi nucleic acid.

In one embodiment, the lung cancer proteins of the present invention may be used to generate polyclonal and monoclonal antibodies to lung cancer proteins. Similarly, the lung cancer proteins can be coupled, using standard technology, to affinity chromatography columns. These columns may then be used to purify lung cancer antibodies useful for production, diagnostic, or therapeutic purposes. In a preferred embodiment, the antibodies are generated to epitopes unique to a lung cancer protein; that is, the antibodies show little or no cross-reactivity to other proteins. The lung cancer antibodies may be coupled to standard affinity chromatography columns and used to purify lung cancer proteins. The antibodies may also be used as blocking polypeptides, as outlined above, since they will specifically bind to the lung cancer protein.

### **Methods of identifying variant lung cancer-associated sequences**

Without being bound by theory, expression of various lung cancer sequences is correlated with lung cancer. Accordingly, disorders based on mutant or variant lung cancer genes may be determined. In one embodiment, the invention provides methods for



identifying cells containing variant lung cancer genes, e.g., determining all or part of the sequence of at least one endogenous lung cancer genes in a cell. In a preferred embodiment, the invention provides methods of identifying the lung cancer genotype of an individual, e.g., determining all or part of the sequence of at least one lung cancer gene of the individual.

- 5 This is generally done in at least one tissue of the individual, and may include the evaluation of a number of tissues or different samples of the same tissue. The method may include comparing the sequence of the sequenced lung cancer gene to a known lung cancer gene, i.e., a wild-type gene.

10 The sequence of all or part of the lung cancer gene can then be compared to the sequence of a known lung cancer gene to determine if any differences exist. This can be done using known homology programs, such as Bestfit, etc. In a preferred embodiment, the presence of a difference in the sequence between the lung cancer gene of the patient and the known lung cancer gene correlates with a disease state or a propensity for a disease state, as outlined herein.

- 15 In a preferred embodiment, the lung cancer genes are used as probes to determine the number of copies of the lung cancer gene in the genome.

In another preferred embodiment, the lung cancer genes are used as probes to determine the chromosomal localization of the lung cancer genes. Information such as chromosomal localization finds use in providing a diagnosis or prognosis in particular when  
20 chromosomal abnormalities such as translocations, and the like are identified in the lung cancer gene locus.

### **Administration of pharmaceutical and vaccine compositions**

- 25 In one embodiment, a therapeutically effective dose of a lung cancer protein or modulator thereof, is administered to a patient. By “therapeutically effective dose” herein is meant a dose that produces effects for which it is administered. The exact dose will depend on the purpose of the treatment, and will be ascertainable by one skilled in the art using known techniques (e.g., Ansel, et al. (1992) Pharmaceutical Dosage Forms and Drug Delivery; Lieberman, Pharmaceutical Dosage Forms (vols. 1-3), Dekker, ISBN 0824770846,  
30 082476918X, 0824712692, 0824716981; Lloyd (1999) The Art, Science and Technology of Pharmaceutical Compounding; and Pickar (1999) Dosage Calculations). Adjustments for lung cancer degradation, systemic versus localized delivery, and rate of new protease synthesis, as well as the age, body weight, general health, sex, diet, time of administration,



drug interaction and the severity of the condition may be necessary, and will be ascertainable with routine experimentation by those skilled in the art.

A "patient" for the purposes of the present invention includes both humans and other animals, particularly mammals. Thus the methods are applicable to both human therapy and  
5 veterinary applications. In the preferred embodiment the patient is a mammal, preferably a primate, and in the most preferred embodiment the patient is human.

The administration of the lung cancer proteins and modulators thereof of the present invention can be done in a variety of ways, including, but not limited to, orally, subcutaneously, intravenously, intranasally, transdermally, intraperitoneally, intramuscularly,  
10 intrapulmonary, vaginally, rectally, or intraocularly. In some instances, e.g., in the treatment of wounds and inflammation, the lung cancer proteins and modulators may be directly applied as a solution or spray.

The pharmaceutical compositions of the present invention comprise a lung cancer protein in a form suitable for administration to a patient. In the preferred embodiment, the  
15 pharmaceutical compositions are in a water soluble form, such as being present as pharmaceutically acceptable salts, which is meant to include both acid and base addition salts. "Pharmaceutically acceptable acid addition salt" refers to those salts that retain the biological effectiveness of the free bases and that are not biologically or otherwise undesirable, formed with inorganic acids such as hydrochloric acid, hydrobromic acid,  
20 sulfuric acid, nitric acid, phosphoric acid and the like, and organic acids such as acetic acid, propionic acid, glycolic acid, pyruvic acid, oxalic acid, maleic acid, malonic acid, succinic acid, fumaric acid, tartaric acid, citric acid, benzoic acid, cinnamic acid, mandelic acid, methanesulfonic acid, ethanesulfonic acid, p-toluenesulfonic acid, salicylic acid and the like. "Pharmaceutically acceptable base addition salts" include those derived from inorganic bases  
25 such as sodium, potassium, lithium, ammonium, calcium, magnesium, iron, zinc, copper, manganese, aluminum salts and the like. Particularly preferred are the ammonium, potassium, sodium, calcium, and magnesium salts. Salts derived from pharmaceutically acceptable organic non-toxic bases include salts of primary, secondary, and tertiary amines, substituted amines including naturally occurring substituted amines, cyclic amines and basic  
30 ion exchange resins, such as isopropylamine, trimethylamine, diethylamine, triethylamine, tripropylamine, and ethanolamine.

The pharmaceutical compositions may also include one or more of the following: carrier proteins such as serum albumin; buffers; fillers such as microcrystalline cellulose,



lactose, corn and other starches; binding agents; sweeteners and other flavoring agents; coloring agents; and polyethylene glycol.

The pharmaceutical compositions can be administered in a variety of unit dosage forms depending upon the method of administration. For example, unit dosage forms  
5 suitable for oral administration include, but are not limited to, powder, tablets, pills, capsules and lozenges. It is recognized that lung cancer protein modulators (e.g., antibodies, antisense constructs, ribozymes, small organic molecules, etc.) when administered orally, should be protected from digestion. This is typically accomplished either by complexing the  
10 molecule(s) with a composition to render it resistant to acidic and enzymatic hydrolysis, or by packaging the molecule(s) in an appropriately resistant carrier, such as a liposome or a protection barrier. Means of protecting agents from digestion are well known in the art.

The compositions for administration will commonly comprise a lung cancer protein modulator dissolved in a pharmaceutically acceptable carrier, preferably an aqueous carrier. A variety of aqueous carriers can be used, e.g., buffered saline and the like. These solutions  
15 are sterile and generally free of undesirable matter. These compositions may be sterilized by conventional, well known sterilization techniques. The compositions may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions such as pH adjusting and buffering agents, toxicity adjusting agents and the like, e.g., sodium acetate, sodium chloride, potassium chloride, calcium chloride, sodium lactate  
20 and the like. The concentration of active agent in these formulations can vary widely, and will be selected primarily based on fluid volumes, viscosities, body weight and the like in accordance with the particular mode of administration selected and the patient's needs (e.g., Remington's Pharmaceutical Science (15th ed., 1980) and Hardman, et al. (eds. 1996) Goodman and Gilman: The Pharmacological Basis of Therapeutics).

Thus, a typical pharmaceutical composition for intravenous administration would be  
25 about 0.1 to 10 mg per patient per day. Dosages from 0.1 up to about 100 mg per patient per day may be used, particularly when the drug is administered to a secluded site and not into the blood stream, such as into a body cavity or into a lumen of an organ. Substantially higher dosages are possible in topical administration. Actual methods for preparing parenterally  
30 administrable compositions will be known or apparent to those skilled in the art, e.g., Remington's Pharmaceutical Science and Goodman and Gilman, The Pharmacological Basis of Therapeutics, *supra*.



The compositions containing modulators of lung cancer proteins can be administered for therapeutic or prophylactic treatments. In therapeutic applications, compositions are administered to a patient suffering from a disease (e.g., a cancer) in an amount sufficient to cure or at least partially arrest the disease and its complications. An amount adequate to accomplish this is defined as a “therapeutically effective dose.” Amounts effective for this use will depend upon the severity of the disease and the general state of the patient’s health. Single or multiple administrations of the compositions may be administered depending on the dosage and frequency as required and tolerated by the patient. In any event, the composition should provide a sufficient quantity of the agents of this invention to effectively treat the patient. An amount of modulator that is capable of preventing or slowing the development of cancer in a mammal is referred to as a “prophylactically effective dose.” The particular dose required for a prophylactic treatment will depend upon the medical condition and history of the mammal, the particular cancer being prevented, as well as other factors such as age, weight, gender, administration route, efficiency, etc. Such prophylactic treatments may be used, e.g., in a mammal who has previously had cancer to prevent a recurrence of the cancer, or in a mammal who is suspected of having a significant likelihood of developing cancer based, at least in part, upon gene expression profiles. Vaccine strategies may be used, in either a DNA vaccine form, or protein vaccine.

It will be appreciated that the present lung cancer protein-modulating compounds can be administered alone or in combination with additional lung cancer modulating compounds or with other therapeutic agent, e.g., other anti-cancer agents or treatments.

In numerous embodiments, one or more nucleic acids, e.g., polynucleotides comprising nucleic acid sequences set forth in the tables, such as antisense or RNAi polynucleotides or ribozymes, will be introduced into cells, *in vitro* or *in vivo*. The present invention provides methods, reagents, vectors, and cells useful for expression of lung cancer-associated polypeptides and nucleic acids using *in vitro* (cell-free), *ex vivo*, or *in vivo* (cell or organism-based) recombinant expression systems.

The particular procedure used to introduce the nucleic acids into a host cell for expression of a protein or nucleic acid is application specific. Many procedures for introducing foreign nucleotide sequences into host cells may be used. These include the use of calcium phosphate transfection, spheroplasts, electroporation, liposomes, microinjection, plasma vectors, viral vectors and other well known methods for introducing cloned genomic DNA, cDNA, synthetic DNA or other foreign genetic material into a host cell (see, e.g.,



Berger and Kimmel, Guide to Molecular Cloning Techniques, Methods in Enzymology volume 152 (Berger), Ausubel, et al. (eds. 1999) Current Protocols (supplemented through 1999), and Sambrook, et al. (1989) Molecular Cloning - A Laboratory Manual (2nd ed., Vol. 1-3).

5 In a preferred embodiment, lung cancer proteins and modulators are administered as therapeutic agents, and can be formulated as outlined above. Similarly, lung cancer genes (including both the full-length sequence, partial sequences, or regulatory sequences of the lung cancer coding regions) can be administered in a gene therapy application. These lung cancer genes can include antisense or inhibitory applications, e.g., as inhibitory RNA or gene  
10 therapy (e.g., for incorporation into the genome) or as antisense compositions.

Lung cancer polypeptides and polynucleotides can also be administered as vaccine compositions to stimulate HTL, CTL, and antibody responses.. Such vaccine compositions can include, e.g., lipidated peptides (see, e.g., Vitiello, et al. (1995) J. Clin. Invest. 95:341), peptide compositions encapsulated in poly(DL-lactide-co-glycolide) ("PLG") microspheres  
15 (see, e.g., Eldridge, et al. (1991) Molec. Immunol. 28:287-294; Alonso, et al. (1994) Vaccine 12:299-306; Jones, et al. (1995) Vaccine 13:675-681), peptide compositions contained in immune stimulating complexes (ISCOMS) (see, e.g., Takahashi, et al. (1990) Nature 344:873-875; Hu, et al. (1998) Clin Exp Immunol. 113:235-243), multiple antigen peptide systems (MAPs) (see, e.g., Tam (1988) Proc. Natl. Acad. Sci. U.S.A. 85:5409-5413; Tam  
20 (1996) J. Immunol. Methods 196:17-32), peptides formulated as multivalent peptides; peptides for use in ballistic delivery systems, typically crystallized peptides, viral delivery vectors (Perkus, et al., p. 379 In: Kaufmann (ed. 1996) Concepts in vaccine development; Chakrabarti, et al. (1986) Nature 320:535; Hu, et al. (1986) Nature 320:537; Kieny, et al. (1986) AIDS Bio/Technology 4:790; Top, et al. (1971) J. Infect. Dis. 124:148; Chanda, et al.  
25 (1990) Virology 175:535), particles of viral or synthetic origin (see, e.g., Kofler, et al. (1996) J. Immunol. Methods 192:25; Eldridge, et al. (1993) Sem. Hematol. 30:16; Faló, et al. (1995) Nature Med. 7:649), adjuvants (Warren, et al. (1986) Annu. Rev. Immunol. 4:369; Gupta, et al. (1993) Vaccine 11:293), liposomes (Reddy, et al. (1992) J. Immunol. 148:1585; Rock (1996) Immunol. Today 17:131), or, naked or particle absorbed cDNA (Ulmer, et al. (1993) Science 259:1745; Robinson, et al. (1993) Vaccine 11:957; Shiver, et al., p. 423 In:  
30 Kaufmann (ed. 1996) Concepts in vaccine development; Cease and Berzofsky (1994) Annu. Rev. Immunol. 12:923 and Eldridge, et al. (1993) Sem. Hematol. 30:16). Toxin-targeted



delivery technologies, also known as receptor mediated targeting, such as those of Avant Immunotherapeutics, Inc. (Needham, Massachusetts) may also be used.

Vaccine compositions often include adjuvants. Many adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, *Bordetella pertussis* or *Mycobacterium tuberculosis* derived proteins. Certain adjuvants are commercially available as, e.g., Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI); Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ); AS-2 (SmithKline Beecham, Philadelphia, PA); aluminum salts such as aluminum hydroxide gel (alum) or aluminum phosphate; salts of calcium, iron or zinc; an insoluble suspension of acylated tyrosine; acylated sugars; cationically or anionically derivatized polysaccharides; polyphosphazenes; biodegradable microspheres; monophosphoryl lipid A and quil A. Cytokines, such as GM-CSF, interleukin-2, -7, -12, and other like growth factors, may also be used as adjuvants.

Vaccines can be administered as nucleic acid compositions wherein DNA or RNA encoding one or more of the polypeptides, or a fragment thereof, is administered to a patient. This approach is described, for instance, in Wolff, et. al. (1990) Science 247:1465 as well as U.S. Patent Nos. 5,580,859; 5,589,466; 5,804,566; 5,739,118; 5,736,524; 5,679,647; WO 98/04720; and in more detail below. Examples of DNA-based delivery technologies include "naked DNA", facilitated (bupivacaine, polymers, peptide-mediated) delivery, cationic lipid complexes, and particle-mediated ("gene gun") or pressure-mediated delivery (see, e.g., U.S. Patent No. 5,922,687).

For therapeutic or prophylactic immunization purposes, the peptides of the invention can be expressed by viral or bacterial vectors. Examples of expression vectors include attenuated viral hosts, such as vaccinia or fowlpox. This approach involves the use of vaccinia virus, e.g., as a vector to express nucleotide sequences that encode lung cancer polypeptides or polypeptide fragments. Upon introduction into a host, the recombinant vaccinia virus expresses the immunogenic peptide, and thereby elicits an immune response. Vaccinia vectors and methods useful in immunization protocols are described in, e.g., U.S. Patent No. 4,722,848. Another vector is BCG (Bacille Calmette Guerin). BCG vectors are described in Stover, et al. (1991) Nature 351:456-460. A wide variety of other vectors useful for therapeutic administration or immunization e.g., adeno and adeno-associated virus vectors, retroviral vectors, *Salmonella typhi* vectors, detoxified anthrax toxin vectors, and the



like, will be apparent to those skilled in the art from the description herein (see, e.g., Shata, et al. (2000) Mol Med Today 6:66-71; Shedlock, et al. (2000) J. Leukoc. Biol. 68:793-806; Hipp, et al. (2000) In Vivo 14:571-85).

Methods for the use of genes as DNA vaccines are well known, and include placing a lung cancer gene or portion of a lung cancer gene under the control of a regulatable promoter or a tissue-specific promoter for expression in a lung cancer patient. The lung cancer gene used for DNA vaccines can encode full-length lung cancer proteins, but more preferably encodes portions of the lung cancer proteins including peptides derived from the lung cancer protein. In one embodiment, a patient is immunized with a DNA vaccine comprising a plurality of nucleotide sequences derived from a lung cancer gene. For example, lung cancer-associated genes or sequence encoding subfragments of a lung cancer protein are introduced into expression vectors and tested for their immunogenicity in the context of Class I MHC and an ability to generate cytotoxic T cell responses. This procedure provides for production of cytotoxic T cell responses against cells which present antigen, including intracellular epitopes.

In a preferred embodiment, DNA vaccines include a gene encoding an adjuvant molecule with the DNA vaccine. Such adjuvant molecules include cytokines that increase the immunogenic response to the lung cancer polypeptide encoded by the DNA vaccine. Additional or alternative adjuvants are available.

In another preferred embodiment lung cancer genes find use in generating animal models of lung cancer. When the lung cancer gene identified is repressed or diminished in metastatic tissue, gene therapy technology, e.g., wherein antisense or inhibitory RNA directed to the lung cancer gene will also diminish or repress expression of the gene. Animal models of lung cancer find use in screening for modulators of a lung cancer-associated sequence or modulators of lung cancer. Similarly, transgenic animal technology including gene knockout technology, e.g., as a result of homologous recombination with an appropriate gene targeting vector, will result in the absence or increased expression of the lung cancer protein. When desired, tissue-specific expression or knockout of the lung cancer protein may be necessary.

It is also possible that the lung cancer protein is overexpressed in lung cancer. As such, transgenic animals can be generated that overexpress the lung cancer protein. Depending on the desired expression level, promoters of various strengths can be employed to express the transgene. Also, the number of copies of the integrated transgene can be determined and compared for a determination of the expression level of the transgene.



Animals generated by such methods will find use as animal models of lung cancer and are additionally useful in screening for modulators to treat lung cancer.

### **Kits for Use in Diagnostic and/or Prognostic Applications**

5           For use in diagnostic, research, and therapeutic applications suggested above, kits are also provided by the invention. In diagnostic and research applications such kits may include at least one of the following: assay reagents, buffers, lung cancer-specific nucleic acids or antibodies, hybridization probes and/or primers, antisense polynucleotides, ribozymes, RNAi, dominant negative lung cancer polypeptides or polynucleotides, small molecule inhibitors of  
10 lung cancer-associated sequences, etc. A therapeutic product may include sterile saline or another pharmaceutically acceptable emulsion and suspension base.

          In addition, the kits may include instructional materials containing instructions (e.g., protocols) for the practice of the methods of this invention. While the instructional materials typically comprise written or printed materials they are not limited to such. A medium  
15 capable of storing such instructions and communicating them to an end user is contemplated by this invention. Such media include, but are not limited to electronic storage media (e.g., magnetic discs, tapes, cartridges, chips), optical media (e.g., CD ROM), and the like. Such media may include addresses to internet sites that provide such instructional materials.

          The present invention also provides for kits for screening for modulators of lung  
20 cancer-associated sequences. Such kits can be prepared from readily available materials and reagents. For example, such kits can comprise one or more of the following materials: a lung cancer-associated polypeptide or polynucleotide, reaction tubes, and instructions for testing lung cancer-associated activity. Optionally, the kit contains biologically active lung cancer protein. A wide variety of kits and components can be prepared according to the present  
25 invention, depending upon the intended user of the kit and the particular needs of the user. Diagnosis would typically involve evaluation of a plurality of genes or products. The genes typically will be selected based on correlations with important parameters in disease which may be identified in historical or outcome data.



## EXAMPLES

## Example 1: Gene Chip Analysis

5 Molecular profiles of various normal and cancerous tissues were determined and analyzed using gene chips. RNA was isolated and gene chip analysis was performed as described (Glynne, et al. (2000) Nature 403:672-676; Zhao, et al. (2000) Genes Dev. 14:981-993).



Tables 1A and 1B were previously filed on April 18, 2001 in USSN 60/284,770 (18501-001500US) and on November 29, 2001 in USSN 60/334,370 (18501-001520US)

5	Table 1A				70% chron/90% NL	70% SQAD/90% NL
	Pkey	ExAccn	UnigenelD	Unigene Title		
	100134	D13264	Hs.49	macrophage scavenger receptor 1	1.61	0.74
	100780	HG3731-HT4001		***Immunoglobulin Heavy Chain, VdJrc Reg	2.68	3.28
10	100971	J02874	Hs.83213	fatty acid binding protein 4; adipocyte	1.96	0.14
	101088	L05568	Hs.553	solute carrier family 6 (neurotransmitte	0.79	0.07
	101102	L07594	Hs.79059	transforming growth factor; beta recepto	2.55	1
	101168	L15388	Hs.211569	G protein-coupled receptor kinase 5	0.88	0.27
	101277	L38486	Hs.118223	microfibrillar-associated protein 4	0.89	0.26
15	101330	L43821	Hs.80261	enhancer of filamentation 1 (cas-like do	0.59	0.29
	101336	L49169	Hs.75678	FBJ murine osteosarcoma viral oncogene h	1.15	0.41
	101345	L76380	Hs.152175	calcitonin receptor-like	0.81	0.31
	101678	M62505	Hs.2161	complement component 5 receptor 1 (C5a I	1.31	0.77
	101764	M80563	Hs.81256	S100 calcium-binding protein A4 (calcium	1.44	0.82
20	101771	M81750	Hs.153837	myeloid cell nuclear differentiation ant	0.96	0.45
	101842	M93221	Hs.75182	mannose receptor; C type 1	1.27	0.37
	102283	U31384	Hs.83381	guanine nucleotide binding protein 11	1.04	0.3
	102363	U39447	Hs.198241	amine oxidase; copper containing 3 (vasc	0.96	0.26
	102507	U52154	Hs.193044	potassium inwardly-rectifying channel; s	2.81	3.45
	102698	U75272	Hs.1867	progastricsin (pepsinogen C)	0.95	0.23
25	103025	X54131	Hs.123641	protein tyrosine phosphatase; receptor t	1.62	0.21
	103280	X79981	Hs.76206	cadherin 5; VE-cadherin (vascular epithe	0.9	0.41
	103496	Y09267	Hs.132821	flavin containing monooxygenase 2	1.27	0.49
	103541	Z11697	Hs.79197	CD83 antigen (activated B lymphocytes; i	1.86	1
30	103554	Z18951	Hs.74034	caveolin 1; caveolae protein; 22kD	1.27	0.47
	104212	AB002298	Hs.173035	KIAA0300 protein	1.17	0.16
	104691	AA011176	Hs.37744	ESTs	1.08	0.35
	104825	AA035613	Hs.141883	ESTs	0.75	0.27
	104857	AA043219	Hs.19058	ESTs	2.6	3.3
35	104865	AA045136	Hs.22575	ESTs	1.23	0.49
	104989	AA102098	Hs.118615	ESTs	0.63	0.32
	105729	AA292694	Hs.3807	ESTs; Weakly similar to PHOSPHOLEMMAN PR	0.86	0.34
	105847	AA398606	Hs.32241	ESTs	1.32	0.4
	105894	AA400979	Hs.25691	calcitonin receptor-like receptor activi	0.78	0.28
40	106490	AA451861	Hs.115537	ESTs; Weakly similar to dipeptidase prec	1.2	0.47
	106536	AA453997	Hs.23804	ESTs	0.82	0.15
	106605	AA457718	Hs.21103	Homo sapiens mRNA; cDNA DKFZp564B076 (fr	0.99	0.07
	106667	AA461086	Hs.16578	ESTs	1.17	0.4
	106773	AA478109	Hs.188833	ESTs	1.46	0.43
45	106797	AA478962	Hs.169943	ESTs	1.18	0.32
	106844	AA485055	Hs.158213	sperm associated antigen 6	0.98	0.51
	106870	AA487576	Hs.26530	serum deprivation response (phosphatidyl	1.05	0.14
	106954	AA496980	Hs.204038	ESTs	1.25	0.33
	107054	AA600150	Hs.14366	ESTs	1.11	0.4
50	107292	T30407	Hs.4789	ESTs; Weakly similar to oxidative-stress	1.07	2.58
	107994	AA036811	Hs.165030	ESTs	0.7	0.21
	107997	AA037388	Hs.82223	Human DNA sequence from clone 141H5 on c	1.02	0.48
	108041	AA041552	Hs.61957	ESTs	1.44	0.51
	108087	AA045709	Hs.40545	ESTs	1.98	1
55	108382	AA074885	Hs.67726	macrophage receptor with collagenous str	1.52	0.72
	108435	AA078787	Hs.194101	ESTs	2.53	1.53
	108480	AA081093	Hs.68055	ESTs	1.56	0.48
	109252	AA194830	Hs.85944	ESTs	2.69	3.18
	109550	F01534	Hs.26981	ESTs	1.19	0.65
60	109613	F03031	Hs.27519	ESTs	1.01	0.29
	109837	H00656	Hs.29792	ESTs	0.81	0.15
	109893	H04768	Hs.30484	ESTs	1.44	0.32
	109984	H09594	Hs.10299	ESTs	0.62	0.14
	110099	H16568	Hs.23748	ESTs	1.01	0.28
65	110837	N30796	Hs.17424	ESTs; Weakly similar to semaphorin F [H.	1.1	0.22
	111247	N69825	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	1.26	0.26
	111341	N80935	Hs.22483	ESTs	1.57	0.52
	111510	R07856	Hs.16355	ESTs	3.96	1
	111737	R25410	Hs.9218	ESTs	0.97	0.24
70	113195	T57112		***yc20g11.s1 Stratagene lung (#937210)	1.22	0.35
	113238	T62979	Hs.189813	ESTs	2.27	0.45
	113540	T90496	Hs.16757	ESTs	1.06	0.22
	113552	T90889	Hs.16026	ESTs	1.16	0.42
	113606	T93093	Hs.17125	ESTs	1.48	0.7
75	113695	T96965	Hs.17948	ESTs	1.54	0.28
	113946	W84753	Hs.37896	ESTs	1.79	0.72
	114251	Z39898	Hs.21948	ESTs	1.95	0.25
	114359	Z41589	Hs.153483	ESTs; Moderately similar to H1 chloride	1.42	0.13
	115230	AA278300	Hs.182980	ESTs	2.62	0.42
80	115279	AA279760	Hs.63671	ESTs	1.79	0.91
	115566	AA398083	Hs.43977	ESTs	0.86	0.2
	115965	AA446661	Hs.173233	ESTs	0.79	0.04
	116166	AA461556	Hs.202949	KIAA1102 protein	2.29	0.68
	116279	AA486073	Hs.57362	ESTs	2.27	0.78
	117023	H88157	Hs.41105	ESTs	1.36	0.16



	117209	H99959	Hs.42768	ESTs	1.46	0.48
	118901	N90719	Hs.94445	ESTs	1.51	1
	118981	N93839	Hs.39288	ESTs	1.34	0.48
5	119073	R32894	Hs.45514	v-els avian erythroblastosis virus E26 o	1.14	0.27
	119221	R98105		***yr30g11.s1 Soares fetal liver spleen	1.32	0.53
	119824	W74536	Hs.184	advanced glycosylation end product-speci	1	0.19
	119861	W80715		ESTs; Moderately similar to !!!! ALU SUB	1.83	0.45
	120041	W92775	Hs.59368	ESTs	1.23	0.55
10	120132	Z38839	Hs.125019	ESTs; Highly similar to KIAA0886 protein	0.91	0.37
	120467	AA251579	Hs.187628	ESTs	1.87	1.91
	121314	AA402799	Hs.182538	ESTs	1.3	0.31
	121643	AA417078	Hs.193767	ESTs	2.31	0.68
	121690	AA418074	Hs.110286	ESTs	1.47	0.51
15	122633	AA454080	Hs.34853	inhibitor of DNA binding 4; dominant neg	1.31	0.63
	123978	C20653	Hs.170278	ESTs	1.52	0.32
	124214	H58608	Hs.151323	ESTs	0.93	0.35
	124357	N22401		***yw37g07.s1 Morton Fetal Cochlea Homo	1.29	1
	124438	N40188	Hs.102550	ESTs	1.36	0.7
20	125167	W45560	Hs.102541	ESTs	1.46	0.69
	125174	W51835	Hs.231082	EST	3.07	3.76
	125422	AA903229	Hs.153717	ESTs	1.34	0.3
	125561	AI417667	Hs.22978	ESTs	1.89	0.63
	125831	D60988		***HUM145B09B Clontech human fetal brain	0.94	0.36
25	127002	R35380	Hs.24979	ESTs	3.02	4.06
	127307	AA369367	Hs.126712	ESTs; Weakly similar to pIL2 hypothetica	1.01	0.69
	127609	AA622559	Hs.150318	ESTs	1.21	0.32
	127959	AI302471	Hs.124292	ESTs	2.5	1
	128458	D52193	Hs.56340	ESTs	1.13	0.33
30	128624	AA479209	Hs.102647	ESTs	1.45	0.58
	128789	AA486567	Hs.105895	ESTs	1.1	0.34
	128798	AF014958	Hs.105938	chemokine (C-C motif) receptor-like 2	1.16	0.55
	128952	R51076	Hs.107361	ESTs; Highly similar to Rap2 interacting	2.04	2.4
	129057	X62466	Hs.214742	CDW52 antigen (CAMPATH-1 antigen)	1.77	0.73
35	129210	AA401654	Hs.202949	KIAA1102 protein	1.11	0.36
	129240	W24360	Hs.237868	interleukin 7 receptor	0.91	0.41
	129402	T63781		***yc21g01.s1 Stratagene lung (#937210)	1.36	0.43
	129565	X77777	Hs.198726	vasoactive intestinal peptide receptor 1	0.67	0.08
40	129593	AA487015	Hs.98314	Homo sapiens mRNA; cDNA DKFZp586L0120 (f	1.3	0.42
	129626	AA447410	Hs.11712	ESTs; Weakly similar to !!!! ALU SUBFAM1	1.28	0.46
	129699	AA458578	Hs.12017	KIAA0439 protein; homolog of yeast ubiqu	1.58	1
	129898	N48595	Hs.13256	ESTs	1.13	0.53
	129958	L20591	Hs.1378	annexin A3	0.81	0.31
45	130273	U59914	Hs.153863	MAD (mothers against decapentaplegic; Dr	0.59	0.22
	130655	N92934	Hs.17409	cysteine-rich protein 1 (intestinal)	1.44	0.76
	130657	T94452	Hs.201591	ESTs	0.96	0.42
	131061	N64328	Hs.22567	ESTs; Moderately similar to HYPOTHETICAL	1.51	0.45
	131066	F09006	Hs.22588	ESTs	0.97	0.37
	131263	R38334	Hs.24950	regulator of G-protein signalling 5	2.34	2.82
50	131589	U52100	Hs.29191	epithelial membrane protein 2	1.2	0.62
	131686	AA157428	Hs.30687	Grb2-associated binder 2	0.95	0.38
	131751	H18335	Hs.31562	ESTs	1.47	0.52
	132430	T23630	Hs.258675	EST	1.86	2.09
	132476	N67192	Hs.49476	Homo sapiens clone TUA8 Cri-du-chat regi	1.73	0.58
55	132836	F09557	Hs.57929	slit (Drosophila) homolog 3	0.91	0.29
	133120	X64559	Hs.65424	telranectin (plasminogen-binding protein	0.82	0.2
	133488	D45370	Hs.74120	adipose specific 2	1.29	0.48
	133565	H57056	Hs.204831	ESTs	2.25	0.57
	133651	U97105	Hs.173381	dihydropyrimidinase-like 2	1.65	0.62
60	133835	AA059489	Hs.76640	ESTs; Highly similar to RGC-32 [R.norveg	1.16	0.34
	133978	W73859	Hs.78061	transcription factor 21	0.79	0.27
	133985	L34657	Hs.78146	platelet/endothelial cell adhesion molec	0.99	0.28
	134299	AA487558	Hs.8135	ESTs	1.02	0.46
	134300	U81984	Hs.166082	endothelial PAS domain protein 1	0.86	0.42
65	134323	AA028976	Hs.8175	Homo sapiens mRNA; cDNA DKFZp564M0763 (f	1.19	0.27
	134343	D50683	Hs.82028	transforming growth factor; beta recepto	1.21	0.67
	134417	D87969	Hs.82921	solute carrier family 35 (CMP-sialic aci	1.28	1
	134561	U76421	Hs.85302	adenosine deaminase; RNA-specific; B1 (h	2.12	0.55
	134624	W67147	Hs.8700	deleted in liver cancer 1	2.35	2.74
70	134696	H88354	Hs.8861	ESTs	1.35	0.33
	134749	L10955	Hs.89485	carbonic anhydrase IV	0.89	0.2
	134786	L06139	Hs.89640	TEK tyrosine kinase; endothelial (venous	0.48	0.21
	134869	T35288	Hs.90421	ESTs; Moderately similar to !!!! ALU SUB	2.14	2.64
	135346	M21056	Hs.992	phospholipase A2; group IB (pancreas)	0.63	0.13
75	100113	D00591	Hs.84746	Chromosome condensation 1	1	2.15
	100147	D13666	Hs.136348	Homo sapiens mRNA for osteoblast specifi	0.5	2
	100280	D42085	Hs.155314	KIAA0095 gene product	1.02	1.39
	100335	D63391	Hs.6793	platelet-activating factor acetylhydrola	1	5.58
	100360	D78335	Hs.75939	Uridine monophosphate kinase	0.91	2.04
80	100372	D79997	Hs.184339	KIAA0175 gene product	0.75	2.03
	100486	HG1112-HT1112		TIGR: ras-like protein TC4	1.09	1.93
	100559	HG2197-HT2267		*collagen, type VII, alpha 1*	0.97	3.6
	100576	HG2290-HT2386		*calcitonin/alpha-CGRP, alt. transcript	1	1
	100668	HG2981-HT3938		*TIGR: CD44 (epican, alt. transcript 12	0.85	1.9
	100906	HG4716-HT5158		Guanosine 5'-Monophosphate Synthase	1.18	2.29
85	100930	HG721-HT4827		*TIGR: placental protein 14, endometrial	1	1.45



	100960	J00124	Hs.117729	keratin 14 (epidermolysis bullosa simple	0.84	2.6
	101031	J05070	Hs.151738	"Matrix metalloproteinase 9 (gelatinase	0.77	1.52
	101111	L08424	Hs.1619	Achaete-scute complex (Drosophila) homol	1	1
5	101124	L10343	Hs.112341	"Protease inhibitor 3, skin-derived (SKA	0.62	2.67
	101175	L18920	Hs.36980	"Melanoma antigen, family A, 2"	1	1
	101204	L24203	Hs.82237	Ataxia-telangiectasia group D-associated	0.74	4.1
	101431	M19888	Hs.1076	Small proline-rich protein 1B (cornifin)	0.85	2.51
	101448	M21389	Hs.195850	keratin 5 (epidermolysis bullosa simplex	0.61	8.83
10	101511	M27826	Hs.267319	Endogenous retroviral protease	1.03	1.13
	101526	M29540	Hs.220529	Carcinoembryonic antigen-related cell ad	1.07	4.61
	101548	M31328	Hs.71642	"Guanine nucleotide binding protein (G p	0.97	1.13
	101625	M57293		"Human parathyroid hormone-related pepti	1	1
	101649	M60047	Hs.1690	Heparin-binding growth factor binding pr	1	2.7
15	101724	M69225	Hs.620	bulbous pemphigoid antigen 1 (230/240kD)	1	8.98
	101748	M76482	Hs.1925	Desmoglein 3 (pemphigus vulgaris antigen	1	2.78
	101759	M80244	Hs.184601	"Solute carrier family 7 (cationic amino	1.07	2.45
	101804	M86699	Hs.169840	TTK protein kinase	1	1
	101806	M86757	Hs.112408	S100 calcium-binding protein A7 (psorias	0.74	1.76
20	101809	M86849		"Homo sapiens connexin 26 (GJB2) mRNA, c	1	7
	101845	M93426	Hs.78867	"Protein tyrosine phosphatase, receptor-	1	1
	101851	M94250	Hs.82045	Midkine (neurite growth-promoting factor	1.13	2.6
	102083	U10323	Hs.75117	"Interleukin enhancer binding factor 2,	1.03	1.61
25	102154	U17760	Hs.75517	"Laminin, beta 3 (nicein (125kD), kalini	0.94	3.62
	102193	U20758	Hs.313	secreted phosphoprotein 1 (osteopontin;	0.34	4.59
	102305	U33286	Hs.90073	chromosome segregation 1 (yeast homolog)	1.45	2.97
	102348	U37519	Hs.87539	Aldehyde dehydrogenase 8	0.52	2.25
	102581	U61145	Hs.77256	Enhancer of zeste (Drosophila) homolog 2	0.91	2.46
	102610	U65011	Hs.30743	Preferentially expressed antigen in mela	1	3.88
30	102623	U66083	Hs.37110	"Melanoma antigen, family A, 9 (MAGE-9)"	1	1
	102669	U71207	Hs.29279	Eyes absent (Drosophila) homolog 2	1	1
	102696	U74612	Hs.239	Forkhead box M1	1.06	2.77
	102829	U91618	Hs.80962	Neurotensin	1	1
35	102888	X04741	Hs.76118	Ubiquitin carboxyl-terminal esterase L1	1.13	2.59
	102913	X07696	Hs.80342	keratin 15	0.7	4.72
	102915	X07820	Hs.2258	Matrix Metalloproteinase 10 (Stromolysin	1.15	3.35
	102963	X15943	Hs.37058	"Calcitonin/calcitonin-related polypepti	1	1
	103021	X53587	Hs.85266	"Integrin, beta 4"	1.38	2.34
40	103036	X54925	Hs.83169	Matrix metalloprotease 1 (interstitial c	1	14.93
	103058	X57348	Hs.184510	Stratillin	1.25	4.17
	103060	X57766	Hs.155324	matrix metalloproteinase 11 (stromelysin	1	1.72
	103119	X63629	Hs.2877	"Cadherin 3, P-cadherin (placental)"	1.16	7.38
	103206	X72755	Hs.77367	monokine induced by gamma interferon	0.71	1.48
45	103242	X76342	Hs.389	"Alcohol dehydrogenase 7 (class IV), mu	1	1
	103312	X82693	Hs.3185	"Lymphocyte antigen 6 complex, locus D;	0.92	1.28
	103478	Y07755	Hs.38991	S100 calcium-binding protein A2	1.05	5.81
	103558	Z19574	Hs.2785	keratin 17	0.65	6.68
	103576	Z26317	Hs.2631	Desmoglein 2	0.79	1.73
	103587	Z29083	Hs.82128	5T4 Oncofetal antigen	1	3.93
50	103594	Z31560	Hs.816	"SRY (sex determining region Y)-box 2, p	0.71	7.23
	103768	AA089997		"ESTs, Highly similar to integral membra	0.99	1.8
	104158	AA454908	Hs.8127	KIAA0144 gene product	0.96	1.29
	104558	R56678	Hs.88959	Human DNA sequence from clone 967N21 on	1.23	7.23
	104689	AA010665		ESTs	0.96	2.11
55	104733	AA019498	Hs.23071	ESTs	1.18	1.88
	104906	AA055809	Hs.26802	Protein kinase domains containing protei	1.11	3.15
	104978	AA088458	Hs.19322	ESTs; Weakly similar to !!!! ALU SUBFAM1	1.64	2.89
	105012	AA116036	Hs.9329	"Homo sapiens mRNA for fls353, complete	1.19	3.91
	105175	AA186804	Hs.25740	ESTs; Weakly similar to unknown [S.cerev	0.9	4.63
60	105263	AA227926	Hs.6682	ESTs	0.95	2.87
	105298	AA233459	Hs.26369	ESTs	1	1.13
	105312	AA233854	Hs.23348	S-phase kinase-associated protein 2 (p45	1.32	3.01
	105719	AA291644	Hs.36793	Hypothetical protein FLJ23188	1.28	2.31
	105743	AA293300	Hs.9598	ESTs	1	1
65	106012	AA411621	Hs.8895	ESTs; same as BFH67	0.94	2.04
	106231	AA429571	Hs.38002	KIAA1355 protein	1.04	1.5
	106540	AA454607	Hs.38114	Hypothetical protein FLJ11100	1.26	2.26
	106575	AA456039	Hs.105421	ESTs	1	2
70	106632	AA459897	Hs.11950	GPI-anchored metastasis-associated prote	0.87	1.32
	106727	AA465342	Hs.34045	Hypothetical protein FLJ20764	0.87	1.59
	106906	AA490237	Hs.222024	Transcription factor BMAL2 (cycle-like f	0.61	1.6
	107059	AA608545	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re	0.48	2.67
	107104	AA609786	Hs.15243	Nucleolar protein 1 (120kD)	1.01	1.44
75	107151	AA621169	Hs.8687	ESTs; procollagen I-N proteinase	0.97	2.89
	107284	S74039	Hs.291904	Accessory proteins BAP31/BAP29	1.15	3.65
	107901	AA026418	Hs.91539	ESTs	0.72	3.44
	107922	AA028028	Hs.61460	Ig superfamily receptor LNIR precursor	1	2.48
	107932	AA029317	Hs.18878	Hypothetical protein FLJ21620	1	1
	108695	AA121315	Hs.70823	KIAA1077 protein	0.91	3.53
80	108857	AA133250	Hs.62180	ESTs	1	1
	108860	AA133334	Hs.129911	ESTs	0.73	7.3
	108990	AA152296	Hs.72045	ESTs	1	1
	109166	AA179845	Hs.73625	"RAB6 interacting, kinesin-like (rabkine	1	4.55
	109424	AA227919	Hs.85962	Hyaluronan synthase 3	1	1.28
85	109665	F05012	Hs.27027	Hypothetical protein DKFZp762H1311	1.42	2
	109970	H09281	Hs.13234	ESTs	1.13	2.16



	110015	H10998	Hs.7164	A disintegrin and metalloproteinase doma	0.84	1.95
	110156	H18957	Hs.4213	ESTs	0.94	1.41
	110561	H59617	Hs.5199	HSPC150 protein similar to ubiquitin-con	0.91	3.18
5	111223	N68921	Hs.34806	ESTs; Weakly similar to neogenin [H.sapi	0.91	3.13
	111345	N89820	Hs.14559	Hypothetical protein FLJ10540	1	1.25
	111876	R38239	Hs.293246	*ESTs, Weakly similar to putative p150 [	0.83	1.27
	111902	R39191	Hs.109445	KIAA1020 protein	0.91	0.91
	112244	R51309	Hs.70823	KIAA1077 protein	0.77	3.01
10	112973	T17271		*cDNA FLJ13308 fis, clone OVARC1001436,	1	1
	112989	T23482	Hs.89981	*Diacylglycerol kinase, zeta (104kd)*	0.55	1.03
	113047	T25867	Hs.7549	ESTs	0.87	2
	113095	T40920	Hs.126733	ESTs	1	1
	113531	T90345	Hs.16740	Hypothetical protein FLJ11036	0.42	1.44
15	113970	W86748	Hs.8109	ESTs	1.17	1.73
	114346	Z41450	Hs.130489	*ATPase, aminophospholipid transporter-I	0.86	0.82
	114407	AA010188	Hs.103305	ESTs	0.8	1.88
	114471	AA028074	Hs.104613	RP42 homolog	1.06	1.34
	114509	AA043551	Hs.101799	KIAA1350 protein	1.82	2.32
20	115060	AA253214	Hs.198249	*Gap junction protein, beta 5 (connexin	0.79	1.49
	115091	AA255900	Hs.184523	KIAA0965 protein	0.72	1.92
	115123	AA256642	Hs.236894	*ESTs, High sim to LRP1_hu low density I	0.59	1.97
	115291	AA279943	Hs.122579	ESTs	1	1.25
	115506	AA292537	Hs.45207	Hypothetical protein KIAA1335	1.15	1.48
25	115522	AA331393	Hs.47378	ESTs	0.5	3.29
	115536	AA347193	Hs.62180	ESTs	1	1
	115697	AA411502	Hs.63325	Homo sapiens type II membrane serine pro	1	6.53
	115909	AA436666	Hs.59761	ESTs	1	6.98
	115978	AA447522	Hs.69517	Differentially expressed in Fanconi anem	1	2.31
30	116028	AA452112	Hs.42644	thioredoxin-like	0.99	1.68
	116107	AA456968	Hs.92030	ESTs	1.14	1.8
	116134	AA460246	Hs.50441	CGI-04 protein	1.11	1.86
	116157	AA461063	Hs.44298	Hypothetical protein	0.99	1.9
	116158	AA461187	Hs.61762	Hypoxia-inducible protein 2	0.44	0.86
35	116335	AA495830	Hs.87013	*Homo sapiens cDNA FLJ10238 fis, clone H	0.62	3.89
	116483	C14092	Hs.76118	Ubiquitin carboxyl-terminal esterase L1	1.04	2.36
	117320	N23239	Hs.211092	LUNX protein; PLUNC(palate lung & nasal	0.51	0.64
	117557	N33920	Hs.44532	Diubiquitin	1.11	2.63
	117693	N40939	Hs.112110	PTD007 protein	0.98	1.79
40	117881	N50073	Hs.260622	Butyrate-induced transcript 1	1	1.43
	118368	N64339	Hs.48956	ESTs	0.67	2.86
	118566	N68558	Hs.42824	Hypothetical protein FLJ10718	1.21	0.83
	118695	N71781	Hs.50081	KIAA1199 see CVA7.doc	0.88	1.63
	119780	W72967	Hs.191381	ESTs; Weakly similar to hypothetical pro	1	1
45	119845	W79920	Hs.58561	G protein-coupled receptor 87	1	1
	120102	W95428	Hs.132927	*ESTs, Moderately similar to p53 regulat	1	1
	120104	W95477	Hs.180479	ESTs	0.69	3.07
	120486	AA253400	Hs.137569	Tumor protein 63 kDa with strong homolog	1.08	12.05
	120859	AA350158	Hs.1619	Achaete-scute complex (Drosophila) homol	1	1
50	120880	AA360240	Hs.97019	EST	1	1
	120948	AA397822	Hs.104650	Hypothetical protein FLJ10292	1.04	2.15
	120983	AA398209	Hs.97587	EST	1	1
	121362	AA405500	Hs.97932	Chondromodulin I precursor	1	1
	121369	AA405657	Hs.128791	CGI-09 protein	1	1.8
55	121791	AA423978	Hs.293317	*ESTs, Weakly similar to JM27 [H.sapiens	1	1
	123005	AA479726	Hs.105577	ESTs	1	1
	123044	AA481549	Hs.130881	B-cell CLL/lymphoma 11A (zinc finger pro	0.95	1.88
	123160	AA488687	Hs.284235	ESTs	1.59	4.98
	123479	AA599469	Hs.135056	clone RP5-850E9 on chromosome 20	1.19	1.64
60	123571	AA608956	Hs.112619	*ESTs, Weakly similar to PQ0109 Purkinje	1.03	1.14
	123829	AA620697	Hs.112208	XAGE-1 protein	1.39	2.2
	124006	D60302	Hs.108977	ESTs	1	4.85
	124059	F13673	Hs.99769	ESTs	1.49	8.62
	124960	T15386	Hs.194766	Seizure related gene 6 (mouse)-like	0.76	0.77
65	125218	W73561	Hs.110024	NADH:ubiquinone oxidoreductase MLRQ subu	1.33	1.77
	125453	R06041	Hs.18048	*Melanoma antigen, family A, 10*	0.8	1.42
	125759	AA425587	Hs.82226	Glycoprotein (transmembrane) nmb	1.52	2.26
	125972	AA434562	Hs.35406	*ESTs, Highly similar to unnamed protein	1.05	2.48
	125994	H55782	Hs.270799	EST	1	1.95
70	126395	N70192	Hs.278956	Hypothetical protein FLJ12929	1	1.35
	126645	AI167942	Hs.61635	STEAP1 (Homo sapiens BAC clone RG041D11	1	2.23
	127221	AI354332	Hs.72365	ESTs	0.73	3.27
	127479	AA513722	Hs.179729	collagen; type X; alpha 1 (Schmid metaph	0.51	1.94
	128192	AI204246		KIAA1085 protein	1.8	3.16
75	128610	L38608	Hs.10247	activated leucocyte cell adhesion molecu	0.89	0.97
	128777	U46006	Hs.10526	Cysteine and glycine-rich protein 2	1	1
	128924	AA234962	Hs.26557	Plakophilin 3	1.3	2.97
	129041	H58873	Hs.169902	*Solute carrier family 2 (facilitated gl	0.84	2.04
	129099	H50398	Hs.108660	*ATP-binding cassette, sub-family C (CFT	0.87	1.04
80	129404	AA172056	Hs.111128	ESTs	1	1
	129466	L42583		*Genbank Homo sapiens keratin 6 isoform	0.72	12.67
	129605	S72493	Hs.115947	Keratin 16 (focal non-epidermolytic palm	0.92	1.5
	129628	U26727	Hs.1174	*Cyclin-dependent kinase inhibitor 2A (m	0.85	1.93
	130023	X13461	Hs.239600	Calmodulin-like 3	0.84	1.22
	130080	X14850	Hs.147097	*H2A histone family, member X*	0.98	1.96
85	130385	AA126474	Hs.155223	stanniocalcin 2	1	1



	130410	V01514	Hs.155421	Alpha-fetoprotein	0.63	0.63
	130441	U35835	Hs.301387	"Human DNA-PK mRNA, partial cds"	1.15	3.65
	130482	L32866	Hs.1578	Baculoviral IAP repeat-containing 5 (sur	1	1.88
5	130553	AA430032	Hs.252587	Pituitary tumor-transforming 1	0.92	1.96
	130577	M35410	Hs.162	Insulin-like growth factor binding prote	1.17	4.7
	130627	L23808	Hs.1695	Matrix metalloproteinase 12 (macrophage	0.69	4.05
	130800	AA223386	Hs.19574	ESTs; Weakly similar to katanin p80 subu	1.13	2.41
	130939	AA598689	Hs.21400	ESTs	0.8	0.89
10	131046	X02530	Hs.2248	INTERFERON-GAMMA INDUCED PROTEIN PRECURS	0.8	1.15
	131244	D38076	Hs.24763	RAN binding protein 1	1.13	1.85
	131877	J04088	Hs.156346	Topoisomerase (DNA) II alpha (170kD)	1	1
	131927	AA461549	Hs.34780	"Doublecortex; lissencephaly, X-linked (	0.81	0.62
	131965	W90146	Hs.35962	ESTs	0.74	3.27
15	131978	D80008	Hs.36232	KIAA0186 gene product	1	1
	132354	L05187	Hs.211913	Small proline-rich protein 1A	0.69	1.43
	132543	AA417152	Hs.5101	ESTs; Highly similar to protein regulati	0.79	4.27
	132632	N59764	Hs.5398	guanine-monophosphate synthetase	1	1.08
	132653	U31201	Hs.54451	"laminin gamma2 chain gene (LAMC2), exon	1	1
20	132659	Z75190	Hs.54481	"Low density lipoprotein receptor-relate	0.89	0.89
	132710	W93726	Hs.55279	"Serine (or cysteine) proteinase inhibit	0.64	4.41
	132758	W52432	Hs.56105	"ESTs, Weakly similar to WDNM RAT WDNM1	1.55	2.08
	132767	L05188	Hs.231622	Small proline-rich protein 2B	0.83	1.66
	132816	M74542	Hs.575	Aldehyde dehydrogenase 3	0.55	0.55
25	132990	AA458761	Hs.18387	transcription factor AP-2 alpha (activat	1	3.53
	133070	U69611	Hs.64311	"A disintegrin and metalloproteinase dom	1.16	2
	133282	U52960	Hs.286145	"SRB7 (suppressor of RNA polymerase B, y	1	2.7
	133317	AA215299	Hs.70830	U6 snRNA-associated Sm-like protein LSM7	0.95	1.42
	133370	AA156897	Hs.72157	Homo sapiens mRNA; cDNA DKFZp56411922	1.12	2.55
30	133391	X57579	Hs.727	H.sapiens activin beta-A subunit (exon 2	1.65	1.76
	133832	H03387	Hs.241305	estrogen-responsive B box protein (EBBP)	1.02	1.39
	134032	Z81326	Hs.78589	"Serine (or cysteine) proteinase inhibit	1	1
	134168	AA398908	Hs.181634	"Homo sapiens cDNA: FLJ23602 fis, clone	0.95	1.53
	134218	AA227480	Hs.80205	Pim-2 oncogene	1.36	2.48
35	134405	R67275	Hs.82772	""collagen, type XI, alpha 1""	0.76	2.86
	134453	X70683	Hs.83484	SRY (sex determining region Y)-box 4	1.89	3.78
	134470	X54942	Hs.83758	CDC28 protein kinase 2	1.82	4.11
	134645	U87459	Hs.167379	"Cancer/testis antigen (NY-ESO-1, CTAG1,	0.82	0.83
	134781	M17183	Hs.89626	Parathyroid hormone-like hormone	1	1
40	135002	U19147	Hs.272484	G antigen 6	1	1
	100040	M97935		AFFX control: STAT1	0.92	1.25
	101201	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin;	2.92	8.5
	101664	M60752	Hs.121017	H2A histone family; member A	1	1
	102025	U03911	Hs.78934	mutS (E. coli) homolog 2 (colon cancer;	0.8	1.61
45	102031	U04898	Hs.2156	RAR-related orphan receptor A	1	1
	102221	U24576		LIM domain only 4	1	1
	102270	U30255	Hs.75888	phosphogluconate dehydrogenase	1.08	1.43
	102339	U37022	Hs.95577	cyclin-dependent kinase 4	0.88	1.32
	102391	U41668	Hs.77494	deoxyguanosine kinase	1.07	1.58
50	103000	X51956	Hs.146580	enolase 2; (gamma; neuronal)	0.91	1.49
	103395	X94754	Hs.119503	methionine-tRNA synthetase	0.89	1.32
	105638	AA281599	Hs.20418	Homo sapiens mRNA for histone H2B; c	0.91	1.25
	105726	AA292328	Hs.9754	activating transcription factor 5	0.94	1.48
	114841	AA234722	Hs.55408	ESTs; Moderately similar to CALCIUM-DEPE	0.78	1.56
55	115206	AA262491	Hs.186572	ESTs	1	1
	115906	AA436616	Hs.82302	ESTs	0.74	2.52
	119132	R49046	Hs.107911	ATP-binding cassette; sub-family B (MDR/	1.1	1.51
	124163	H30539	Hs.189838	ESTs	1	1
	126487	AA482505	Hs.184601	solute carrier family 7 (cationic amino	1.01	1.46
60	127141	AA307960	Hs.75478	KIAA0956 protein	0.85	1.4
	128034	AA905754	Hs.75103	tyrosine 3-monooxygenase/tryptophan 5-mo	1	1.18
	128609	AA234365	Hs.102456	survival of motor neuron protein interac	1	1.5
	128895	R37753	Hs.106985	ESTs	1.7	2
	130199	Z48579	Hs.172028	a disintegrin and metalloprotease domain	1	1
65	130524	U89995	Hs.159234	forkhead box E1	1	1
	133000	U24152	Hs.62402	p21/Cdc42/Rac1-activated kinase 1 (yeast	1	1
	133658	M25756	Hs.75426	secretogranin II (chromogranin C)	1	1
	135047	AA460466	Hs.93597	ESTs	1	1
70	100053	M27830		AFFX control: 28S ribosomal RNA	0.88	1.53
	100114	D00596	Hs.82962	thymidylate synthetase	0.68	1.86
	100128	D11094	Hs.61153	proteasome (prosome; macropain) 26S subu	1.29	2.03
	100154	D14657	Hs.81892	KIAA0101 gene product	0.71	4.26
	100161	D14694	Hs.77329	phosphatidylserine synthase 1	1.02	1.56
	100168	D14874	Hs.394	adrenomedullin	0.46	1.17
75	100187	D17793	Hs.78183	aldo-keto reductase family 1; member C3	1	1
	100188	D21063	Hs.57101	minichromosome maintenance deficient (S,	0.97	1.4
	100217	D26600	Hs.89545	proteasome (prosome; macropain) subunit;	1.13	1.9
	100220	D28364		""Human mRNA for annexin II, 5'UTR (seq	1.11	1.53
	100287	D43950	Hs.1600	chaperonin containing TCP1; subunit 5 (e	1.13	2.09
80	100297	D49489	Hs.182429	protein disulfide isomerase-related prot	0.92	1.78
	100330	D55716	Hs.77152	minichromosome maintenance deficient (S,	1.07	1.61
	100355	D78129		""Homo sapiens mRNA for squalene epoxid	0.96	1.87
	100364	D78586	Hs.154868	carbamoyl-phosphate synthetase 2; aspart	1.49	2.46
	100368	D79987	Hs.153479	extra spindle poles; S. cerevisiae; homo	0.59	1.32
	100398	D84557	Hs.155462	minichromosome maintenance deficient (mi	1.08	1.9
85	100438	D87448	Hs.91417	topoisomerase (DNA) II binding protein	1	2.15



	100455	D87953	Hs.75789	N-myc downstream regulated	0.91	1.48
	100491	HG1153-HT1153		Nucleoside Diphosphate Kinase Nm23-H2s	0.99	1.41
	100518	HG174-HT174		Desmoplakin I	1.28	3.17
5	100528	HG1828-HT1857		***Nexin, Glia-Derived***	0.68	1.9
	100661	HG2874-HT3018		Ribosomal Protein L39 Homolog	1.1	5.44
	100667	HG2981-HT3127		***Epican, Alt. Splice 11***	0.8	1.97
	100830	HG4074-HT4344		Rad2	1.01	2.12
	101061	K03515	Hs.944	glucose phosphate isomerase	0.91	1.79
10	101131	L10838	Hs.167460	splicing factor; arginine/serine-rich 3	1.23	1.87
	101162	L14595	Hs.174203	solute carrier family 1 (glutamate/neutr	1.35	2.73
	101181	L19686	Hs.73798	macrophage migration inhibitory factor (	1.03	1.78
	101183	L19779	Hs.795	H2A histone family; member O	0.57	1.3
	101216	L25876	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK	0.7	2.2
15	101228	L27706	Hs.82916	chaperonin containing TCP1; subunit 6A (	0.99	1.99
	101233	L29008	Hs.878	sorbitol dehydrogenase	0.82	2.11
	101247	L33801	Hs.78802	glycogen synthase kinase 3 beta	1.2	1.91
	101332	L47276		***Homo sapiens (cell line HL-6) alpha t	0.69	2.78
	101342	L76191	Hs.182018	interleukin-1 receptor-associated kinase	1.04	1.84
20	101366	M15796	Hs.78996	proliferating cell nuclear antigen	0.95	3.55
	101423	M18391	Hs.89839	EphA1	1	1.5
	101445	M21259	Hs.1066	small nuclear ribonucleoprotein polypept	1.21	1.96
	101505	M27396	Hs.75692	asparagine synthetase	0.93	1.6
	101525	M29536	Hs.12163	eukaryotic translation initiation factor	1.19	1.93
25	101535	M30448	Hs.251669	casein kinase 2; beta polypeptide	0.96	1.42
	101607	M38690	Hs.1244	CD9 antigen (p24)	1.11	1.25
	101624	M55998		***Human alpha-1 collagen type I gene, 3	1.17	1.98
	101758	M77836	Hs.79217	pyrroline-5-carboxylate reductase 1	1.77	3.45
	101839	M93036	Hs.692	membrane component; chromosomal 4; surfa	0.71	1.45
30	101853	M94362	Hs.76084	lamin B2	0.84	1.19
	101977	S83364		***putative Rab5-interacting protein (cl	0.89	1.9
	101992	U01038	Hs.77597	polo (Drosophila)-like kinase	0.66	1.46
	102009	U02680	Hs.82643	protein tyrosine kinase 9	1.23	3.35
	102012	U03057	Hs.118400	singed (Drosophila)-like (sea urchin fas	0.85	1.88
35	102039	U05861	Hs.201967	aldo-keto reductase family 1; member C1	0.93	2.32
	102123	U14518	Hs.1594	centromere protein A (17kD)	1	4.28
	102130	U15009	Hs.1575	small nuclear ribonucleoprotein D3 polyp	0.89	1.42
	102148	U16954	Hs.75823	ALL1-fused gene from chromosome 1q	0.8	2.95
	102210	U23028	Hs.2437	eukaryotic translation initiation factor	1.01	1.34
40	102220	U24389	Hs.65436	lysyl oxidase-like 1	1.15	2.34
	102260	U28386	Hs.159557	karyopherin alpha 2 (RAG cohort 1; impor	1.14	2.69
	102330	U35451	Hs.77254	chromobox homolog 1 (Drosophila HP1 beta	1.05	1.7
	102423	U44754	Hs.179312	small nuclear RNA activating complex; po	1.14	2.99
	102455	U48705	Hs.75562	discoidin domain receptor family; member	1.05	2.01
45	102499	U51478	Hs.76941	ATPase; Na+/K+ transporting; beta 3 poly	1.27	1.92
	102522	U53347	Hs.183556	solute carrier family 1 (neutral amino a	0.84	1.31
	102590	U62136		***Homo sapiens enterocyte differenti	1.11	1.6
	102676	U72514	Hs.12045	putative protein	1.04	2.17
	102687	U73379	Hs.93002	ubiquitin carrier protein E2-C	0.86	2.28
50	102704	U76638	Hs.54089	BRCA1 associated RING domain 1	1.12	1.63
	102781	U83843		***Human HIV-1 Nef interacting protein (	0.9	1.39
	102784	U85658	Hs.61796	transcription factor AP-2 gamma (activat	0.98	2.16
	102827	U91327	Hs.6456	chaperonin containing TCP1; subunit 2 (b	0.96	1.62
	102935	X13482	Hs.80506	small nuclear ribonucleoprotein polypept	1.21	4.2
55	102972	X16662	Hs.87268	annexin A8	1.25	2.32
	102983	X17620	Hs.118638	non-metastatic cells 1; protein (NM23A)	1.03	1.83
	103023	X53793	Hs.117950	multifunctional polypeptide similar to S	1.58	5.44
	103038	X54941	Hs.77550	CDC28 protein kinase 1	1.32	3.79
	103075	X59543	Hs.2934	ribonucleotide reductase M1 polypeptide	1.11	2.58
60	103168	X68314	Hs.2704	glutathione peroxidase 2 (gastrointestin	0.75	3.05
	103185	X69910	Hs.74368	transmembrane protein (63kD); endoplasm	1.01	1.97
	103212	X73874	Hs.2393	phosphorylase kinase; alpha 1 (muscle)	0.95	1.72
	103223	X74801	Hs.1708	chaperonin containing TCP1; subunit 3 (g	0.97	1.77
	103260	X78416	Hs.3155	casein; alpha	1	1
65	103262	X78565	Hs.204133	hexabrachion (tenascin C; cytotoxicin)	1.23	3.09
	103330	X85373	Hs.77496	small nuclear ribonucleoprotein polypept	1.12	2.25
	103364	X90872	Hs.75854	SULT1C sulfotransferase	2.85	4.62
	103375	X91868	Hs.54416	sine oculis homeobox (Drosophila) homolo	1	2.48
	103391	X94453	Hs.114366	pyrroline-5-carboxylate synthetase (glut	1	1.53
70	103404	X95586	Hs.78596	proteasome (prosome; macropain) subunit;	0.92	1.53
	103437	X98260	Hs.82254	M-phase phosphoprotein 11	0.92	1.54
	103448	X99133	Hs.204238	lipocalin 2 (oncogene 24p3)	0.55	0.96
	103605	Z35402	Hs.194657	cadherin 1; E-cadherin (epithelial)	1.32	2.51
	103646	Z68228	Hs.2340	junction plakoglobin	0.88	1.28
75	103658	Z74615	Hs.172928	collagen; type I; alpha 1	1.06	2.98
	103774	AA092898	Hs.92918	ESTs; Weakly similar to R07G3.8 [C.elega	1.88	4.66
	104261	AF008442	Hs.5409	RNA polymerase I subunit	0.87	2.17
	104276	C02193	Hs.85222	ESTs; Weakly similar to R27090_2 [H.sapi	1.4	2.49
	104289	C16281	Hs.75478	KIAA0956 protein	1.15	1.68
80	104434	L02870	Hs.1640	collagen; type VII; alpha 1 (epidermolys	1.04	1.49
	104453	M19169	Hs.123114	cystatin SN	0.38	0.76
	104611	R98280	Hs.125845	ribose-5-phosphate-3-epimerase	1.08	2.25
	104758	AA024661	Hs.7010	ESTs; Weakly similar to ACYL-COA DEHYDRO	1.14	1.65
	105114	AA156532	Hs.11801	adenosine A2b receptor pseudogene	0.91	1.38
85	105132	AA159501	Hs.247280	HBV associated factor	1.08	1.7
	105174	AA186613	Hs.34744	ESTs	0.95	2.05



	105280	AA232215	Hs.14600	ESTs	1	1.4
	105344	AA235303	Hs.8645	ESTs	0.72	2.02
	105516	AA257971	Hs.21214	ESTs	1.35	3.56
5	105621	AA280865	Hs.6375	Homo sapiens mRNA; cDNA DKFZp564K0222 (f	1.23	1.82
	105698	AA287393	Hs.15202	ESTs; Weakly similar to oligodendrocyte-	0.98	1.28
	105705	AA290767	Hs.101282	Homo sapiens mRNA; cDNA DKFZp434B102 (fr	0.92	1.32
	105724	AA292098	Hs.22934	ESTs; Weakly similar to ZINC FINGER PROT	0.99	1.41
	105782	AA350215	Hs.21580	ESTs	1	1
10	105799	AA372018	Hs.24743	ESTs	1.08	1.78
	105807	AA393803	Hs.16869	ESTs; Moderately similar to COLLAGEN ALP	0.95	1.34
	105891	AA400768	Hs.26662	ESTs; Weakly similar to tumor necrosis f	0.87	2.25
	105936	AA404338		ESTs	1.14	1.46
	106069	AA417741	Hs.29899	ESTs; Weakly similar to ZINC FINGER PROT	1	1
	106103	AA421104	Hs.12094	ESTs	1.04	1.44
15	106140	AA424524	Hs.14912	KIAA0286 protein	1.23	2.11
	106149	AA424881	Hs.256301	ESTs	0.83	1.48
	106154	AA425304	Hs.6994	ESTs	0.77	2.05
	106182	AA426609	Hs.10862	ESTs	0.74	2.23
20	106220	AA428582	Hs.32196	ESTs; Moderately similar to metargidin p	0.97	1.99
	106228	AA429290	Hs.17719	ESTs	0.99	1.54
	106318	AA436570	Hs.9605	pre-mRNA cleavage factor Im (25kD)	0.95	2.09
	106341	AA441798	Hs.5243	ESTs; Moderately similar to pL2 hypothe	0.98	2.66
	106432	AA448850	Hs.17138	ESTs	0.95	1.93
25	106474	AA450212	Hs.42484	Homo sapiens mRNA; cDNA DKFZp564C053 (fr	1	1
	106483	AA451676	Hs.30299	IGF-II mRNA-binding protein 2	1.4	2.29
	106599	AA457235	Hs.12842	ESTs; Moderately similar to non-function	1	1.82
	106611	AA458904	Hs.26267	ESTs; Weakly similar to torsinA [H.sapie	1.49	2.78
	106654	AA460449	Hs.3784	ESTs; Highly similar to phosphoserine am	1	1.4
30	107076	AA609145	Hs.21143	ESTs; Weakly similar to fos39554_1 [H.sa	1.11	1.49
	107115	AA610108	Hs.27693	ESTs; Highly similar to CGI-124 protein	1	1.03
	107129	AA620553	Hs.4756	flap structure-specific endonuclease 1	1.13	3.63
	107159	AA621340	Hs.10600	ESTs; Weakly similar to ORF YKR081c [S.c	1.05	2.09
	107444	W28391	Hs.5181	proliferation-associated 2G4; 38kD	1.18	1.9
35	107481	W58247	Hs.27437	Homo sapiens kinesin superfamily motor K	0.99	2.74
	107516	X56597	Hs.99853	fibrillarin	0.94	1.77
	107529	Y12065	Hs.5092	nucleolar protein (KKE/D repeat)	1.05	2.29
	107531	Y13936	Hs.17883	protein phosphatase 1G (formerly 2C); ma	1.06	1.62
40	107801	AA019433	Hs.173100	ESTs	1.03	1.4
	107957	AA031948	Hs.57548	ESTs	0.95	1.46
	108565	AA085342	Hs.1526	ATPase; Ca++ transporting; cardiac muscl	0.59	1.35
	108780	AA128561	Hs.117938	collagen; type XVII; alpha 1	1	7.63
	108828	AA131584	Hs.71435	DKFZP564O0463 protein	1.33	2.56
	109060	AA160879	Hs.241551	chloride channel; calcium activated; fam	0.67	1.42
45	109112	AA169379	Hs.72865	ESTs	1.03	2.31
	109344	AA213696	Hs.86559	poly(A)-binding protein-like 1	0.97	1.55
	109412	AA227145	Hs.209473	ESTs; Weakly similar to REGULATOR OF MIT	0.76	1.87
	110780	N23174	Hs.22891	solute carrier family 7 (cationic amino	0.9	0.95
	110958	N50550	Hs.24587	signal transduction protein (SH3 contain	1.17	2.26
50	111018	N54067	Hs.3628	mitogen-activated protein kinase kinase	1.21	1.85
	111337	N79612	Hs.16607	ESTs; Highly similar to Myosin heavy cha	1	1.45
	112305	R54822	Hs.26244	ESTs	1	1
	112401	R61279	Hs.237536	ESTs; Weakly similar to F25B5.3 [C.elega	1.24	1.64
	112853	T02843	Hs.4351	EST	1.56	1.96
55	112869	T03313	Hs.4747	dyskeratosis congenita 1; dyskerin	1.03	1.57
	112992	T23513	Hs.7147	ESTs	1	1
	113048	T25895	Hs.184008	ESTs; Weakly similar to RNA-binding prot	1.37	2.26
	113063	T32438	Hs.5027	ESTs	1	1
	113179	T55182	Hs.152571	ESTs; Highly similar to IGF-II mRNA-bind	1.33	2.7
60	113573	T91166	Hs.15990	ESTs	0.76	1.47
	113811	W44928	Hs.4878	ESTs	0.79	1.51
	114086	Z38266	Hs.12770	Homo sapiens PAC clone DJ0777O23 from 7p	0.9	1.34
	114587	AA070827	Hs.180320	ESTs; Weakly similar to GOLGI 4-TRANSMEM	1.02	1.76
	114846	AA234929	Hs.44343	ESTs	1.32	2.36
65	114964	AA243873	Hs.82184	ring finger protein 3	1.1	1.84
	115047	AA252627	Hs.22554	homeo box B5	1.01	2.36
	115166	AA258409	Hs.198907	myelin protein zero-like 1	1.05	2.31
	115167	AA258421	Hs.43728	hypothetical protein	1.52	2.52
	115239	AA278650	Hs.73291	ESTs; Weakly similar to similar to the b	0.7	2.57
70	115278	AA279757	Hs.67466	ESTs; Weakly similar to BACN32G11.d [D.m	1.14	2.12
	115652	AA405098	Hs.38178	ESTs	0.82	4.67
	115875	AA433943	Hs.43946	ESTs; Weakly similar to Weak similarity	1.2	1.98
	116004	AA449122	Hs.76086	ESTs; Highly similar to small zinc finge	0.96	1.31
	116121	AA459254	Hs.48855	ESTs	0.97	1.55
75	116129	AA459956	Hs.49163	ESTs; Highly similar to putative ribonuc	1.08	2.73
	116190	AA464963	Hs.67776	ESTs	0.8	1.57
	116312	AA490494	Hs.65403	ESTs	1.37	2.65
	116732	F13779	Hs.165909	ESTs	0.92	1.8
	117602	N35020	Hs.44685	ESTs; Weakly similar to GOLIATH PROTEIN	1.15	1.84
80	117950	N51394	Hs.75478	KIAA0956 protein	1.04	2.36
	117992	N52000	Hs.172089	Homo sapiens mRNA; cDNA DKFZp586B0222 (f	0.62	1.29
	118785	N75386	Hs.111867	GLI-Kruppel family member GLI2	1	1
	119717	W69134	Hs.57987	ESTs	1	1.4
	119814	W74069	Hs.58350	ESTs	0.78	1.77
85	120128	Z38499	Hs.91448	MKP-1 like protein tyrosine phosphatase	0.86	1.46
	120242	Z98443	Hs.86366	ESTs	0.83	2.01



	120483	AA252994	Hs.1578	apoptosis inhibitor 4 (survivin)	0.74	1.64
	121054	AA398604	Hs.97387	ESTs	1.05	1.93
	121326	AA404246	Hs.97031	ESTs; Weakly similar to Similar to phyto	0.98	1.3
5	121376	AA405699	Hs.166232	ESTs; Moderately similar to SODIUM- AND	0.91	1.83
	121457	AA411448	Hs.208985	ESTs	0.91	1.59
	121780	AA422086	Hs.124660	ESTs	0.46	0.55
	121781	AA422150	Hs.98370	cytochrome P540 family member predicted	1.07	1.54
	121844	AA425732	Hs.98485	gap junction protein; beta 2; 26kD (conn	0.94	1.4
10	122059	AA431737	Hs.98749	EST	1.93	2.33
	122338	AA443311	Hs.98998	ESTs	1	1
	122354	AA443772	Hs.186692	ESTs	0.88	1.39
	122591	AA453265	Hs.99311	ESTs; Weakly similar to MRJ [H.sapiens]	2.28	2.93
	122790	AA460156	Hs.99556	ESTs	0.88	1.3
	123398	AA521265	Hs.105514	ESTs	1	1.93
15	123518	AA608531	Hs.170313	ESTs	1	1
	123673	AA609471	Hs.112712	ESTs	1	1.15
	124000	D57317	Hs.74861	activated RNA polymerase II transcriptio	0.74	1.12
	124367	N24006	Hs.99348	distal-less homeo box 5	0.67	1.1
	124447	N48000	Hs.140945	Homo sapiens mRNA; cDNA DKFZp586L141 (fr	1.19	1.7
20	125756	W25498	Hs.81634	ATP synthase; H+ transporting; mitochond	0.93	1.59
	125769	AI382972	Hs.82128	5T4 oncofetal trophoblast glycoprotein	1.65	6.76
	125852	H09290	Hs.76550	Homo sapiens mRNA; cDNA DKFZp564B1264 (f	0.72	2.26
	125924	AA526849	Hs.82109	syndecan 1	1.22	2.25
25	126037	M85772	Hs.6066	KIAA1112 protein	1.36	1.63
	126214	N29455	Hs.74316	desmoplakin (DPI; DPII)	1.93	3.55
	126414	N78770	Hs.223439	ESTs	1.21	1.66
	126737	AA488132	Hs.62741	ESTs	1	1
	126743	AA179253	Hs.172182	poly(A)-binding protein; cytoplasmic 1	1.3	2.16
30	126926	AA179546	Hs.832	ESTs; Highly similar to INTEGRIN BETA-8	2.53	2.8
	127432	AA501734	Hs.170311	heterogeneous nuclear ribonucleoprotein	1.57	2.12
	128218	H02682	Hs.99189	ESTs; Moderately similar to recombinatio	1.24	2.09
	128527	M31523	Hs.101047	transcription factor 3 (E2A immunoglobul	1.08	1.78
	128568	X60673	Hs.247568	adenylate kinase 3	1.23	3.48
35	128584	M11433	Hs.101850	retinol-binding protein 1; cellular	0.87	2.42
	128628	C14037	Hs.251978	EST	1.22	1.9
	128691	W27939	Hs.103834	ESTs	1.1	1.73
	128714	V00599	Hs.179661	Homo sapiens clone 24703 beta-tubulin mR	0.92	1.17
40	128733	AA328993	Hs.104558	ESTs	1.34	1.94
	128781	X85372	Hs.105465	small nuclear ribonucleoprotein polypept	0.9	1.34
	129052	AA496297	Hs.182740	ribosomal protein S11	2.59	3.19
	129095	L12350	Hs.108623	thrombospondin 2	1.04	3.2
	129241	AA435665	Hs.109706	ESTs; Moderately similar to HN1 [M.muscu	0.95	1.61
	129665	M88458	Hs.118778	KDEL (Lys-Asp-Glu-Leu) endoplasmic retic	1.28	2.63
45	129703	AA401348	Hs.179999	ESTs	0.97	1.63
	129720	AA476582	Hs.12152	ESTs; Moderately similar to SIGNAL RECOG	1.09	1.79
	129850	N20593	Hs.56845	GDP dissociation inhibitor 2	0.74	1.68
	129896	AA043021	Hs.13225	UDP-Gal:betaGlcNAc beta 1,4- galactosylt	1.43	4.19
	130069	AA055896	Hs.146428	collagen; type V; alpha 1	1.17	1.98
50	130405	H88359	Hs.155396	nuclear factor (erythroid-derived 2)-lik	1.26	1.79
	130541	X05608	Hs.211584	neurofilament; light polypeptide (68kD)	1	1
	130599	M91670	Hs.174070	ubiquitin carrier protein	1.07	1.66
	130867	J04093	Hs.2056	UDP glycosyltransferase 1	1	4.8
	131009	AA063596	Hs.22142	ESTs; Weakly similar to NADH-CYTOCHROME	0.93	1.05
55	131028	U20240	Hs.2227	CCAAT/enhancer binding protein (C/EBP);	1	1.23
	131083	U66661	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	1.1	1.8
	131091	T35341	Hs.22880	ESTs; Highly similar to dipeptidyl pepti	1.28	1.98
	131144	C14412	Hs.23528	ESTs; Highly similar to HSPC038 protein	1.43	2.06
	131148	C00038	Hs.23579	ESTs	0.88	3.38
60	131164	Y00503	Hs.182265	keratin 19	1.19	2.77
	131185	M25753	Hs.23960	cyclin B1	0.86	3.84
	131219	C00476	Hs.24395	small inducible cytokine subfamily B (Cy	0.66	2.96
	131454	AA455896	Hs.2699	glypican 1	0.99	1.54
	131687	L11066	Hs.3069	heat shock 70kD protein 9B (mortalin-2)	1	1.18
65	131689	AA599653	Hs.30696	transcription factor-like 5 (basic helix	1	1.95
	131692	D50914	Hs.30736	KIAA0124 protein	1.55	2.39
	131786	AA135554	Hs.32125	ESTs	1	1.33
	131843	AA195893	Hs.184062	ESTs; Moderately similar to putative Rab	0.83	1.63
	131860	U02082	Hs.334	Oncogene TIM	1.08	2.2
70	131884	H90124	Hs.3463	ribosomal protein S23	1.23	1.24
	131903	AA481723	Hs.3436	deleted in oral cancer (mouse; homolog)	0.91	1.18
	131945	M87339	Hs.35120	replication factor C (activator 1) 4 (37	1	2.8
	131958	AA093998	Hs.3566	ESTs; Highly similar to phosphorylation	0.87	1.36
	131964	W42508	Hs.3593	ESTs	1	1.25
75	132001	J00277	Hs.37003	v-Ha-ras Harvey rat sarcoma viral onco	1.12	1.43
	132040	AA146843	Hs.172894	BH3 interacting domain death agonist	1	1.55
	132065	D82226	Hs.211594	proteasome (prosome; macropain) 26S subu	0.89	1.27
	132109	AA599801	Hs.40098	ESTs	1	1.05
	132112	AA150661	Hs.40154	jumonji (mouse) homolog	0.99	1.44
80	132123	AA447123	Hs.250705	ESTs	1.06	2.46
	132162	H89551	Hs.41241	ESTs	1.08	2.46
	132180	AA405569	Hs.418	fibroblast activation protein; alpha; se	1.02	4.56
	132309	AA460917	Hs.2780	jun D proto-oncogene	1.16	1.8
	132371	AA235448	Hs.46677	ESTs	0.8	1.26
85	132618	AA253330	Hs.5344	adaptor-related protein complex 1; gamma	0.5	1.49
	132736	U68019	Hs.211578	MAD (mothers against decapentaplegic; Dr	1.21	1.81



	132771	AA488432	Hs.56407	phosphoserine phosphatase	1	1.3
	132833	U78525	Hs.57783	eukaryotic translation initiation factor	0.91	1.43
	132922	T23641	Hs.6066	KIAA1112 protein	1.16	1.53
5	132959	AA028103	Hs.61472	ESTs; Weakly similar to unknown [S.cerev	1.02	1.88
	132994	AA505133	Hs.7594	solute carrier family 2 (facilitated glu	0.72	2.97
	133005	C21400	Hs.103329	KIAA0970 protein	0.88	1.34
	133065	X62535	Hs.172690	diacylglycerol kinase; alpha (80kD)	0.93	1.23
	133083	N70633	Hs.6456	chaperonin containing TCP1; subunit 2 (b	1.14	1.76
10	133086	L17131	Hs.139800	high-mobility group (nonhistone chromoso	0.97	1.43
	133134	T89703	Hs.65648	RNA binding motif protein 8	1.1	1.8
	133195	AA350744	Hs.181409	KIAA1007 protein	2.29	2.69
	133313	AA249427	Hs.70704	ESTs	1.07	1.68
	133331	T62039	Hs.158675	ribosomal protein L14	0.85	1.18
15	133438	D13370	Hs.73722	APEX nuclease (multifunctional DNA repai	0.91	1.45
	133445	T99303	Hs.73797	guanine nucleotide binding protein (G pr	0.94	1.68
	133483	X52426	Hs.74070	keratin 13	0.85	1.14
	133492	L40397	Hs.74137	transmembrane trafficking protein	1.1	1.69
	133504	W95070	Hs.74316	desmoplakin (DP1; DP11)	0.7	6.21
20	133517	X52947	Hs.74471	gap junction protein; alpha 1; 43kD (con	0.95	1.3
	133540	D78151	Hs.74619	proteasome (prosome; macropain) 26S subu	0.91	1.25
	133594	L07758	Hs.172589	nuclear phosphoprotein similar to S. cer	0.84	1.29
	133627	U09587	Hs.75280	glycyl-tRNA synthetase	1.09	1.99
	133671	T25747	Hs.75471	zinc finger protein 146	1.02	1.5
25	133859	U86782	Hs.178761	26S proteasome-associated pad1 homolog	1.11	3.33
	133865	F09315	Hs.170290	discs; large (Drosophila) homolog 5	1.84	6.7
	133913	W84712	Hs.7753	calumenin	1.15	1.86
	133963	L34587	Hs.184693	transcription elongation factor B (SIII)	1.3	1.91
	133982	U47621	Hs.207251	nucleolar autoantigen (55kD) similar to	1.3	1.99
30	134100	L07540	Hs.171075	replication factor C (activator 1) 5 (36	0.72	1.65
	134110	U41060	Hs.79136	LIV-1 protein; estrogen regulated	1.04	1.62
	134158	U15174	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	1	1.55
	134161	U97188	Hs.79440	IGF-II mRNA-binding protein 3	0.82	1.95
	134193	F09570	Hs.7980	ESTs	0.98	1.48
35	134367	X54199	Hs.82285	phosphoribosylglycinamide formyltransfer	1	2.8
	134402	U25165	Hs.82712	fragile X mental retardation; autosomal	1.26	2
	134457	D86963	Hs.174044	dishevelled 3 (homologous to Drosophila	1	1.47
	134469	X17567	Hs.83753	small nuclear ribonucleoprotein polypept	0.94	1.57
40	134498	M63180	Hs.84131	threonyl-tRNA synthetase	1.2	2.64
	134501	W84870	Hs.211568	eukaryotic translation initiation factor	0.84	1.36
	134507	M63488	Hs.84318	replication protein A1 (70kD)	1.7	2.93
	134548	U41515	Hs.85215	Deleted in split-hand/split-foot 1 regio	1.46	2.73
	134599	X99226	Hs.86297	Fanconi anemia; complementation group A	1.36	2.22
45	134692	R73567	Hs.8850	a disintegrin and metalloproteinase doma	0.77	1.64
	134693	N70361	Hs.8854	ESTs	1.09	1.82
	134806	Z49099	Hs.89718	spermine synthase	0.98	1.35
	134821	Z34974	Hs.198382	plakophilin 1 (ectodermal dysplasia/skin	0.99	1.4
	134864	Y08999	Hs.90370	actin related protein 2/3 complex; subun	0.95	1.42
	134914	U29615	Hs.91093	chitinase 1 (chitotriosidase)	1.16	1.29
50	134953	L10678	Hs.91747	profilin 2	0.95	1.76
	134993	AA282343	Hs.9242	purine-rich element binding protein B	0.98	1.73
	135051	C15324	Hs.93668	ESTs	1.35	2.11
	135158	U51711		Human desmocollin-2 mRNA; 3' UTR	0.86	1.16

Table 1B shows the accession numbers for those pkeys in Table 1A lacking unigenelD's. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the Accession column.

Pkey: Unique Eos probeset identifier number  
CAT number: Gene cluster number  
Accession: Genbank accession numbers

Pkey	CAT	Accessions
65	100661 23182_1 100667 26401_3	BE623001 L05096 AA383604 AW966416 N53295 AA460213 AW571519 AA603655 L05424 X56794 S66400 X55150 W60071 AW351820 X55938 M83326 BE005289 BE070059 M83324 BE005248 BE069717 BE181648 BE069700 AW606203 BE069721 AW382138 AW803776 BE463954 BE005334 BE005274 T27386 AA932714 AA972695 AW377728 AI632506 T29066 AI783934 AW377727 BE163715 AL047291 AA279047 AA523003 BE008048 BE440141 W23614 BE090519 BE092193 N29181 N20358 N44153 BE546944 T69231 AW377441 AA907406 H50799 AW051416 AI420712 BE620922 AI279161 AA992549 W47198 BE005241 AI342696 H50700 AI969974 AI863855 AA374490 AW130675 AI950633 AA146687 H99482 X55150 BE005414 BE005339 N28294 AI673068 AI887890 AW804171 AI675961 AW804172 AA778841 AL048050 AI127757 AI095568 AW204965 AW468978 W31898 AI052595 AI278771 BE464018 AI081503 AI824196 AA513211 AA411062 AW084376 N48752 AA703209 N35580 AW059918 AA054563 AI280942 T27619 BE621435 N66010 AW589527 AI160414 AA283090 AA962536 H82726 W52115 W45432 W60433 AA577548 AA146714 BE150994 AA054615 AW796025 AW382768 BE565671 C00444 AA054555
75	100668 26401_3	L05424 X56794 S66400 X55150 W60071 AW351820 X55938 M83326 BE005289 BE070059 M83324 BE005248 BE069717 BE181648 BE069700 AW606203 BE069721 AW382138 AW803776 BE463954 BE005334 BE005274 T27386 AA932714 AA972695 AW377728 AI632506 T29066 AI783934 AW377727 BE163715 AL047291 AA279047 AA523003 BE008048 BE440141 W23614 BE090519 BE092193 N29181 N20358 N44153 BE546944 T69231 AW377441 AA907406 H50799 AW051416 AI420712 BE620922 AI279161 AA992549 W47198 BE005241 AI342696 H50700 AI969974 AI863855 AA374490 AW130675 AI950633 AA146687 H99482 X55150 BE005414 BE005339 N28294 AI673068 AI887890 AW804171 AI675961 AW804172 AA778841 AL048050 AI127757 AI095568 AW204965 AW468978 W31898 AI052595 AI278771 BE464018 AI081503 AI824196 AA513211 AA411062 AW084376 N48752 AA703209 N35580 AW059918 AA054563 AI280942 T27619 BE621435 N66010 AW589527 AI160414 AA283090 AA962536 H82726 W52115 W45432 W60433 AA577548 AA146714 BE150994 AA054615 AW796025 AW382768 BE565671 C00444 AA054555
80		J04088 NM_001067 AF071747 AJ011741 N85424 AL042407 AA218572 BE296748 BE083981 AL040877 AW499918 AW675045 H17813 BE081283 AA670403 AW504327 BE094229 AA104024 AI471482 AI970337 AA737616 AI827444 AW003286 AI742333 AI344044 AI765634
85	101332 25130_1	



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AW674920 N57176 AA026480 AW576767 H93284 AA026863 AW177787 AA026654 AW177786 BE092134 BE092137 BE092136 AW177784  
AI022862 BE091653 AW376811 AW848592 AA040018 BE185331 BE182164 AA368564 AW951576 T29918 AA131077 W95048 W25458  
AW205789 H90899 N29754 W32490 R20904 BE167181 BE167165 N84767 H27408 H30146 AI190590 C03378 AI554403 AI205263 AA128470  
AI392926 AF139065 AW370813 AW370827 AW798417 AW798780 AW798883 AW798569 R33557 AA149190 C03029 AW177783 AA088866  
AW370829 AA247685 BE002273 AI760816 AI439101 AW879451 AI700963 AA451923 AI340326 AI590975 T48793 AI568096 AI142882 AA039975  
AI470146 AA946936 BE067737 BE067786 W19287 AA644381 AA702424 AI417612 AI306554 AI686869 AI568892 AW190555 AI571075 AI220573  
AA056527 AI471874 AI304772 AW517828 AI915596 AI627383 AI270345 AW021347 AW166807 AW105614 AI346078 AA552300 W95070  
AI494059 AI911702 AA149191 AA026864 AI830049 AI887258 AW780435 AI910434 AI819984 AI858282 AI078449 AI025932 AI860584 AI635878  
AA026047 AA703232 D12062 AW192085 AA658154 AW514597 AW591892 T87181 AA782066 AW243815 AW150038 AW268383 AW004633  
AI927207 AA782109 AW473233 AI804485 AW169216 AI572669 AA602182 AW015480 AW771865 AI270027 AA961816 AA283207 AI076962  
AI498487 AI348053 AI783914 H44405 AW799118 AA128330 AA515500 AA918281 W02156 AI905927 AA022701 W38382 R20795 T77861  
AW860878  
100528 45979\_1 BE386801 AU077299 AA143755 BE302747 AA853375 U30162 BE274163 BE277479 BE408180 BE274874 C15000 AA047476 N27099 AI359165  
AI638794 AI151283 AI863925 AW444977 AI207392 AA931263 AA443112 R40138 AW068538 AA351008 AA676972 R62503 AA916492 AW001865  
H42334 H38280 AA121497 AA114137 AI750938 M17783 AA383786 BE274462 AI753182 C05975 AA347404 AW069298 AI754351 AI754044  
AA188808 AA186879 AA565243 AL040655 AA456177 AI750722 AA045756 AA213580 C16936 AW578747 AW753731 H41632 N44761 R58560  
R61260 AA039902 N59721 AW992543 R68380 AA149686 T29017 H03739 BE383822 BE387105 BE408251 BE410425 H41560 AA247591  
BE389677 AI752233 AI566195 AA868004 AI424523 AW753720 AA852159 BE386803  
100559 2260\_1 NM\_000094 L02870 D13694 S51236 M96984 AW946290 M65158 AI285422 D29523 AL119886 AW630655 L06862 AI884355 AW168737 T29085  
AW797005 AW801340 AI355504 AW079048 AW801337 AI690455 AI972063 AW268565 W68588 AA587326 AA883498 AI033523 AW510356  
AW591998 H98463 AL043852 AI150055 AI566239 AI624803 AA844717 H40670 AA922334 AI864424 AW615094 AW451233 AI302203 F31221  
AI872170 W68589 AA904478 AI917631 AW014208 AW450759 AA847625 AI284033 AA848176 AA598507  
100576 9986\_1 X00356 NM\_001741 M26095 X03662 M12667 X02330 X02330 AA716058 AW296074 X04861 AI695720 AA719597  
124357 genbank\_N22401 N22401  
101624 entrez\_M55998 M55998  
101625 entrez\_M57293 M57293  
135158 57963\_1 AL037551 AI804716 AW439811 AI569470 AA075299 AI738572 AI270388 AI816783 AW263026 AI633951 AI655285 AI990572 AI950425  
AW241533 AA916883 AA576693 AA160156 AA613783 AW078884 AI888282 AI275241 AI133467 AA164921



Tables 2A-8C were previously filed on November 9, 2001 in USSN 60/339,245 (18501-004100US)

Table 2A shows 504 genes down-regulated in lung tumors relative to normal lung and chronically diseased lung. Chronically diseased lung samples represent chronic non-malignant lung diseases such as fibrosis, emphysema, and bronchitis. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Pkey: Unique Eos probeset identifier number  
 ExAccn: Exemplar Accession number, Genbank accession number  
 UnigenelD: Unigene number  
 Unigene Title: Unigene gene title  
 R1: 90th percentile of AI for normal lung samples divided by the 80th percentile of AI for adenocarcinoma and squamous cell carcinoma lung tumor samples.  
 R2: median of AI for normal lung samples divided by 90th percentile of AI for adenocarcinoma and squamous cell carcinoma lung tumor samples.  
 R3: median of AI for normal lung samples minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples divided by the 90th percentile of AI for adenocarcinoma and squamous cell carcinoma lung tumor samples minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples.  
 R4: average of AI for normal lung samples divided by average AI for squamous cell carcinoma and adenocarcinoma lung tumors.  
 R5: median of AI for normal lung samples divided by the 90th percentile of AI for adenocarcinomas.  
 R6: median of AI for normal lung samples minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples divided by the 90th percentile of AI for adenocarcinomas minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples.  
 R7: average of AI for normal lung samples divided by the 90th percentile of AI for squamous cell carcinomas.  
 R8: median of AI for normal lung samples minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples divided by the 90th percentile of AI for squamous cell carcinomas minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples.

Pkey	ExAccn	UnigenelD	Unigene Title	R1	R2	R3	R4	R5	R6	R7	R8
100095	Z97171	Hs.78454	myocilin; trabecular meshwork inducible	40.20							
100115	NM_002084	Hs.336920	glutathione peroxidase 3 (plasma)								3.46
100138	U83508	Hs.2463	angiopoietin 1			2.30					
100299	D49493	Hs.2171	growth differentiation factor 10		11.00						
100306	U86749	Hs.80598	transcription elongation factor A (SII);						3.06		
100447	NM_014767	Hs.74583	KIAA0275 gene product								3.16
100458	S74019	Hs.247979	Vpre-B	42.40							
100862	AA005247	Hs.285754	Hepatocyte Growth Factor Receptor						4.13		
100959	AA359129	Hs.118127	actin; alpha; cardiac muscle				125.60				
101032	BE206854	Hs.46039	phosphoglycerate mutase 2 (muscle)	36.40							
101081	AF047347	Hs.4880	amyloid beta (A4) precursor protein-bind				34.60				
101088	X70697	Hs.553	solute carrier family 6 (neurotransmitter)				193.20				
101125	AJ250562	Hs.82749	transmembrane 4 superfamily member 2						3.10		
101180	U11874	Hs.846	interleukin 8 receptor; beta				54.86				
101308	L41390		"Homo sapiens core 2 beta-1,6-N-acetylgl	33.20							
101330	L43821	Hs.80261	enhancer of filamentation 1 (cas-like do				36.40				
101345	NM_005795	Hs.152175	Calcitonin receptor-like			2.29					
101346	AI738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(N				70.55				
101397	M26380	Hs.180878	lipoprotein lipase								3.54
101414	NM_000066	Hs.38069	complement component 8; beta polypeptide							3.81	
101435	NM_001100	Hs.1288	actin; alpha 1; skeletal muscle				34.60				
101507	X16896	Hs.82112	interleukin 1 receptor; type I				37.60				
101530	M29874	Hs.1360	cytochrome P450; subfamily IIB (phenobar								4.25
101537	AI469059	Hs.184915	zinc finger protein; Y-linked			2.54					
101542	NM_000102	Hs.1363	cytochrome P450; subfamily XVII (steroid		5.50						
101545	BE246154	Hs.154210	EDG1; endothelial differentiation, sphin	39.40							
101554	BE207611	Hs.123078	thyroid stimulating hormone receptor		13.00						
101560	AW958272	Hs.83733	Intercellular adhesion molecule 2, exon								3.38
101574	M34182	Hs.158029	protein kinase; cAMP-dependent; catalyti						4.37		
101805	M37984	Hs.118845	troponin C; slow								3.80
101621	BE391804	Hs.62661	guanylate binding protein 1; interferon-	30.20							
101680	AA299330	Hs.1042	Sjogren syndrome antigen A1 (52kD; ribon							2.75	
101829	AW452398	Hs.129763	solute carrier family 8 (sodium/calcium						3.37		
101842	M93221	Hs.75182	mannose receptor; C type 1				38.20				
101961	AW004056	Hs.168357	"Hs-TBX2=T-box gene (T-box region) [huma			2.32					6.85
101994	T92248	Hs.2240	uteroglobin								
102020	AU077315	Hs.154970	transcription factor CP2			2.45					
102091	BE280901	Hs.83155	aldehyde dehydrogenase 7								6.75
102112	AW025430	Hs.155591	forkhead box F1	54.60							
102190	AA723157	Hs.73769	folate receptor 1 (adult)								3.98
102202	NM_000507	Hs.574	fructose-bisphosphatase 1								3.62
102241	NM_007351	Hs.268107	Multimerin			2.32					
102310	U33839		Accession not listed in Genbank		7.00						
102397	U41898		"Human sodium cotransporter RKST1 mRNA,	29.40							
102571	U60115	Hs.239069	"Homo sapiens skeletal muscle LIM-protei								3.75
102620	AA976427	Hs.121513	Human clone W2-6 mRNA from chromosome X						3.07		
102636	U67092		"Human ataxia-telangiectasia locus prote			2.40					
102667	U70867	Hs.83974	solute carrier family 21 (prostaglandin			3.15					
102675	U72512	Hs.7771	"Human B-cell receptor associated protei						3.56		
102698	M18667	Hs.1867	progastricin (pepsinogen C)								4.51
102727	U79251	Hs.99902	opioid-binding protein/cell adhesion mol					12.00			
102852	V00571	Hs.75294	corticotropin releasing hormone	37.40							
103026	X54162	Hs.79386	thyroid and eye muscle autoantigen D1 (6					13.00			
103028	X54380	Hs.74094	pregnancy-zone protein	28.80							
103098	M86361		Human mRNA for T cell receptor; clone IG					10.00			
103117	X63578	Hs.295449	parvalbumin		6.00						
103241	X76223		H.sapiens MAL gene exon 4			2.47					
103280	U84722	Hs.76206	Cadherin 5, VE-cadherin (vascular epithe			2.69					
103360	Y16791	Hs.73082	keratin; hair; acidic; 5							2.16	



	103496	Y09267	Hs.132821	flavin containing monooxygenase 2				5.97
	103508	Y10141		"H.sapiens DAT1 gene, partial, VNTR"		3.27		
	103561	NM_001843	Hs.143434	contactin 1	2.40			
5	103569	NM_005512	Hs.151641	glycoprotein A repetitions predominant	2.99			
	103575	Z26256		"H.sapiens isoform 1 gene for L-type cal		4.18		
	103627	Z48513		H.sapiens XG mRNA (clone PEP6)		3.44		
	103767	BE244667	Hs.296155	CGI-100 protein			2.25	
	103850	AA187101	Hs.213194	Hypothetical protein MGC10895; sim to SR	46.55			
10	104078	AA402801	Hs.303276	ESTs		3.05		
	104326	AW732858	Hs.143067	ESTs		3.54		
	104352	BE219898	Hs.173135	dual-specificity tyrosine-(Y)-phosphoryl		3.16		
	104398	AI423930	Hs.36790	ESTs; Weakly similar to putative p150 [H	64.80			
	104473	AI904823	Hs.31297	ESTs			3.38	
	104493	AW960427	Hs.79059	ESTs; Moderately similar to TGF-BETA REC	2.47			
15	104495	AW975687	Hs.292979	ESTs	28.60			
	104595	AI799603	Hs.271568	ESTs		3.42		
	104597	AI364504	Hs.93967	ESTs; Weakly similar to Slit-1 protein [	6.00			
	104659	AW969769	Hs.105201	ESTs	34.00			
20	104686	AA010539	Hs.18912	ESTs	11.00			
	104691	U29690	Hs.37744	ESTs; Beta-1-adrenergic receptor	56.80			
	104764	AI039243	Hs.278585	ESTs		60.40		
	104776	AA026349		ESTs	34.20			
	104825	AA035613	Hs.141883	ESTs		3.03		
	104865	T79340	Hs.22575	Homo sapiens cDNA: FLJ21042 fis, clone C	41.20			
25	104942	NM_016348	Hs.10235	ESTs			3.27	
	104989	R65998	Hs.285243	ESTs		40.00		
	105062	AW954355	Hs.36529	ESTs			3.20	
	105101	H63202	Hs.38163	ESTs	34.20			
30	105173	U54617	Hs.8364	ESTs			4.17	
	105194	R06780	Hs.19800	ESTs	16.00			
	105226	R58958	Hs.26608	ESTs		2.34		
	105256	AA430650	Hs.16529	transmembrane 4 superfamily member (tet		2.72		
	105394	BE245812	Hs.8941	ESTs		2.61		
35	105647	Y09306	Hs.30148	homeodomain-interacting protein kinase 3	33.60			
	105789	AF106941	Hs.18142	arrestin; beta 2			3.59	
	105817	AA397825		synaptopodin		4.46		
	105847	AW964490	Hs.32241	ESTs		35.40		
	105894	AI904740	Hs.25691	calcitonin receptor-like receptor activi	3.43			
40	105999	BE268786	Hs.21543	ESTs	7.00			
	106075	AA045290	Hs.25930	ESTs		42.60		
	106178	AL049935	Hs.301763	KIAA0554 protein	34.80			
	106381	AB040916	Hs.24106	ESTs		12.00		
	106467	AA450040	Hs.154162	ADP-ribosylation factor-like 2			3.69	
45	106536	AA329648	Hs.23804	ESTs		96.40		
	106569	R20909	Hs.300741	sorcin		47.20		
	106605	AW772298	Hs.21103	Homo sapiens mRNA; cDNA DKFZp564B076 (fr		220.40		
	106842	AF124251	Hs.26054	novel SH2-containing protein 3		2.55		
	106844	AA485055	Hs.158213	sperm associated antigen 6	39.20			
50	106870	AI983730	Hs.26530	serum deprivation response (phosphatidyl		2.28		
	106943	AW888222	Hs.9973	ESTs			4.28	
	106954	AF128847	Hs.204038	ESTs			4.32	
	107106	AA862496	Hs.28482	ESTs		10.45		
	107163	AF233588	Hs.27018	ESTs		2.57		
55	107201	D20378	Hs.30731	EST			3.84	
	107238	D59362	Hs.330777	EST	8.00			
	107376	U90545	Hs.327179	solute carrier family 17 (sodium phospho	10.67			
	107530	Y13622	Hs.85087	latent transforming growth factor beta b		2.32		
	107688	AW082221	Hs.60536	ESTs		34.60		
60	107706	AA015579	Hs.29276	ESTs	28.40			
	107723	AA015967		EST			3.29	
	107727	AA149707	Hs.173091	DKFZP434K151 protein		80.80		
	107750	AA017291	Hs.60781	ESTs		51.40		
	107751	AA017301	Hs.235390	ESTs			3.14	
65	107873	AK000520	Hs.143811	ESTs	9.00			
	107899	BE019261	Hs.83869	ESTs; Weakly similar to !!!! ALU SUBFAM			3.65	
	107994	AA036811	Hs.48469	ESTs		44.60		
	107997	AL049176	Hs.82223	Human DNA sequence from clone 141H5 on c		32.00		
	108041	AW204712	Hs.61957	ESTs		30.80		
70	108048	AI797341	Hs.165195	ESTs			4.75	
	108338	AA070773		"zm53g11.s1 Stratagene fibroblast (#9372	2.33			
	108434	AA078899		"zm94b1.s1 Stratagene colon HT29 (#93722			2.92	
	108447	AA079126		"zm92a11.s1 Stratagene ovarian cancer (#			3.06	
	108480	AL133092	Hs.68055	ESTs		34.00		
75	108499	AA083103		"zn1b12.s1 Stratagene hNT neuron (#93723				3.36
	108535	R13949	Hs.226440	Homo sapiens clone 24881 mRNA sequence		19.00		
	108550	AA084867		"zn11f6.s1 Stratagene hNT neuron (#93723		12.00		
	108604	AA934589	Hs.49696	ESTs	2.33			
	108625	AW972330	Hs.283022	ESTs				5.82
80	108629	AA102425		"zn24c6.s1 Stratagene neuroepithelium NT			3.42	
	108655	AA099960		"zm65c6.s1 Stratagene fibroblast (#93721	7.00			
	108756	AA127221	Hs.117037	Homo sapiens mRNA; cDNA DKFZp564N1164 (f	6.05			
	108864	AI733852	Hs.199957	ESTs	28.80			
	108895	AL138272	Hs.62713	ESTs	32.80			
	108921	AI568801	Hs.71721	ESTs		57.80		
85	108967	AA142989	Hs.71730	ESTs	28.80			



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	109001	AI056548	Hs.72116	ESTs, Moderately similar to hedgehog-int	2.57				
	109003	AA147497	Hs.71825	ESTs				2.11	
	109004	AA156235	Hs.139077	EST	5.60				
5	109065	AA161125	Hs.252739	EST		10.00			
	109250	H83784	Hs.62113	ESTs; Weakly similar to PHOSPHATIDYLETHA				3.44	
	109490	AA233416	Hs.139202	ESTs				2.92	
	109510	AI798863	Hs.87191	ESTs	2.40				
	109578	F02208	Hs.27214	ESTs	10.00				
10	109601	F02695	Hs.311662	EST		40.80			
	109613	H47315	Hs.27519	ESTs		54.40			
	109650	R31770	Hs.23540	ESTs	31.20				
	109682	H18017	Hs.22869	ESTs	8.40				
	109724	D59899	Hs.127842	ESTs		29.40			
15	109782	AB020644	Hs.14945	long fatty acyl-CoA synthetase 2 gene		8.00			
	109833	R79864	Hs.29889	ESTs	10.00				
	109837	H00656	Hs.29792	ESTs	6.49				
	109977	T64183	Hs.282982	ESTs				2.75	
	109984	AI796320	Hs.10299	ESTs		107.00			
20	110146	H41324	Hs.31581	ESTs; Moderately similar to SYNTAXIN 1B				2.22	
	110271	H28985	Hs.31330	ESTs			3.48		
	110280	AW874263	Hs.32468	ESTs	44.20				
	110420	R93141	Hs.184261	ESTs		32.00			
	110578	T62507	Hs.11038	ESTs	28.40				
25	110634	R98905	Hs.35992	ESTs		20.00			
	110726	AW961818	Hs.24379	potassium voltage-gated channel; shaker-				4.15	
	110837	H03109	Hs.108920	ESTs; Weakly similar to semaphorin F [H.		56.80			
	110875	N35070	Hs.26401	tumor necrosis factor (ligand) superfam	3.13				
	110894	R92356	Hs.66881	ESTs; Moderately similar to cytoplasmic	5.33				
30	110971	AI760098	Hs.21411	ESTs		44.60			
	111023	AV655386	Hs.7645	ESTs	32.40				
	111057	T79639	Hs.14629	ESTs		17.14			
	111247	AW058350	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f			4.58		
	111330	BE247767	Hs.18166	KIAA0870 protein				3.42	
35	111374	BE250726	Hs.283724	ESTs; Moderately similar to HYA22 [H.sap				3.91	
	111442	AW449573	Hs.181003	ESTs		33.20			
	111737	H04607	Hs.9218	ESTs		53.00			
	111747	AI741471	Hs.23666	ESTs	46.20				
40	111807	R33508	Hs.18827	ESTs	16.00				
	111862	R37472	Hs.21559	EST			3.91		
	112045	AI372588	Hs.8022	TU3A protein				2.74	
	112057	R43713	Hs.22945	EST				4.92	
	112214	AW148652	Hs.167398	ESTs		13.00			
	112263	R52393	Hs.25917	ESTs					
45	112314	AW206093	Hs.748	ESTs	9.00				
	112324	R55965	Hs.26479	limbic system-associated membrane protei		14.00			
	112362	AW300887	Hs.26638	ESTs; Weakly similar to CD20 receptor [H					
	112380	H63010	Hs.5740	ESTs					
	112425	AA324998	Hs.321677	ESTs; Weakly similar to !!!! ALU SUBFAM	8.00				
50	112473	R65993	Hs.279798	pregnancy specific beta-1-glycoprotein 9			4.53		
	112492	N51620	Hs.28694	ESTs		29.80			
	112541	AF038392	Hs.116674	ESTs			3.62		
	112620	R80552	Hs.29040	ESTs	2.37				
	112623	AW373104	Hs.25094	ESTs	2.26				
55	112867	T03254	Hs.167393	ESTs		12.00			
	112894	T08188	Hs.3770	ESTs	6.50				
	112954	AA928953	Hs.6655	ESTs	7.00				
	113029	AW081710	Hs.7369	ESTs; Weakly similar to !!!! ALU SUBFAM				4.39	
	113086	AA346839	Hs.209100	DKFZP434C171 protein				4.47	
60	113140	T50405	Hs.175967	ESTs		10.00			
	113252	NM_004469	Hs.11392	c-fos induced growth factor (vascular en	14.00				
	113257	AI821378	Hs.159367	ESTs			3.72		
	113394	T81473	Hs.177894	ESTs			3.60		
	113437	T85349	Hs.15923	EST	35.00				
65	113454	AI022166	Hs.16188	ESTs	6.00				
	113502	T89130	Hs.16026	ESTs	39.60				
	113552	AI654223	Hs.333181	ESTs				3.88	
	113645	T95358	Hs.17932	EST		38.20		2.58	
70	113691	T96935	Hs.269192	ESTs			3.09		
	113706	AA004693	Hs.11958	oxidative 3 alpha hydroxysteroid dehydro					
	113883	U89281	Hs.170056	Homo sapiens mRNA; cDNA DKFZp586B0220 (f	30.40				
	113924	BE178285	Hs.269181	ESTs		13.00			
	114035	W92798	Hs.114727	ESTs					
	114058	AK002016	Hs.12248	ESTs		40.60			
75	114084	AA708035	Hs.25425	ESTs					
	114121	H05785	Hs.125019	Human lymphoid nuclear protein (LAF-4)	7.00				
	114124	W57554	Hs.306117	interleukin 13 receptor; alpha 1	6.00				
	114275	AW515443	Hs.173091	DKFZP434K151 protein		48.80			
	114297	AA149707	Hs.33532	ESTs; Highly similar to Miz-1 protein [H			3.45		
80	114427	AA017176	Hs.243010	*ze63b11.s1 Soares retina N2b4HR Homo sa		10.00			
	114449	AA020736		ESTs, Moderately similar to RTC0_HUMAN G	14.00				
	114452	AI369275		*zm97a5.s1 Stratagene colon HT29 (#93722			3.13		
	114609	AA079505		*zn25b3.s1 Stratagene neuroepithelium NT		35.40			
	114648	AA101056		Homo sapiens HNF-3beta mRNA for hepatocy				3.42	
85	114731	BE094291	Hs.155651	ESTs	33.00				
	114762	AA146979	Hs.288464	ESTs					



	114776	AA151719	Hs.95834	ESTs	34.40				
	115009	AA251561	Hs.48689	ESTs	30.20				
	115272	AW015947		ESTs; Weakly similar to hypothetical L1	32.60				
5	115279	AW964897	Hs.290825	ESTs		6.00			
	115302	AL109719	Hs.47578	ESTs			12.00		
	115365	AW976252	Hs.268391	ESTs				3.32	
	115559	AL079707	Hs.207443	ESTs			48.00		
	115566	AI142336	Hs.43977	ESTs			56.20		
10	115683	AF255910	Hs.54650	ESTs, Weakly similar to (define not ava	31.40				
	115744	AA418538	Hs.43945	ESTs; Highly similar to dJ1178H5.3 [H.sa			33.60		
	115819	AA486620	Hs.41135	Endomucin 2			74.40		
	115949	AI478427	Hs.43125	ESTs		3.18			
	115965	AA001732	Hs.173233	ESTs			388.80		
15	116035	AA621405	Hs.184664	ESTs			33.20		
	116049	AA454033	Hs.41644	ESTs			45.80		
	116081	AI190071	Hs.55278	ESTs				3.57	
	116082	AB029496	Hs.59729	ESTs		3.06			
	116213	AA292105	Hs.326740	leucine rich repeat (in FLII) interactin	50.60				
20	116228	AI767947	Hs.50841	ESTs; Weakly similar to tuftelin [M.musc		3.85			
	116250	N76712	Hs.44829	ESTs		6.00			
	116419	AI613480	Hs.47152	ESTs; Weakly similar to testicular tekti			30.00		
	116617	D80761	Hs.45220	EST		2.27			
	116784	AB007979	Hs.301281	tenascin R (restrictin; janusin)	47.20				
25	116835	N39230	Hs.38218	ESTs			41.20		
	116970	AB023179	Hs.9059	KIAA0962 protein			91.00	11.00	
	117023	AW070211	Hs.102415	ESTs					
	117027	AW085208	Hs.130093	ESTs	49.40				
	117036	H88908	Hs.41192	EST			32.60		
30	117110	AA160079	Hs.172932	ESTs		8.67			
	117209	W03011	Hs.306881	ESTs			30.60		
	117325	N23599	Hs.43396	ESTs				9.29	
	117454	N29569	Hs.44055	ESTs					3.19
	117475	N30205	Hs.93740	ESTs	44.00				
35	117543	BE219453	Hs.42722	ESTs		16.00			
	117567	AW444761	Hs.44555	ESTs			12.00		
	117570	N48649	Hs.44583	ESTs			11.00		
	117600	N34963	Hs.44676	EST				3.74	
	117730	N45513	Hs.46608	ESTs		6.00			
40	117791	N48325	Hs.93956	EST		9.00			
	117929	N51075	Hs.47191	ESTs			29.20		
	117990	AA446167	Hs.47385	ESTs		8.00			
	118224	N62275	Hs.48503	EST	31.40				
	118244	N62516	Hs.48556	ESTs	32.80				
45	118357	AL109667	Hs.124154	Homo sapiens mRNA full length insert cDN		2.40			
	118446	N66361	Hs.269121	ESTs		2.28			
	118447	N66399	Hs.49193	EST	30.80				
	118530	N67900	Hs.118446	ESTs				3.10	
	118549	N68163	Hs.322954	EST				3.41	
50	118823	W03754	Hs.50813	ESTs; Weakly similar to long chain fatty		3.94			
	118862	W17065	Hs.54522	ESTs				3.58	
	118935	AI979247	Hs.247043	KIAA0525 protein			33.00		
	118944	AI734233	Hs.226142	ESTs; Weakly similar to !!!! ALU SUBFAM				11.43	
	118995	N94591	Hs.323056	ESTs		14.00			
55	119073	BE245360	Hs.279477	ERG-2/ERG-1; V-ets avian erythroblastosi			52.60		
	119268	T16335	Hs.65325	EST	31.40				
	119514	W37937		Accession not listed in Genbank				3.50	
	119824	W74536	Hs.184	advanced glycosylation end product-speci		2.75			
	119831	AL117664	Hs.58419	DKFZP586L2024 protein				3.21	
60	119861	W78816	Hs.49943	ESTs; Moderately similar to !!!! ALU SUB			33.80		
	119889	W84346	Hs.58671	ESTs			30.03		
	119921	W86192	Hs.58815	ESTs	29.00				
	120082	H80286	Hs.40111	ESTs				3.80	
	120094	AA811339	Hs.124049	ESTs		6.00			
65	120132	W57554	Hs.125019	Human lymphoid nuclear protein (LAF-4)		12.00	36.60		
	120378	AA223249	Hs.285728	ESTs					
	120404	AB023230	Hs.96427	KIAA1013 protein	39.40			8.00	
	120504	AA256837		ESTs					
	120512	N55761	Hs.194718	ESTs	33.00				
70	120667	AA287740	Hs.78335	microtubule-associated protein; RP/EB fa				4.18	
	120777	AA287702	Hs.10031	KIAA0955 protein			46.60		
	121082	AA398722		ESTs			39.00		
	121191	AA400205	Hs.104447	ESTs	41.60				
	121248	AA400914	Hs.97827	EST				5.08	
75	121363	AI287280	Hs.97933	ESTs			12.00		
	121366	AI743515		ESTs			20.00		
	121483	AI660332	Hs.25274	ESTs; Moderately similar to putative sev				3.32	
	121518	AA412155		ESTs			30.20		
	121545	AA412442	Hs.98132	ESTs		2.29			
80	121622	AA416931	Hs.126065	ESTs		9.00			
	121665	AA416556	Hs.98234	ESTs			34.80		
	121709	AI338247	Hs.98314	Homo sapiens mRNA; cDNA DKFZp586L0120 (f	34.80				
	121730	AI140683	Hs.98328	ESTs	38.80				
	121740	AA421138	Hs.98334	EST		7.00			
85	121772	AI590770	Hs.110347	Homo sapiens mRNA for alpha integrin bin	36.20				
	121821	AL040235	Hs.3346	ESTs				3.61	



	121835	AB033030	Hs.300670	ESTs		2.34			
	121841	AA427794	Hs.104864	ESTs		2.61			
	121885	AA934883	Hs.98467	ESTs				2.25	
	121888	AA426429	Hs.98463	ESTs				2.92	
5	121938	AA428659	Hs.98610	ESTs			46.80		
	121950	AA429515		EST			31.40		
	122030	AA431310	Hs.98724	ESTs	34.40				
	122054	AA431725	Hs.98746	EST				3.58	
10	122211	AA300900	Hs.98849	ESTs; Moderately similar to bithoraxoid-	49.40				
	122233	AA436455	Hs.98872	EST	29.80				
	122247	AA436676	Hs.98890	EST			39.80		
	122253	AA436703	Hs.104936	ESTs; Weakly similar to hypothetical pro		9.00			
	122266	AA436840	Hs.98907	EST				3.60	
15	122285	AA436981	Hs.121602	EST				3.14	
	122409	AA446830	Hs.99081	ESTs	30.80				
	122485	AA524547	Hs.160318	phospholemman					
	122697	AA420683	Hs.98321	Homo sapiens cDNA FLJ14103 fis, clone MA		15.00	2.65		
	122772	AW117452	Hs.99489	ESTs		6.67			
20	122831	AI857570	Hs.5120	ESTs				3.37	
	122913	AI638774	Hs.105328	ESTs			32.20		
	123049	BE047680	Hs.211869	ESTs			41.80		
	123076	AI345569	Hs.190046	ESTs	35.80				
	123136	AW451999	Hs.194024	ESTs				2.58	
25	123309	N52937	Hs.102679	ESTs			19.00		
	123455	AA353113	Hs.112497	ESTs			82.80		
	123691	AA609579	Hs.112724	ESTs				3.95	
	123756	AA609971	Hs.112795	EST	35.40				
	123802	AA620448		Homo sapiens clone 24760 mRNA sequence	58.00				
30	123837	AI807243	Hs.112893	ESTs			32.40		
	123844	AA938905	Hs.120017	olfactory receptor; family 7; subfamily		2.63			
	123936	NM_004673	Hs.241519	ESTs	29.00				
	123987	C21171	Hs.95497	ESTs; Weakly similar to GLUCOSE TRANSPOR			70.60		
	124013	AI521936	Hs.107149	ESTs; Weakly similar to PTB-ASSOCIATED S	28.40				
35	124160	R40290	Hs.124685	ESTs			13.00		
	124205	H77570	Hs.108135	ESTs				4.74	
	124226	AA618527	Hs.190266	ESTs		2.35			
	124246	H67680	Hs.270962	ESTs			29.40		
40	124348	AI796320	Hs.10299	ESTs	17.00				
	124358	AW070211	Hs.102415	"yw35g11.s1 Morton Fetal Cochlea Homo sa		3.07			
	124409	AI814166	Hs.107197	ESTs				3.14	
	124442	AW663632	Hs.285625	TATA box binding protein (TBP)-associate		2.48			
	124468	N51413	Hs.109284	ESTs			30.80		
	124479	AB011130	Hs.127436	calcium channel; voltage-dependent; alph				6.03	
45	124519	AI670056	Hs.137274	ESTs; Weakly similar to SPLICEOSOME ASSO		2.50			
	124711	NM_004657	Hs.26530	serum deprivation response (phosphatidyl	59.20				
	124866	AI768289	Hs.304389	ESTs		8.00			
	124874	BE550182	Hs.127826	ESTs			37.60		
	125097	AW576389	Hs.335774	ESTs			10.00		
50	125179	AW206468	Hs.103118	ESTs				3.12	
	125200	AW836591	Hs.103156	ESTs				2.79	
	125299	T32982	Hs.102720	ESTs			34.20		
	125400	AL110151	Hs.128797	DKFZP586D0824 protein	29.00				
	125810	H00083		aryl hydrocarbon receptor-interacting pr	32.20				
55	126176	BE242256	Hs.2441	KIAA0022 gene product		12.00			
	126303	D78841		HUM525A05B Human placenta polyA+ (TFu)			33.60		
	126403	AW629054	Hs.125976	ESTs; Weakly similar to metalloprotease/	35.80				
	126507	AL040137	Hs.23964	ESTs; Weakly similar to HC1 ORF [M.muscu			29.80		
	126773	AA648284	Hs.187584	ESTs	39.60				
60	127307	AW962712	Hs.126712	ESTs; Weakly similar to pIL2 hypothetica	28.80				
	127462	AA760776	Hs.293977	aa59b04.s1 NCI_CGAP_GCB1 Homo sapiens c			34.40		
	127486	AW002846	Hs.105468	ESTs		9.00			
	127572	AA594027	Hs.191788	ESTs		2.36			
	127609	X80031	Hs.530	ESTs			29.40		
65	127832	AW976035	Hs.292396	ESTs			37.20		
	127898	AA774725	Hs.128970	ESTs				4.42	
	128073	AW340720	Hs.125983	ESTs			38.40		
	128101	AA905730	Hs.128254	ESTs		7.33			
70	128149	NM_012214	Hs.177576	mannosyl (alpha-1;3-)-glycoprotein beta-				2.58	
	128212	W27411	Hs.336920	glutathione peroxidase 3 (plasma)		3.09			
	128333	W68800	Hs.12126	ESTs; Weakly similar to LR8 [H.sapiens]			34.40		
	128364	N76462	Hs.269152	ESTs; Weakly similar to ZINC FINGER PROT		10.00			
	128426	AI265784	Hs.145197	ESTs				4.31	
	128598	AA305407	Hs.102308	potassium inwardly-rectifying channel; s	31.20				
75	128634	AA464918		ESTs; Moderately similar to !!!! ALU SUB			41.60		
	128687	AW271273	Hs.23767	ESTs			87.00		
	128726	AI311238	Hs.104476	ESTs				4.02	
	128773	NM_004131	Hs.1051	granzyme B (granzyme 2; cytotoxic T-lymp			9.00		
	128833	W26667	Hs.184581	ESTs				3.76	
80	128870	H39537	Hs.75309	eukaryotic translation elongation factor		2.66			
	128878	R25513	Hs.10683	ESTs				3.10	
	128885	AF134803	Hs.180141	cofilin 2 (muscle)			11.00		
	128998	W04245	Hs.107761	ESTs; Weakly similar to PUTATIVE RHO/RAC				3.21	
	129000	AA744902	Hs.107767	ESTs; Moderately similar to CaM-KII inh				3.68	
85	129038	AW156903	Hs.108124	ribosomal protein L41				3.17	
	129098	AW580945	Hs.330466	ESTs	34.60				



	129210	AL039940	Hs.202949	KIAA1102 protein					4.09
	129240	AA361258	Hs.237868	interleukin 7 receptor	2.29				
	129262	BE222198	Hs.109843	ESTs		3.30			
5	129301	AF182277	Hs.330780	Human cytochrome P450-11B (h11B3) mRNA;					4.05
	129331	AW167668	Hs.279772	ESTs; Highly similar to CGI-38 protein [					4.09
	129381	AW245805	Hs.110903	claudin 5 (transmembrane protein deleted	2.93				
	129565	X77777	Hs.198726	vasoactive intestinal peptide receptor 1		160.80			
	129595	U09550	Hs.1154	oviductal glycoprotein 1; 120kD		10.00			
10	129613	AW978517	Hs.172847	ESTs; Weakly similar to collagen alpha 1			3.40		
	129782	AW016932	Hs.104105	EST	9.00				
	129950	F07783	Hs.1369	decay accelerating factor for complement			87.80		
	129958	R27496	Hs.1378	annexin A3			44.60		
	129959	AL036554	Hs.274463	defensin; alpha 1; myeloid-related seque	2.72				
15	130160	AA305688	Hs.267695	UDP-Gal:betaGlcNAc beta 1;3-galactosyltr			42.20		
	130259	NM_000328	Hs.153614	retinitis pigmentosa GTPase regulator	2.54				
	130273	AW972422	Hs.153863	MAD (mothers against decapentaplegic; Dr		51.60			
	130312	AF056195	Hs.15430	DKFZP586G1219 protein			3.16		
	130436	NM_001928	Hs.155597	D component of complement (adipsin)					4.11
20	130523	AA999702	Hs.214507	ESTs			4.77		
	130799	AB028945	Hs.12696	ESTs	6.00				
	130885	NM_005883	Hs.20912	adenomatous polyposis coli like			3.54		
	131002	AL050295	Hs.22039	KIAA0758 protein					3.50
	131012	AL039940	Hs.202949	KIAA1102 protein	20.00				
25	131031	NM_001650	Hs.288650	aquaporin 4	41.20				
	131061	N64328	Hs.268744	ESTs; Moderately similar to KIAA0273 [H.		31.40			
	131066	AW169287	Hs.22588	ESTs		29.60			
	131082	AI091121	Hs.246218	ESTs; Weakly similar to zinc finger prot		9.00			
	131087	AF147709	Hs.22824	ESTs; Weakly similar to p160 myb-binding					3.86
30	131161	AF033382	Hs.23735	potassium voltage-gated channel; subfami			3.14		
	131179	AA171388	Hs.184482	DKFZP586D0624 protein			3.80		
	131182	AI824144	Hs.23912	ESTs					3.67
	131205	NM_003102	Hs.2420	superoxide dismutase 3; extracellular	2.98				
	131277	AA131466	Hs.23767	ESTs	3.15				
35	131281	AA251716	Hs.25227	ESTs		32.20			
	131282	X03350	Hs.4	alcohol dehydrogenase 3 (class I); gamma					3.44
	131285	AI567943	Hs.25274	ESTs; Moderately similar to putative sev			6.40		
	131355	R52804	Hs.25956	DKFZP564D206 protein	8.00				
	131391	AW085781	Hs.26270	ESTs	10.00				
40	131461	AA992841	Hs.27263	butyrate response factor 2 (EGF-response	28.80				
	131487	F13036	Hs.27373	Homo sapiens mRNA; cDNA DKFZp564O1763 (f				4.03	
	131517	AB037789	Hs.263395	ESTs; Highly similar to semaphorin VIa [	39.00				
	131545	AL137432	Hs.28564	ESTs			11.00		
	131583	AK000383	Hs.323092	ESTs; Weakly similar to dual specificity			10.00		
45	131647	AA359615	Hs.30089	ESTs	2.47				
	131675	H15205	Hs.30509	ESTs			3.06		
	131676	AI126821	Hs.30514	ESTs	45.80				
	131708	S60415	Hs.30941	calcium channel; voltage-dependent; beta	2.28				
	131717	X94630	Hs.3107	CD97 antigen					3.78
50	131756	AA443966	Hs.31595	ESTs		40.60			
	131762	AA744902	Hs.107767	ESTs; Moderately similar to CaM-KII inhi					3.67
	131821	AA017247	Hs.164577	ESTs	2.87				
	131839	AB014533	Hs.33010	KIAA0633 protein				3.48	
	131861	AL096858	Hs.184245	KIAA0929 protein Msx2 interacting nuclea	54.00				
55	132015	AI418006	Hs.3731	ESTs			49.20		
	132070	BE622641	Hs.38489	ESTs			34.80		
	132242	AA332697	Hs.42721	ESTs	2.68				
	132334	AW080704	Hs.45033	lacrima proline rich protein	4.66				
	132476	AL119844	Hs.49476	Homo sapiens clone TUA8 Cri-du-chat regi	34.20				
60	132490	NM_001290	Hs.4980	LIM binding domain 2					
	132533	AI922988	Hs.172510	ESTs	13.00				
	132598	X80031	Hs.530	collagen; type IV; alpha 3 (Goodpasture		30.60			
	132619	H28855	Hs.53447	ESTs; Moderately similar to kinesin ligh			4.02		
	132652	N41739	Hs.61260	ESTs			3.18		
65	132726	N52298	Hs.55608	ESTs; Weakly similar to cDNA EST yk484g1		11.43			
	133028	R51604	Hs.300842	ESTs	2.37				
	133071	BE384932	Hs.64313	ESTs	2.27				
	133120	NM_003278	Hs.65424	tetranectin (plasminogen-binding protein	2.63				
70	133129	AA428580	Hs.65551	ESTs					5.49
	133147	AA026533	Hs.66	interleukin 1 receptor-like 1	6.20				
	133151	NM_014051	Hs.94896	ESTs			3.69		
	133213	AA903424	Hs.6786	ESTs		31.40			
	133276	AW978439	Hs.69504	ESTs		9.00			
75	133377	AJ131245	Hs.7239	SEC24 (S. cerevisiae) related gene famil	41.20				
	133407	AF017987	Hs.7306	secreted frizzled-related protein 1	50.20				
	133535	AL134030	Hs.284180	protocadherin 2 (cadherin-like 2)			3.72		
	133537	U41518	Hs.74602	aquaporin 1 (channel-forming integral pr					3.35
	133656	BE149455	Hs.75415	Accession not listed in Genbank	2.65				
	133689	NM_001872	Hs.75572	carboxypeptidase B2 (plasma)		90.80			
80	133779	T58486	Hs.222566	ESTs			3.05		
	133978	AF035718	Hs.78061	transcription factor 21	2.92				
	133985	L34657	Hs.78146	platelet/endothelial cell adhesion molec					3.45
	134000	AW175787	Hs.334841	selenium binding protein 1					4.05
	134111	AI372588	Hs.8022	TU3A protein	4.49				
85	134185	AA285136	Hs.301914	Homo sapiens mRNA; cDNA DKFZp586K1220 (f				3.27	
	134204	AI873257	Hs.7994	ESTs; Weakly similar to CGI-69 protein [		40.80			



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	134641	AI092634	Hs.156114	protein tyrosine phosphatase; non-recept				3.76
	134677	AA251363	Hs.177711	ESTs		32.20		
	134745	NM_000685	Hs.89472	angiotensin receptor 1B	15.00			
5	134749	T28499	Hs.89485	carbonic anhydrase IV		3.05		
	134786	T29618	Hs.89640	angiotensin 1 receptor; TEK tyrosine ki			57.80	
	134825	U33749	Hs.197764	thyroid transcription factor 1				3.73
	134978	AI829008	Hs.333383	ficolin (collagen/fibrinogen domain-cont		2.52		
	135010	N50465	Hs.92927	ESTs			31.60	
10	135053	AW796190	Hs.93678	ESTs				3.21
	135081	AF069517	Hs.173993	RNA binding motif protein 6	28.80			
	135091	AA493650	Hs.94367	ESTs				4.24
	135135	AA775910	Hs.95011	syntrophin; beta 1 (dystrophin-associate		8.00		
	135203	C15737	Hs.269386	ESTs				4.31
15	135236	AI636208	Hs.96901	ESTs	43.00			
	135266	R41179	Hs.97393	Human mRNA for KIAA0328 gene; partial cd				6.42
	135346	NM_000928	Hs.992	phospholipase A2; group IB (pancreas)		3.82		
	135378	AW961818	Hs.24379	potassium voltage-gated channel; shaker-		4.15		
	135387	NM_001972	Hs.99863	elastase 2; neutrophil	37.20			
20	135388	W27965	Hs.99865	EST	38.80			
	135402	L12398	Hs.99922	dopamine receptor D4				4.21

25 TABLE 2B shows the accession numbers for those primekeys lacking unigenelD's for Table 2A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

30 Pkey: Unique Eos probeset identifier number  
CAT number: Gene cluster number  
Accession: Genbank accession numbers

Pkey	CAT number	Accessions
35	108447	43452_-7 AA079126
	108550	120073_1 AA084867 AA084996
	108655	127522_1 AA099960 AA113013
	102397	44371_-1 U41898
40	126303	1525933_1 D78841 D78880
	125810	1554054_1 H00083 R81062
	103627	2615_2 Z48513 Z48512
	121366	280401_1 AI743515 AA405617 AW276706
	114609	116777_1 AA079505 AA079537
	115272	172113_1 AW015947 AA211890 AA279425
45	108338	112186_1 AA070773 AA070774
	108434	114012_1 AA078899 AA078782 AA075788
	123802	genbank_AA620448 AA620448
	102310	NOT_FOUND_entrez_U33839 U33839
	102636	entrez_U67092 U67092
50	104776	genbank_AA026349 AA026349
	120504	genbank_AA256837 AA256837
	113502	genbank_T89130T89130
	108499	genbank_AA083103 AA083103
	101308	entrez_L41390 L41390
55	108629	genbank_AA102425 AA102425
	103098	221_215 M86361 Z26593 X02850 D13070 AE000659 M17649 M87869 M87871 X61077 M16286 AF018169 X61079 S59351 X60142 AF043169
	103241	entrez_X76223 X76223
	103508	entrez_Y10141 Y10141
	103575	entrez_Z26256 Z26256
60	119514	NOT_FOUND_entrez_W37937 W37937
	121082	genbank_AA398722 AA398722
	128634	AA464918_at AA464918
	105817	genbank_AA397825 AA397825
	121518	genbank_AA412155 AA412155
65	114449	genbank_AA020736 AA020736
	114648	genbank_AA101056 AA101056
	121950	genbank_AA429515 AA429515
	107723	genbank_AA015967 AA015967



Table 3A shows 452 genes up-regulated in chronically diseased lung relative to normal lung. Chronically diseased lung samples represent chronic non-malignant lung diseases such as fibrosis, emphysema, and bronchitis. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

5	Pkey:	Unique Eos probeset identifier number					
	ExAccn:	Exemplar Accession number, Genbank accession number					
	UnigenelD:	Unigene number					
	Unigene Title:	Unigene gene title					
10	R1:	80th percentile of AI for chronically diseased lung samples divided by the 90th percentile of AI for normal lung samples.					
	R2:	80th percentile of AI for chronically diseased lung samples divided by the 90th percentile of normal lung samples, squamous cell carcinomas and adenocarcinomas					
	R3:	70th percentile of AI for chronically diseased lung samples minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples divided by the 90th percentile of normal lung samples, squamous cell carcinomas and adenocarcinomas minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples					
15							
	Pkey	ExAccn	UnigenelD	Unigene Title	R1	R2	R3
20	135423	U50531	Hs.138751	Human BRCA2 region, mRNA sequence CG030	12.40		
	135378	AW961818	Hs.24379	MUM2 protein			2.13
	135346	NM_000928	Hs.992	phospholipase A2, group IB (pancreas)			
	135235	AW298244	Hs.293507	ESTs	12.40		
	135057	U90268	Hs.93810	cerebral cavernous malformations 1	11.67		
25	134951	BE305081	Hs.169358	hypothetical protein		8.00	
	134799	M36821	Hs.89690	GRO3 oncogene		8.20	
	134786	T29618	Hs.89640	TEK tyrosine kinase, endothelial (venous			
	134772	NM_000829	Hs.163697	glutamate receptor, ionotropic, AMPA 4	29.80		
	134752	BE246762	Hs.89499	arachidonate 5-lipoxygenase			1.93
	134749	T28499	Hs.89485	carbonic anhydrase IV			2.07
30	134696	BE326276	Hs.8861	ESTs			
	134636	NM_005582	Hs.87205	lymphocyte antigen 64 (mouse) homolog, r	13.60		
	134627	AI018768	Hs.12482	glyceronephosphate O-acyltransferase			1.92
	134622	AW975159	Hs.293097	ESTs, Weakly similar to A55380 faciogeni			1.92
35	134570	U66615	Hs.172280	SWI/SNF related, matrix associated, acti	13.20		
	134561	U76421	Hs.85302	adenosine deaminase, RNA-specific, B1 (h			1.78
	134468	NM_001772	Hs.83731	CD33 antigen (gp67)		6.20	
	134417	NM_006416	Hs.82921	solute carrier family 35 (CMP-sialic aci			
	134343	D50683	Hs.82028	transforming growth factor, beta recepto			
40	134323	BE170651	Hs.8700	deleted in liver cancer 1			
	134300	NM_001430	Hs.8136	endothelial PAS domain protein 1			
	134299	AW580939	Hs.97199	complement component C1q receptor			
	134253	X52075	Hs.80738	sialophorin (gpL115, leukosialin, CD43)	20.60		
	134182	D52059	Hs.7972	KIAA0871 protein	12.20		
45	133985	L34657	Hs.78146	platelet/endothelial cell adhesion molec			
	133978	AF035718	Hs.78061	transcription factor 21			
	133835	AI677897	Hs.76640	RGC32 protein			
	133651	AI301740	Hs.173381	dihydropyrimidinase-like 2			
	133633	D21262	Hs.75337	nucleolar and colled-body phosphprotein	15.20		
50	133565	AW955776	Hs.313500	ESTs, Moderately similar to ALU7_HUMAN A			
	133548	AW946384	Hs.178112	DNA segment, single copy probe LNS-CAI/L			1.77
	133488	AA335295	Hs.74120	adipose specific 2			
	133478	X83703	Hs.31432	cardiac ankyrin repeat protein			2.08
	133337	AF085983	Hs.293676	ESTs		9.60	
55	133200	AB037715	Hs.183639	hypothetical protein FLJ10210			1.77
	133153	AF070592	Hs.66170	HSKM-B protein	30.60		
	133130	AI128606	Hs.6557	zinc finger protein 161	22.60		
	133120	NM_003278	Hs.65424	tetranectin (plasminogen-binding protein			
	132928	AW168082	Hs.169449	protein kinase C, alpha	13.80		
60	132836	AB023177	Hs.29900	KIAA0960 protein			
	132799	W73311	Hs.169407	SAC2 (suppressor of actin mutations 2,	41.60		
	132742	AA025480	Hs.292812	ESTs, Weakly similar to T33468 hypotheti	40.40		
	132548	X12830	Hs.193400	interleukin 6 receptor		7.20	
	132476	AL119844	Hs.49476	Homo sapiens clone TUA8 Cri-du-chat regi		4.76	
	132439	AK001942	Hs.4863	hypothetical protein DKFZp566A1524			1.88
65	132240	AB018324	Hs.42676	KIAA0781 protein	21.20		
	132210	NM_007203	Hs.42322	A kinase (PRKA) anchor protein 2			1.99
	132199	AL041299	Hs.165084	ESTs	15.20		
	131751	T96555	Hs.31562	ESTs			1.76
70	131745	AI828559	Hs.31447	ESTs, Moderately similar to A46010 X-II	27.80		
	131694	NM_000246	Hs.3076	MHC class II transactivator		4.00	
	131686	NM_012296	Hs.30687	GRB2-associated binding protein 2			
	131676	AI126821	Hs.30514	ESTs		6.20	
	131629	Z45794	Hs.238809	ESTs	21.40		
75	131589	C18825	Hs.29191	epithelial membrane protein 2			
	131536	AA019201	Hs.269210	ESTs		9.40	
	131517	AB037789	Hs.263395	sema domain, transmembrane domain (TM),		3.59	
	131355	R52804	Hs.25956	DKFZP564D206 protein		4.48	
	131253	R71802	Hs.24853	ESTs	15.00		
80	131207	AF104266	Hs.24212	latrophilin			1.75
	131156	AI472209	Hs.323117	ESTs			1.84
	131066	AW169287	Hs.22588	ESTs		3.54	
	131061	N64328	Hs.268744	KIAA1796 protein			
	131053	AA348541	Hs.296261	guanine nucleotide binding protein (G pr			1.93
85	130895	AA641767	Hs.21015	hypothetical protein DKFZp564L0864 simil	16.60		
	130762	D84371	Hs.1898	paraonoxase 1	12.00		



	130657	AW337575	Hs.201591	ESTs			
	130655	AI831962	Hs.17409	cysteine-rich protein 1 (intestinal)			
	130589	AL110226	Hs.16441	DKFZP434H204 protein		2.08	
5	130562	D50402	Hs.182611	solute carrier family 11 (proton-coupled		1.91	
	130555	R69743	Hs.116774	integrin, alpha 1	9.60		
	130365	W56119	Hs.155103	eukaryotic translation initiation factor	11.60		
	130273	AW972422	Hs.153863	MAD (mothers against decapentaplegic, Dr	6.60		
	130259	NM_000328	Hs.153614	refinitis pigmentosa GTPase regulator		1.91	
10	130090	H97878	Hs.132390	zinc finger protein 36 (KOX 18)	21.20		
	129958	R27496	Hs.1378	annexin A3	5.05		
	129898	AI672731	Hs.13256	ESTs			
	129875	AA181018	Hs.13056	hypothetical protein FLJ13920	18.60		
	129699	AB007899	Hs.12017	homolog of yeast ubiquitin-protein ligas			
15	129626	F13272	Hs.111334	ferritin, light polypeptide			
	129598	N30436	Hs.11556	Homo sapiens cDNA FLJ12566 fis, clone NT	22.63		
	129593	AI338247	Hs.98314	Homo sapiens mRNA; cDNA DKFZp586L0120 (f			
	129565	X77777	Hs.198726	vasoactive intestinal peptide receptor 1		2.53	
	129527	AA769221	Hs.270847	delta-tubulin	39.20		
20	129402	W72062	Hs.111112	ESTs		2.11	
	129385	AA172106	Hs.110950	Rag C protein	15.20		
	129315	NM_014563	Hs.174038	spondyloepiphyseal dysplasia, late	12.40		
	129312	T97579	Hs.110334	ESTs, Weakly similar to I78885 serine/th	20.83		
	129240	AA361258	Hs.237868	interleukin 7 receptor		1.95	
25	129210	AL039940	Hs.202949	KIAA1102 protein			
	129122	AW958473	Hs.301957	nudix (nucleoside diphosphate linked moi	4.20		
	129057	N90866	Hs.276770	CDW52 antigen (CAMPATH-1 antigen)			
	128946	Y13153	Hs.107318	kynurenine 3-monooxygenase (kynurenine 3	5.20		
	128798	AF015525	Hs.302043	chemokine (C-C motif) receptor-like 2			
30	128789	AW368576	Hs.139851	caveolin 2		2.24	
	128778	AA504776	Hs.186709	ESTs, Weakly similar to I38022 hypothet	12.20		
	128766	AW160432	Hs.296460	craniofacial development protein 1	26.40		
	128631	R44238	Hs.155546	KIAA1080 protein; Golgi-associated, gamm			
	128624	BE154765	Hs.102647	ESTs, Weakly similar to TRHY_HUMAN TRICH		1.78	
35	128609	NM_003616	Hs.102456	survival of motor neuron protein interac	16.00		
	128603	NM_004915	Hs.10237	ATP-binding cassette, sub-family G (WHIT	12.80		
	128598	AA305407	Hs.102308	potassium inwardly-rectifying channel, s		4.00	
	128458	H55864	Hs.56340	ESTs			
40	128061	AF150882	Hs.186877	sodium channel, voltage-gated, type XII,	17.20		
	127968	AA830201	Hs.124347	ESTs	21.30		
	127959	AI302471	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L			
	127944	AI557081	Hs.262476	S-adenosylmethionine decarboxylase 1	10.60		
	127925	AA805151	Hs.3628	mitogen-activated protein kinase kinase	13.40		
45	127896	AI689586	Hs.222194	ESTs		7.00	
	127859	AA761802	Hs.291559	ESTs	14.00		
	127817	AA836641	Hs.163085	ESTs	14.00		
	127742	AW293496	Hs.180138	ESTs	11.00		
	127628	AI240102	Hs.322430	NDRG family, member 4	11.10		
50	127609	X80031	Hs.530	collagen, type IV, alpha 3 (Goodpasture			
	127582	AA908954	Hs.130844	ESTs	19.60		
	127543	AK000787	Hs.157392	Homo sapiens cDNA FLJ20780 fis, clone CO	15.40		
	127535	AA568424	Hs.164450	ESTs	17.50		
	127404	AI379920	Hs.270224	ESTs	14.60		
	127396	L31968	Hs.187991	DKFZP564A122 protein	15.40		
55	127374	AA442797	Hs.312110	ESTs, Weakly similar to I38022 hypothet	14.60		
	127346	AA203616	Hs.44896	DnaJ (Hsp40) homolog, subfamily B, membe	21.00		
	127340	BE047653	Hs.119183	ESTs, Weakly similar to ZN91_HUMAN ZINC	15.80		
	127307	AW962712	Hs.126712	ESTs, Weakly similar to AF191020 1 E2IG5			
	127242	AW390395	Hs.181301	cathepsin S	22.60		
60	127167	AA625690	Hs.190272	ESTs	21.40		
	127046	AA321948	Hs.293968	ESTs	41.20		
	126928	AA480902	Hs.137401	ESTs	11.00		
	126900	AF137386	Hs.12701	plasmolipin		1.78	
65	126852	AA399961		gb:zu68c01.r1 Soares_testis_NHT Homo sap	5.60		
	126816	AA248234		gb:csq2228.seq.F Human fetal heart, Lamb	12.20		
	126812	AB037860	Hs.173933	nuclear factor I/A	17.19		
	126666	AA648886	Hs.151999	ESTs	13.57		
	126645	AA316181	Hs.61635	six transmembrane epithelial antigen of	15.40		
70	126592	AI611153	Hs.6093	Homo sapiens cDNA: FLJ22783 fis, clone K	4.67		
	126556	AF255303	Hs.112227	membrane-associated nucleic acid binding	18.00		
	126433	AA325606		gb:EST28707 Cerebellum II Homo sapiens c	16.77		
	126299	AW979155	Hs.298275	amino acid transporter 2	14.60		
	126218	AL049801	Hs.13649	Novel human gene mapping to chromosome 13		3.50	
75	126182	AA721331	Hs.293771	ESTs	13.40		
	126177	AW752782	Hs.129750	hypothetical protein FLJ10546	18.20		
	126142	H86261	Hs.40568	ESTs	14.00		
	126077	M78772	Hs.210836	ESTs	16.59		
	125994	AI990529	Hs.270799	ESTs	17.40		
	125934	AA193325	Hs.32646	hypothetical protein FLJ21901	13.00		
80	125847	AW161885	Hs.249034	ESTs	49.57		
	125831	H04043		gb:yj45c03.r1 Soares_placenta Nb2HP Homo			
	125731	R61771	Hs.26912	ESTs	13.20		
	125676	BE612918	Hs.151973	hypothetical protein FLJ23511	11.20		
	125561	F18572	Hs.22978	ESTs, Weakly similar to ALU4_HUMAN ALU S			
85	125552	H09701	Hs.278366	ESTs, Weakly similar to I38022 hypotheti	12.60		
	125489	H49193	Hs.124984	ESTs, Moderately similar to ALU7_HUMAN A	33.40		



	125422	AA903229	Hs.153717	ESTs		1.80
	125331	AI422996	Hs.161378	ESTs	38.00	
	125309	T12411	Hs.183745	hypothetical protein FLJ13456	18.20	
5	125167	AL137540	Hs.102541	netrin 4		1.95
	125139	AW194933	Hs.9788	hypothetical protein MGC10924 similar to		1.84
	125042	T78906	Hs.269432	ESTs, Moderately similar to ALU1_HUMAN	21.80	
	124711	NM_004657	Hs.26530	serum deprivation response (phosphatidyl		10.60
	124631	NM_014053	Hs.270594	FLVCR protein	23.20	
10	124578	N68321	Hs.231500	EST	21.43	
	124574	AL036596	Hs.42322	A kinase (PRKA) anchor protein 2		1.77
	124472	N52517	Hs.102670	EST	37.20	
	124438	BE178536	Hs.11090	membrane-spanning 4-domains, subfamily A		
	124357	N22401		gb:yyw37g07.s1 Morton Fetal Cochlea Homo	14.64	
15	124306	AW973078	Hs.293039	ESTs		4.00
	124214	H58608	Hs.151323	ESTs		
	124097	AW298235	Hs.101689	ESTs	27.20	
	123978	T89832	Hs.170278	ESTs		2.03
	123972	T46848	Hs.70337	immunoglobulin superfamily, member 4	6.00	
20	123961	AL050184	Hs.21610	DKFZP434B203 protein		1.79
	123936	NM_004673	Hs.241519	angiotensin-like 1	15.80	
	123802	AA620448		gb:ae58c09.s1 Stratagene lung carcinoma	4.23	
	123734	AA609861	Hs.312447	ESTs	4.20	
	123619	AA602964		gb:no97c02.s1 NCI_CGAP_Pr2 Homo sapiens	33.60	
25	123596	AA421130	Hs.112640	EST	10.93	
	123476	AA384564	Hs.108829	ESTs		2.18
	123340	AA504264	Hs.182937	peptidylprolyl isomerase A (cyclophilin	11.20	
	123190	AA489212	Hs.105228	EST	14.20	
	123136	AW451999	Hs.194024	ESTs		7.00
30	123073	AA485061	Hs.105852	ESTs	31.20	
	123055	AA482005	Hs.105102	ESTs, Weakly similar to reverse transcri		4.80
	122699	AA456130	Hs.301721	KIAA1255 protein		5.00
	122679	AA811286	Hs.192837	ESTs, Weakly similar to ALU5_HUMAN ALU S	14.40	
	122633	NM_001546	Hs.34853	inhibitor of DNA binding 4, dominant neg		
35	122553	AA451884	Hs.190121	ESTs	40.00	
	122544	AW973253	Hs.292689	ESTs	15.40	
	122485	AA524547	Hs.160318	FXFD domain-containing ion transport reg		1.81
	122211	AA300900	Hs.98849	ESTs, Moderately similar to AF161511.1 H	12.10	
	122127	AW207175	Hs.106771	ESTs		1.95
40	122011	AA431082		gb:zw78a10.s1 Soares_testis_NHT Homo sap		1.89
	121992	AI860775	Hs.98506	ESTs		3.60
	121989	W56487	Hs.193784	Homo sapiens mRNA; cDNA DKFZp586K1922 (f		2.01
	121835	AB033030	Hs.300670	KIAA1204 protein		1.85
	121726	AF241254	Hs.178098	angiotensin I converting enzyme (peptidy	12.43	
45	121690	AV660305	Hs.110286	ESTs		1.82
	121643	AA640987	Hs.193767	ESTs		
	121633	AA417011	Hs.98175	EST	14.00	
	121622	AA416931	Hs.126065	ESTs		16.40
	121497	AA412031	Hs.97901	EST	11.20	
50	121351	AW206227	Hs.287727	hypothetical protein FLJ23132	12.20	
	121314	W07343	Hs.182538	phospholipid scramblase 4		1.83
	121242	AA400857	Hs.97509	ESTs	22.40	
	121059	AA393283		gb:zl74e03.r1 Soares_testis_NHT Homo sap	14.80	
	120934	AA226198		gb:nc26a07.s1 NCI_CGAP_Pr1 Homo sapiens	21.20	
55	120755	AA312934	Hs.190745	Homo sapiens cDNA: FLJ21326 fis, clone		1.79
	120637	AA811804		gb:ob39a05.s1 NCI_CGAP_GCB1 Homo sapiens	20.00	
	120484	AA253170	Hs.96473	EST	40.20	
	120336	N85785	Hs.181165	eukaryotic translation elongation factor		6.60
	120266	AI807264	Hs.205442	ESTs, Weakly similar to T34036 hypotheti	16.80	
60	120132	W57554	Hs.125019	ESTs		4.73
	120041	AA830882	Hs.59368	ESTs		1.75
	119996	W88996	Hs.59134	EST		7.20
	119970	AA767718	Hs.93581	hypothetical protein FLJ10512	11.20	
	119861	W78816	Hs.49943	ESTs, Weakly similar to S65657 alpha-1C-		3.78
65	119824	W74536	Hs.184	advanced glycosylation end product-speci		
	119740	AW021407	Hs.21068	hypothetical protein	20.20	
	119271	AI061118	Hs.65328	Fanconi anemia, complementation group F	15.20	
	119221	C14322	Hs.250700	tryptase beta 1		
	119126	R45175	Hs.117183	ESTs	12.60	
70	119073	BE245360	Hs.279477	ESTs		
	118928	AA312799	Hs.283689	activator of CREM in testis		10.00
	118901	AW292577	Hs.94445	ESTs		3.96
	118661	AL137554	Hs.49927	protein kinase NYD-SP15		9.60
	118607	AI377444	Hs.54245	ESTs, Weakly similar to S65824 reverse t	10.40	
75	118449	AI813865	Hs.164478	hypothetical protein FLJ21939 similar to		1.90
	118416	N66028	Hs.49105	FKBP-associated protein	16.20	
	118379	N64491	Hs.48990	ESTs		4.00
	118329	N63520		gb:yy62f01.s1 Soares_multiple_sclerosis_		6.60
	118320	N63451	Hs.141600	ESTs, Weakly similar to alternatively s		3.80
80	118253	AA497044	Hs.20887	hypothetical protein FLJ10392	17.60	
	118124	N56968	Hs.46707	chromosome 21 open reading frame 37	14.00	
	118056	AB037746	Hs.42768	hypothetical protein DKFZp761O0113		1.86
	118032	N52802	Hs.47544	EST		5.00
	117840	T26379	Hs.48802	Homo sapiens clone 23632 mRNA sequence		4.00
85	117404	N39725	Hs.15220	zinc finger protein 106		1.90
	117314	N32498	Hs.42829	ESTs	14.20	



	117209	W03011	Hs.306881	MSTP043 protein			
	117023	AW070211	Hs.102415	Homo sapiens mRNA; cDNA DKFZp586N0121 (f		2.31	
	116814	H50834		gb:yp86a10.s1 Soares fetal liver spleen	20.20		
5	116784	AB007979	Hs.301281	Homo sapiens mRNA, chromosome 1 specific		3.51	
	116766	AI608657	Hs.95097	ESTs	16.20		
	116712	AW901618	Hs.61935	Homo sapiens mRNA; cDNA DKFZp7611071 (fr		6.80	
	116707	H10344	Hs.49050	ESTs, Weakly similar to A Chain A, Human	18.60		
	116351	AL133623	Hs.82501	similar to mouse Xm1 / Dhml2 protein	19.40		
10	116279	AW971248	Hs.291289	ESTs, Weakly similar to ALU1_HUMAN ALU S			
	116166	AL039940	Hs.202949	KIAA1102 protein		2.13	
	116152	AL040521	Hs.15220	zinc finger protein 106		1.75	
	116117	BE613410	Hs.31575	SEC53, endoplasmic reticulum translocon	13.20		
	116107	AL133916	Hs.172572	hypothetical protein FLJ20093	30.11		
15	115965	AA001732	Hs.173233	hypothetical protein FLJ10970		2.36	
	115955	AF263613	Hs.44198	intracellular membrane-associated calciu	18.20		
	115844	AI373062	Hs.332938	hypothetical protein MGC5370	18.57		
	115683	AF255910	Hs.54650	junctional adhesion molecule 2		23.00	
	115673	AA406341	Hs.269908	Homo sapiens cDNA FLJ11991 fis, clone HE	11.82		
20	115672	AI889110	Hs.73251	ESTs	10.60		
	115566	AI142336	Hs.43977	Human DNA sequence from clone RP11-196N1		1.76	
	115313	AA808001	Hs.184411	albumin	25.20		
	115279	AW964897	Hs.290825	ESTs		8.00	
	115230	AA278300	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L		1.80	
25	115110	AK001671	Hs.11387	KIAA1453 protein	14.20		
	114999	BE246481	Hs.87856	ESTs	19.20		
	114930	AA237022	Hs.188717	ESTs		5.60	
	114922	AA235672	Hs.87491	ESTs		3.60	
	114837	BE244930	Hs.166895	ESTs	43.70		
30	114769	AA149060	Hs.296100	ESTs	11.00		
	114761	AA143781	Hs.126280	hypothetical protein FLJ23393	14.00		
	114736	AI610347	Hs.103812	ESTs, Moderately similar to ALU1_HUMAN A		4.20	
	114596	AA310162	Hs.169248	cytochrome c	10.71		
	114518	AW163267	Hs.106469	suppressor of var1 (S.cerevisiae) 3-like	20.40		
35	114455	H37908	Hs.271616	ESTs, Weakly similar to ALU8_HUMAN ALU S	20.40		
	114452	AI369275	Hs.243010	Homo sapiens cDNA FLJ14445 fis, clone HE		17.20	
	114359	NM_016929	Hs.283021	chloride intracellular channel 5		2.09	
	114357	R41677	Hs.6107	Homo sapiens cDNA FLJ14839 fis, clone OV	12.40		
40	114251	H15261	Hs.21948	ESTs		2.00	
	114138	AW384793	Hs.15740	Homo sapiens mRNA; cDNA DKFZp434E033 (fr		11.40	
	114124	W57554	Hs.125019	ESTs		6.04	
	113946	AW083883	Hs.37896	Homo sapiens cDNA FLJ13510 fis, clone PL		1.82	
	113695	T96965	Hs.17948	ESTs, Weakly similar to ALUB_HUMAN !!!!			
	113606	NM_013343	Hs.278951	NAG-7 protein		2.15	
45	113590	R49642	Hs.142447	ESTs, Weakly similar to ALU1_HUMAN ALU S		3.60	
	113560	T91015	Hs.268626	ESTs	32.00		
	113552	AI654223	Hs.16026	hypothetical protein FLJ23191			
	113540	AW152618	Hs.16757	ESTs			
	113502	T89130		gb:ye12d01.s1 Stratagene lung (937210) H		8.35	
50	113288	AI076838	Hs.12967	ESTs	12.40		
	113252	NM_004469	Hs.11392	c-fos induced growth factor (vascular en		4.27	
	113238	R45467	Hs.189813	ESTs			
	113203	AA743563	Hs.10305	ESTs	21.20		
	113195	H83265	Hs.8881	ESTs, Weakly similar to S41044 chromosom		1.92	
55	113089	T40707	Hs.270862	ESTs	14.33		
	113076	AF033199	Hs.8198	zinc finger protein 204		6.00	
	113009	T23699	Hs.7246	ESTs		9.40	
	112937	AI694320	Hs.6295	ESTs, Weakly similar to T17248 hypotheti		12.20	
	112891	T03927	Hs.293147	ESTs, Moderately similar to A46010 X-li	10.57		
60	112794	R97018		gb:yq74b08.s1 Soares fetal liver spleen	26.60		
	112691	R88708	Hs.220647	ESTs	15.33		
	112602	AW004045	Hs.203365	ESTs	15.60		
	112366	AF035318	Hs.12533	Homo sapiens clone 23705 mRNA sequence	15.40		
	112210	R49645	Hs.7004	ESTs	14.00		
65	112064	AL049390	Hs.22689	Homo sapiens mRNA; cDNA DKFZp586O1318 (f	13.00		
	111998	R42379	Hs.138283	ESTs	11.00		
	111987	NM_015310	Hs.6763	KIAA0942 protein	22.40		
	111803	AA593731	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A		1.77	
	111737	H04607	Hs.9218	ESTs		1.86	
70	111605	T91061	Hs.194178	ESTs, Moderately similar to PC4259 ferri	23.00		
	111510	R07856	Hs.16355	ESTs	11.02		
	111341	AL157484	Hs.22483	Homo sapiens mRNA; cDNA DKFZp762M127 (fr		1.88	
	111280	AA373527	Hs.19385	CGI-58 protein	18.40		
	111247	AW058350	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f			
75	111232	AI247763	Hs.16928	ESTs	27.60		
	110942	R63503	Hs.28419	ESTs	14.80		
	110924	AW058463	Hs.12940	zinc-fingers and homeoboxes 1	24.71		
	110837	H03109	Hs.108920	HT018 protein		2.18	
	110824	AI767183	Hs.26942	ESTs	12.20		
80	110776	AB032417	Hs.19545	frizzled (Drosophila) homolog 4		1.75	
	110576	H60869	Hs.37889	ESTs	13.00		
	110369	AK000768	Hs.107872	hypothetical protein FLJ20761		5.60	
	110099	R44557	Hs.23748	ESTs		2.31	
	109984	AI796320	Hs.10299	Homo sapiens cDNA FLJ13545 fis, clone PL			
85	109958	AA001266	Hs.133521	ESTs	11.25		
	109893	AA884208	Hs.30484	ESTs		2.68	



5	109842	AW818436	Hs.23590	solute carrier family 16 (monocarboxylic	23.83		
	109837	H00656	Hs.29792	ESTs, Weakly similar to I38022 hypothe		17.20	3.91
	109796	AI800515	Hs.12024	ESTs		9.60	
	109688	R41900	Hs.22245	ESTs			
	109648	H17800	Hs.7154	ESTs	22.80		
10	109613	H47315	Hs.27519	ESTs			
	109550	AW021488	Hs.26981	ESTs			
	109523	AW193342	Hs.24144	ESTs			1.89
	109472	AK001989	Hs.91165	hypothetical protein		6.00	
	109355	AA524525	Hs.48297	DKFZP586C1620 protein	15.00		
15	109260	AW978515	Hs.131915	KIAA0863 protein	25.60		
	108781	AA128654		gb:zn98g07.s1 Stratagene fetal retina 93	14.20		
	108663	BE219231	Hs.292653	ESTs, Weakly similar to T26845 hypothe	11.00		
	108573	AA086005		gb:zl84c04.s1 Stratagene colon (937204)	26.00		
	108480	AL133092	Hs.68055	hypothetical protein DKFZp434i0428			
20	108382	NM_006770	Hs.67726	macrophage receptor with collagenous str			1.83
	108174	AA055632	Hs.303070	ESTs	15.20		
	108138	AL049990	Hs.51515	Homo sapiens mRNA; cDNA DKFZp564G112 (fr		3.60	
	108087	AA045708	Hs.40545	ESTs	15.44		
	108048	AI797341	Hs.165195	Homo sapiens cDNA FLJ14237 fis, clone NT		11.40	
25	108041	AW204712	Hs.61957	ESTs			
	107997	AL049176	Hs.82223	chordin-like		4.76	
	107994	AA036811	Hs.48469	LIM domains containing 1			
	107922	BE153855	Hs.61460	Ig superfamily receptor LNIR	14.20		
	107681	BE379594	Hs.49136	ESTs, Moderately similar to ALU7_HUMAN A	51.80		
30	107666	AA010611	Hs.60418	EST	29.20		
	107332	T87750	Hs.183297	DKFZP566F2124 protein	10.73		
	107292	BE166479	Hs.4789	Homo sapiens serologically defined breas	32.00		
	107230	AI034467	Hs.34650	ESTs	17.40		
	107168	W57578	Hs.237955	RAB7, member RAS oncogene family	10.43		
35	107160	AA314490	Hs.27669	KIAA1563 protein	11.40		
	107054	AI076459	Hs.15978	KIAA1272 protein			
	107029	AF264750	Hs.288971	myeloid/lymphoid or mixed-lineage leukem	21.40		
	106999	H93281	Hs.10710	hypothetical protein FLJ20417	35.80		
	106954	AF128847	Hs.204038	indolethylamine N-methyltransferase			1.76
40	106870	AI983730	Hs.26530	serum deprivation response (phosphatidyl			
	106865	AW192535	Hs.19479	ESTs	13.40		
	106844	AA485055	Hs.158213	sperm associated antigen 6		7.13	
	106820	NM_016831	Hs.12592	period (Drosophila) homolog 3		7.00	
	106818	AK002135	Hs.3542	hypothetical protein FLJ11273	13.00		
45	106797	AI768801	Hs.169943	Homo sapiens cDNA FLJ13569 fis, clone PL			2.05
	106773	AA478109	Hs.188833	ESTs			
	106747	NM_007118	Hs.171957	triple functional domain (PTPRF interact	12.60		
	106743	BE613328	Hs.21938	hypothetical protein FLJ12492	10.60		
	106667	AW360847	Hs.16578	ESTs			
50	106605	AW772298	Hs.21103	Homo sapiens mRNA; cDNA DKFZp564B076 (fr			2.40
	106567	AW450408	Hs.86412	chromosome 9 open reading frame 5			1.78
	106562	AL031846	Hs.152151	plakophilin 4			1.76
	106536	AA329648	Hs.23804	ESTs, Weakly similar to PN0099 son3 prot			2.19
	106533	AL134708	Hs.145998	ESTs	23.20		
55	106507	AA259068	Hs.267819	protein phosphatase 1, regulatory (inhib	15.20		
	106490	AA404265	Hs.115537	putative dipeptidase			
	106474	BE383668	Hs.42484	hypothetical protein FLJ10618	10.44		
	106211	AA428240	Hs.126083	ESTs		29.80	
	105986	AB037722	Hs.8707	KIAA1301 protein		3.70	
60	105894	AI904740	Hs.25691	receptor (calcitonin) activity modifying			1.94
	105847	AW964490	Hs.32241	ESTs, Weakly similar to S65657 alpha-1C-			1.75
	105803	AW747996	Hs.160999	ESTs, Moderately similar to A56194 throm			2.47
	105731	AA834664	Hs.29131	nuclear receptor coactivator 2	10.71		
	105729	H46612	Hs.293815	Homo sapiens HSPC285 mRNA, partial cds			
65	105688	AI299139	Hs.17517	ESTs	23.40		
	105510	Z42047	Hs.283978	Homo sapiens PRO2751 mRNA, complete cds	37.20		
	105101	H63202	Hs.38163	ESTs		8.30	
	104989	R65998	Hs.285243	hypothetical protein FLJ22029		8.09	
	104986	AW088826	Hs.117176	poly(A)-binding protein, nuclear 1			1.92
70	104969	AI670947	Hs.78406	phosphatidylinositol-4-phosphate 5-kinas		5.40	
	104903	AI436323	Hs.31141	Homo sapiens mRNA for KIAA1568 protein,		7.60	
	104896	AW015318	Hs.23165	ESTs	13.80		
	104865	T79340	Hs.22575	Homo sapiens cDNA: FLJ21042 fis, clone C			
	104825	AA035613	Hs.141883	ESTs			1.87
75	104781	AA099904	Hs.21610	DKFZP434B203 protein			1.93
	104776	AA026349		gb:zj99i01.s1 Soares_pregnant_uterus_NbH		10.20	
	104691	U29690	Hs.37744	Homo sapiens beta-1 adrenergic receptor		5.69	
	104667	AI239923	Hs.30098	ESTs		3.82	
	104404	H58762		gb:EST00057 HE6W Homo sapiens cDNA clone		4.20	
80	104392	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	27.20		
	104212	AB002298	Hs.173035	KIAA0300 protein			1.91
	104074	AL162039	Hs.31422	Homo sapiens mRNA; cDNA DKFZp434M229 (fr	11.20		
	103749	AL135301	Hs.8768	hypothetical protein FLJ10849	10.86		
	103645	AW246253	Hs.7043	succinate-CoA ligase, GDP-forming, alpha	12.00		
85	103554	AI878826	Hs.323469	caveolin 1, caveolae protein, 22kD			1.80
	103541	AI815601	Hs.79197	CD83 antigen (activated B lymphocytes, i			
	103496	Y09267	Hs.132821	flavin containing monooxygenase 2			
	103428	BE383507	Hs.78921	A kinase (PRKA) anchor protein 1	11.20		
	103353	X89399	Hs.119274	RAS p21 protein activator (GTPase activa	19.80		



	103295	X81479	Hs.2375	egf-like module containing, mucin-like,	3.60	
	103280	U84722	Hs.76206	cadherin 5, type 2, VE-cadherin (vascula		
	103100	NM_005574	Hs.184585	LIM domain only 2 (rhombotin-like 1)	1.76	
5	103025	NM_002837	Hs.123641	protein tyrosine phosphatase, receptor t	2.15	
	102698	M18667	Hs.1867	progastricsin (pepsinogen C)		
	102659	BE245169	Hs.211610	CUG triplet repeat, RNA-binding protein	11.00	
	102580	U60808	Hs.152981	CDP-diacylglycerol synthase (phosphatida	25.40	
	102417	AA034127	Hs.153487	signal transducing adaptor molecule (SH3	14.00	
10	102363	NM_003734	Hs.198241	amine oxidase, copper containing 3 (vasc		
	102302	AA306342	Hs.69171	protein kinase C-like 2	10.86	
	102283	AW161552	Hs.83381	guanine nucleotide binding protein 11		
	102188	U20350	Hs.78913	chemokine (C-X3-C) receptor 1	7.40	
	102151	T27013	Hs.3132	steroidogenic acute regulatory protein	16.40	
15	101957	L28824	Hs.74101	spleen tyrosine kinase	15.40	
	101842	M93221	Hs.75182	mannose receptor, C type 1		
	101771	NM_002432	Hs.153837	myeloid cell nuclear differentiation ant		
	101764	AI198550	Hs.81256	S100 calcium-binding protein A4 (calcium	1.78	
	101716	AF050658	Hs.25663	tachykinin, precursor 1 (substance K, su	18.80	
20	101678	M62505	Hs.2161	complement component 5 receptor 1 (C5a I	2.22	
	101447	M21305		gb:Human alpha satellite and satellite 3	504.80	
	101383	NM_000132	Hs.79345	coagulation factor VIII, procoagulant co	31.00	
	101346	AI738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(N	1.75	
	101345	NM_005795	Hs.152175	calcitonin receptor-like		
25	101336	NM_006732	Hs.75678	FBJ murine osteosarcoma viral oncogene h	2.24	
	101330	L43821	Hs.80261	enhancer of filamentation 1 (cas-like do		
	101277	BE297626	Hs.296049	microfibrillar-associated protein 4		
	101262	L35854		gb:Human dystrophin (dp140) mRNA, 5' end	19.00	
	101168	NM_005308	Hs.211569	G protein-coupled receptor kinase 5	2.01	
30	101102	NM_003243	Hs.79059	transforming growth factor, beta recepto		
	101088	X70697	Hs.553	solute carrier family 6 (neurotransmitte	7.52	
	101066	AW970254	Hs.889	Charot-Leyden crystal protein	19.38	
	100971	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte	1.91	
	100893	BE245294	Hs.180789	S164 protein	15.40	
35	100770	W25797.comp	Hs.177486	amyloid beta (A4) precursor protein (pro	11.20	
	100716	X89887	Hs.172350	HIR (histone cell cycle regulation defec	14.80	
	100555	M69181		gb:Human nonmuscle myosin heavy chain-B	33.00	
	100425	NM_014747	Hs.78748	KIAA0237 gene product	16.20	
40	100408	D86640	Hs.56045	src homology three (SH3) and cysteine ri	4.00	
	100382	D83407	Hs.156007	Down syndrome critical region gene 1-lik	4.24	
	100351	D64158			6.20	
	100299	D49493	Hs.2171	growth differentiation factor 10	21.20	
	100134	AA305746	Hs.49	macrophage scavenger receptor 1		
	100108	U09577	Hs.76873	hyaluronoglucosaminidase 2	1.79	
45	100095	Z97171	Hs.78454	myocilin, trabecular meshwork inducible	5.40	
	100066				11.29	

TABLE 3B shows the accession numbers for those primekeys lacking unigenelD's for Table 3A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number  
CAT number: Gene cluster number  
Accession: Genbank accession numbers

60	Pkey	CAT number	Accessions
	123619	371681_1	AA602964 AA609200
	126433	127143_1	AA325606 AA099517 N89423
	125831	1522905_1	H04043 D60988 D60337
65	126816	122973_1	AA248234 AA090985
	126852	136135_1	AA399961 AA128347
	121059	273450_1	AA393283 AA398628
	120637	200885_1	AA811804 AA809404 AA286907 AW977624
	122011	7617_-2	AA431082
70	120934	177521_1	AA226198 AA226513 AA383773
	123802	genbank_AA620448	AA620448
	116814	genbank_H50834	H50834
	118329	genbank_N63520	N63520
	104404	H58762_at	H58762
75	104776	genbank_AA026349	AA026349
	113502	genbank_T89130T89130	
	101262	entrez_L35854 L35854	
	108573	genbank_AA086005	AA086005
	101447	entrez_M21305 M21305	
80	124357	genbank_N22401	N22401
	108781	genbank_AA128654	AA128654
	112794	genbank_R97018	R97018
	100351	entrez_D64158 D64158	
85	100555	tigr_HT2245 M69181 M81105 U51039	



Table 4A shows 202 genes up-regulated in samples from patients treated with chemotherapy or radiotherapy. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Pkey: Unique Eos probeset identifier number  
 ExAccn: Exemplar Accession number, Genbank accession number  
 UnigenelD: Unigene number  
 Unigene Title: Unigene gene title  
 R1: average of AI for samples from patients treated with chemotherapy or radiotherapy divided by the average of AI for normal lung samples.

Pkey	ExAccn	UnigenelD	Unigene Title	R1
100113	NM_001269	Hs.84746	chromosome condensation 1	27.20
100187	D17793	Hs.78183	aldo-keto reductase family 1, member C3	20.60
100210	D26361	Hs.3104	KIAA0042 gene product	20.40
100225	D28539	Hs.167185	glutamate receptor, metabotropic 5	20.60
100269	NM_001949	Hs.1189	E2F transcription factor 3	29.40
100438	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	23.50
100877	X80821	Hs.27973	KIAA0874 protein	35.56
100893	BE245294	Hs.180789	S164 protein	43.40
101273	Z11933	Hs.182505	POU domain, class 3, transcription facto	21.80
101447	M21305		gb:Human alpha satellite and satellite 3	193.60
101649	AW959908	Hs.1690	heparin-binding growth factor binding pr	38.40
101724	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	198.80
101748	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen	78.60
101809	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	162.20
101879	AA176374	Hs.243886	nuclear autoantigenic sperm protein (his	50.00
101915	AF207881	Hs.155185	cytosolic ovarian carcinoma antigen 1	26.00
101973	U41514	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polyp	37.20
102025	U04045	Hs.78934	mutS (E. coli) homolog 2 (colon cancer,	
102031	U04898	Hs.2156	RAR-related orphan receptor A	32.00
102052	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma	51.20
102391	AA296874	Hs.77494	deoxyguanosine kinase	13.90
102420	U44060	Hs.14427	Homo sapiens cDNA: FLJ21800 fis, clone H	28.80
102610	U65011	Hs.30743	preferentially expressed antigen in mela	110.60
102829	NM_006183	Hs.80962	neurotensin	116.80
103000	NM_001975	Hs.146580	enolase 2, (gamma, neuronal)	2.30
103036	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	181.40
103507	AJ000512	Hs.296323	serum/glucocorticoid regulated kinase	49.20
103587	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	86.60
104660	BE298665	Hs.14846	Homo sapiens mRNA; cDNA DKFZp564D016 (fr	42.60
104896	AW015318	Hs.23165	ESTs	29.40
105038	AW503733	Hs.9414	KIAA1488 protein	21.50
105298	BE387790	Hs.26369	hypothetical protein FLJ20287	32.80
105510	Z42047	Hs.283978	Homo sapiens PRO2751 mRNA, complete cds	20.20
105667	AA767526	Hs.22030	paired box gene 5 (B-cell lineage specif	28.40
106073	AL157441	Hs.17834	downstream neighbor of SON	25.40
106205	AW965058	Hs.111583	ESTs, Weakly similar to I38022 hypotheti	32.00
106516	AL137311	Hs.234074	Homo sapiens mRNA; cDNA DKFZp761G02121 (	40.60
106533	AL134708	Hs.145998	ESTs	59.80
106575	AW970602	Hs.105421	ESTs	43.40
106654	AW075485	Hs.286049	phosphoserine aminotransferase	50.80
106851	AI458623		gb:tk04g09.x1 NCI_CGAP_Lu24 Homo sapiens	53.40
106995	AB023139	Hs.37892	KIAA0922 protein	20.88
107332	T87750	Hs.183297	DKFZP566F2124 protein	23.60
107532	AA443473	Hs.173684	Homo sapiens mRNA; cDNA DKFZp762G207 (fr	57.20
107922	BE153855	Hs.61460	Ig superfamily receptor LNIR	49.00
108609	BE409857	Hs.69499	hypothetical protein	19.67
108780	AU076442	Hs.117938	collagen, type XVII, alpha 1	48.17
109166	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rakines	59.20
109260	AW978515	Hs.131915	KIAA0863 protein	28.60
109280	AK001355	Hs.279610	hypothetical protein FLJ10493	22.80
109292	AW975746	Hs.188662	KIAA1702 protein	
109384	AA219172	Hs.86849	ESTs	21.00
109415	U80736	Hs.110826	trinucleotide repeat containing 9	31.60
109445	AA232103	Hs.189915	ESTs	24.20
109502	AW967069	Hs.211556	hypothetical protein MGC5487	21.40
109633	AW003785	Hs.170267	ESTs	20.40
109786	AI989482	Hs.146286	kinesin family member 13A	19.60
109958	AA001266	Hs.133521	ESTs	24.00
110920	N47224	Hs.20521	HMT1 (hnRNP methyltransferase, S. cerevi	28.40
110924	AW058463	Hs.12940	zinc-fingers and homeoboxes 1	36.00
111084	H44186	Hs.15456	PDZ domain containing 1	61.20
111132	AB037807	Hs.83293	hypothetical protein	24.60
111229	AW389845	Hs.110855	ESTs	27.20
111337	AA837396	Hs.263925	LIS1-interacting protein NUDE1, rat homo	48.00
111987	NM_015310	Hs.6763	KIAA0942 protein	37.80
112046	AA383343	Hs.22116	CDC14 (cell division cycle 14, S. cerevi	26.80
112268	W39609	Hs.22003	solute carrier family 6 (neurotransmitte	63.80
112685	R87650	Hs.33439	ESTs, Weakly similar to ALU1_HUMAN ALU	26.40
112871	AL110216	Hs.12285	ESTs, Weakly similar to I55214 salivary	47.64
112897	AW206453	Hs.3782	ESTs	22.00
112973	AB033023	Hs.318127	hypothetical protein FLJ10201	65.00
112992	AL157425	Hs.133315	Homo sapiens mRNA; cDNA DKFZp761J1324 (f	42.00
113073	N39342	Hs.103042	microtubule-associated protein 1B	55.40



	113494	T91451	Hs.86538	ESTs	22.80
	113560	T91015	Hs.268626	ESTs	22.80
	113849	AA457211	Hs.8858	bromodomain adjacent to zinc finger doma	51.80
5	113950	AI267652	Hs.30504	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	28.20
	114339	AA782845	Hs.22790	ESTs	20.20
	114365	H42169	Hs.18653	hypothetical protein FLJ14627	21.00
	114455	H37908	Hs.271616	ESTs, Weakly similar to ALU8_HUMAN ALU S	25.80
	114518	AW163267	Hs.106469	suppressor of var1 (S.cerevisiae) 3-like	23.60
10	114824	AA960961	Hs.305953	zinc finger protein 83 (HPF1)	27.20
	114837	BE244930	Hs.166895	ESTs	30.20
	114974	AW966931	Hs.179662	nucleosome assembly protein 1-like 1	20.80
	115075	AA814043	Hs.88045	ESTs	30.60
	115084	BE383668	Hs.42484	hypothetical protein FLJ10618	28.86
15	115291	BE545072	Hs.122579	hypothetical protein FLJ10461	38.00
	115313	AA808001	Hs.184411	albumin	22.60
	115697	D31382	Hs.63325	transmembrane protease, serine 4	173.60
	115909	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	27.77
	116090	AI591147	Hs.61232	ESTs	20.80
20	116107	AL133916	Hs.172572	hypothetical protein FLJ20093	164.20
	116399	AA889120	Hs.110637	homeo box A10	38.00
	117099	H93699		gb:yy16a11.s1 Soares fetal liver spleen	21.60
	117881	AF161470	Hs.260622	butyrate-induced transcript 1	49.40
	118091	AW005054	Hs.47883	ESTs, Weakly similar to KCC1_HUMAN CALCI	22.40
25	118138	AA374756	Hs.93560	Homo sapiens mRNA for KIAA1771 protein,	22.00
	118720	N73515		gb:za49d07.s1 Soares fetal liver spleen	20.00
	118873	AI824009	Hs.44577	ESTs	19.40
	119126	R45175	Hs.117183	ESTs	111.20
	119717	AA918317	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	33.00
30	119940	AI050097	Hs.272531	DKFZP586B0319 protein	31.00
	120266	AI807264	Hs.205442	ESTs, Weakly similar to T34036 hypotheti	20.20
	120515	AA258356		gb:zr59c10.s1 Soares_NhHMPu_S1 Homo sapi	25.00
	120859	AA825434	Hs.1619	achaete-scute complex (Drosophila) homol	95.40
	120983	AA398209	Hs.97587	EST	105.20
35	121054	AW976570	Hs.97387	ESTs	38.80
	121369	AW450737	Hs.128791	CGI-09 protein	41.60
	122335	AA443258	Hs.241551	chloride channel, calcium activated, fam	30.80
	122612	AA974832	Hs.128708	ESTs	19.60
40	123130	AA487200		gb:ab19f02.s1 Stratagene lung (937210) H	33.20
	123440	AI733692	Hs.112488	ESTs	23.17
	123596	AA421130	Hs.112640	EST	23.00
	123619	AA602964		gb:nc097c02.s1 NCI_CGAP_Pr2 Homo sapiens	28.80
	124006	AI147155	Hs.270016	ESTs	77.60
	124169	BE079334	Hs.271630	ESTs	22.20
45	124281	AI333756	Hs.111801	arsenate resistance protein ARS2	42.20
	124472	N52517	Hs.102670	EST	32.60
	124617	AW628168	Hs.152684	ESTs	21.80
	124631	NM_014053	Hs.270594	FLVCR protein	30.40
	124839	R55784	Hs.140942	ESTs	21.20
50	125186	AA610620	Hs.181244	major histocompatibility complex, class	42.80
	125321	T86652	Hs.178294	ESTs	27.00
	125535	NM_013243	Hs.22215	secretogranin III	23.80
	125646	AA628962	Hs.75209	protein kinase (cAMP-dependent, catalyti	23.20
	125684	AW589427	Hs.158849	Homo sapiens cDNA: FLJ21663 fis, clone C	21.20
55	125724	AL360190	Hs.295978	Homo sapiens mRNA full length insert cDN	48.80
	125847	AW161885	Hs.249034	ESTs	31.00
	125934	AA193325	Hs.32646	hypothetical protein FLJ21901	21.20
	126077	M78772	Hs.210836	ESTs	49.80
	126299	AW979155	Hs.298275	amino acid transporter 2	21.80
60	126395	AI468004	Hs.278956	hypothetical protein FLJ12929	71.00
	126433	AA325606		gb:EST28707 Cerebellum II Homo sapiens c	23.20
	126509	R47400	Hs.23850	ESTs	23.80
	126538	AB030656	Hs.17377	coronin, actin-binding protein, 1C	23.10
	126666	AA648886	Hs.151999	ESTs	36.00
65	126812	AB037860	Hs.173933	nuclear factor I/A	20.80
	126872	AW450979		gb:UI-H-BI3-ala-a-12-0-UI.s1 NCI_CGAP_Su	46.29
	127046	AA321948	Hs.293968	ESTs	22.80
	127431	AW771958	Hs.175437	ESTs, Moderately similar to PC4259 ferri	30.00
	127489	AA650250	Hs.272076	ESTs	20.80
70	127521	AW297206	Hs.164018	ESTs	25.20
	127742	AW293496	Hs.180138	ESTs	28.00
	127925	AA805151	Hs.3628	mitogen-activated protein kinase kinase	21.20
	127930	AA809672	Hs.123304	ESTs	20.54
	127968	AA830201	Hs.124347	ESTs	28.20
75	127987	AI022103	Hs.124511	ESTs	19.60
	128116	H07103	Hs.286014	Homo sapiens, clone IMAGE:3867243, mRNA	20.40
	128609	NM_003616	Hs.102456	survival of motor neuron protein interac	34.40
	128777	AI878918	Hs.10526	cysteine and glycine-rich protein 2	53.80
	128949	AA009647	Hs.8850	a disintegrin and metalloproteinase doma	23.00
80	129168	AI132988	Hs.109052	chromosome 14 open reading frame 2	37.60
	129404	AI267700	Hs.317584	ESTs	28.60
	129527	AA769221	Hs.270847	delta-tubulin	40.80
	129574	AA026815	Hs.11463	UMP-CMP kinase	31.20
	129598	N30436	Hs.11556	Homo sapiens cDNA FLJ12566 fis, clone NT	29.60
85	129785	H19006	Hs.184780	ESTs	72.20
	129970	AV655806	Hs.296198	chromosome 12 open reading frame 4	22.20



5	130149	AW067805	Hs.172665	methylenetetrahydrofolate dehydrogenase	29.60
	130199	Z48579	Hs.172028	a disintegrin and metalloproteinase doma	27.60
	130441	U63630	Hs.155637	protein kinase, DNA-activated, catalytic	28.36
	130466	W19744	Hs.180059	Homo sapiens cDNA FLJ20653 fis, clone KA	20.20
	130482	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	22.40
	130617	M90516	Hs.1674	glutamine-fructose-6-phosphate transamin	19.60
	130703	R77776	Hs.18103	ESTs	19.40
	130732	AW890487	Hs.63984	cadherin 13, H-cadherin (heart)	21.40
10	130867	NM_001072	Hs.284239	UDP glycosyltransferase 1 family, polype	110.00
	131028	AI879165	Hs.2227	CCAAAT/enhancer binding protein (C/EBP),	25.20
	131086	AL035461	Hs.2281	chromogranin B (secretogranin 1)	40.60
	131284	NM_001429	Hs.25272	E1A binding protein p300	24.60
	131775	AB014548	Hs.31921	KIAA0648 protein	21.00
15	131860	BE383676	Hs.334	Rho guanine nucleotide exchange factor (	33.40
	131945	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	60.80
	132040	NM_001196	Hs.315689	Homo sapiens cDNA: FLJ22373 fis, clone H	20.40
	132084	NM_002267	Hs.3886	karyopherin alpha 3 (importin alpha 4)	29.40
	132389	AA310393	Hs.190044	ESTs	32.40
20	132437	AA152106	Hs.4859	cyclin L ania-6a	27.40
	132550	AW969253	Hs.170195	bone morphogenetic protein 7 (osteogenic	75.60
	132617	AF037335	Hs.5338	carbonic anhydrase XII	31.36
	132632	AU076916	Hs.5398	guanine monophosphate synthetase	32.40
	132672	W27721	Hs.54697	Cdc42 guanine exchange factor (GEF) 9	23.40
25	132742	AA025480	Hs.292812	ESTs, Weakly similar to T33468 hypothi	61.20
	132771	Y10275	Hs.56407	phosphoserine phosphatase	22.33
	133070	U92649	Hs.64311	a disintegrin and metalloproteinase doma	23.50
	133153	AF070592	Hs.66170	HSKM-B protein	30.00
	133181	X91662	Hs.66744	twist ( <i>Drosophila</i> ) homolog (acrocephalos	23.80
30	133282	AA449015	Hs.286145	SRB7 (suppressor of RNA polymerase B, ye	51.60
	133350	AI499220	Hs.71573	hypothetical protein FLJ10074	33.00
	133592	AV652066	Hs.75113	general transcription factor IIIA	82.00
	133658	AA319146	Hs.75426	secretogranin II (chromogranin C)	
35	133865	AB011155	Hs.170290	discs, large ( <i>Drosophila</i> ) homolog 5	69.33
	134032	NM_005025	Hs.78589	serine (or cysteine) proteinase inhibito	33.20
	134125	NM_014781	Hs.50421	KIAA0203 gene product	31.60
	134158	U15174	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	30.60
	134321	BE538082	Hs.8172	ESTs, Moderately similar to A46010 X-lin	23.40
40	134367	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	49.20
	134570	U66615	Hs.172280	SWI/SNF related, matrix associated, acti	20.20
	134753	NM_006482	Hs.173135	dual-specificity tyrosine-(Y)-phosphoryl	20.80
	135002	AA448542	Hs.251677	G antigen 7B	37.60
45	135029	H58818	Hs.187579	hydroxysteroid (17-beta) dehydrogenase	53.40
	135047	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	31.60
	135345	X53655	Hs.99171	neurotrophin 3	28.80

TABLE 4B shows the accession numbers for those primekeys lacking unigenelD's for Table 4A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number  
CAT number: Gene cluster number  
Accession: Genbank accession numbers

Pkey	CAT number	Accessions
123619	371681_1	AA602964 AA609200
126433	127143_1	AA325606 AA099517 N89423
126872	142696_1	AW450979 AA136653 AA136656 AW419381 AA984358 AA492073 BE168945 AA809054 AW238038 BE011212 BE011359
		BE011367 BE011368 BE011362 BE011215 BE011365 BE011363
106851	322947_1	AI458623 AA639708 AA485409 R22065 AA485570
118720	genbank_N73515	N73515
120515	genbank_AA258356	AA258356
117099	321871_1	H93699 H97976 H80036
101447	entrez_M21305	M21305
123130	genbank_AA487200	AA487200



Table 5A shows 680 genes up-regulated in squamous cell carcinoma or adenocarcinoma lung tumors relative to normal lung and chronically diseased lung. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

5	Pkey:	Unique Eos probeset identifier number							
	ExAccn:	Exemplar Accession number, Genbank accession number							
	UnigeneID:	Unigene number							
	Unigene Title:	Unigene gene title							
10	R1:	70th percentile of AI for squamous cell carcinoma and adenocarcinoma lung tumor samples divided by the 90th percentile of AI for normal and chronically diseased lung samples.							
	R2:	80th percentile of AI adenocarcinoma lung tumor samples divided by the 90th percentile of AI for normal and chronically diseased lung samples.							
	R3:	80th percentile of AI squamous cell carcinoma lung tumor samples divided by the 90th percentile of AI for normal and chronically diseased lung samples.							
	R4:	80th percentile of AI adenocarcinoma lung tumor samples divided by the 80th percentile of AI for squamous cell carcinoma lung tumor samples.							
15	R5:	70th percentile of AI for squamous cell carcinoma and adenocarcinoma lung tumor samples minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples divided by 90th percentile of AI for normal and chronically diseased lung samples minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples							
20	Pkey	ExAccn	UnigeneID	Unigene Title	R1	R2	R3	R4	R5
	100035			AFFX control: GAPDH					6.76
	100036			AFFX control: GAPDH					5.77
	100037			AFFX control: GAPDH					5.75
25	100071	A28102		Human GABAA receptor alpha-3 subunit		8.00			
	100114	X02308	Hs.82962	thymidylate synthetase					5.71
	100154	H60720	Hs.81892	KIAA0101 gene product	3.84				
	100187	D17793	Hs.78183	aldo-keto reductase family 1, member C3	3.33				
	100188	AW247090	Hs.57101	minichromosome maintenance deficient (S.					4.52
	100202	BE294407	Hs.99910	phosphofructokinase, platelet					5.49
30	100216	AA489908	Hs.1390	proteasome (prosome, macropain) subunit,					5.67
	100269	NM_001949	Hs.1189	E2F transcription factor 3	2.55				
	100287	AU076657	Hs.1600	chaperonin containing TCP1, subunit 5 (e					5.66
	100297	AU077258	Hs.182429	protein disulfide isomerase-related prot					3.81
	100330	AW410976	Hs.77152	minichromosome maintenance deficient (S.					4.50
35	100335	AW247529	Hs.6793	platelet-activating factor acetylhydrola	5.07				
	100360	W70171	Hs.75939	uridine monophosphate kinase					4.82
	100372	NM_014791	Hs.184339	KIAA0175 gene product					3.79
	100474	NM_000699	Hs.300280	amylase, alpha 2A; pancreatic				15.65	
40	100486	T19006	Hs.10842	RAN, member RAS oncogene family					5.49
	100491	D56165	Hs.275163	non-metastatic cells 2, protein (NM23B)					4.17
	100516	D90278	Hs.11	carcinoembryonic antigen-related cell ad		7.20			
	100522	X51501	Hs.99949	prolactin-induced protein				14.20	
	100559	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys	3.10				
	100576	X00356	Hs.37058	calcitonin/calcitonin-related polypeptid				9.30	
45	100629	AA015693	Hs.21291	mitogen-activated protein kinase kinase				20.60	
	100661	BE623001	Hs.132748	Homo sapiens ribosomal protein L39 mRNA,	3.85				
	100677	AA353686	Hs.57813	zinc ribbon domain containing, 1		8.60			
	100696	L24887	Hs.121686	general transcription factor IIA, 1 (37k				10.00	
	100709	N26539	Hs.100469	myeloid/lymphoid or mixed-lineage leukem			24.80		
50	100761	BE208491	Hs.295112	KIAA0618 gene product		7.60			
	100830	AC004770	Hs.4756	flap structure-specific endonuclease 1					7.99
	100867	U14622		gb:Human transketolase-like protein gene		10.20			
	100902	M16029	Hs.287270	ret proto-oncogene (multiple endocrine n		8.00			
55	100906	AU076916	Hs.5398	guanine monphosphate synthetase					5.16
	100960	J00124	Hs.117729	keratin 14 (epidermolysis bullosa simple	2.57				
	101045	J05614		gb:Human proliferating cell nuclear anti					4.69
	101061	NM_000175	Hs.180532	glucose phosphate isomerase					4.19
	101071	L02840	Hs.84244	potassium voltage-gated channel, Shab-re		12.91			
60	101124	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	3.12				
	101175	U82671	Hs.36980	melanoma antigen, family A, 2	3.50				
	101181	BE262621	Hs.73798	macrophage migration inhibitory factor (					5.69
	101204	L24203	Hs.82237	ataxia-telangiectasia group D-associated	4.08				
	101210	L29301	Hs.2353	opioid receptor, mu 1			6.40		
65	101216	AA284166	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK	2.53				
	101228	AA333387	Hs.82916	chaperonin containing TCP1, subunit 6A (					7.90
	101233	AL135173	Hs.878	sorbitol dehydrogenase					4.45
	101273	Z11933	Hs.182505	POU domain, class 3, transcription facto	8.50				
	101342	U52112	Hs.182018	interleukin-1 receptor-associated kinase					4.17
70	101346	A1738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(N				21.89	
	101369	NM_000892	Hs.1901	kallikrein B, plasma (Fletcher factor) 1				12.80	
	101396	BE267931	Hs.78996	proliferating cell nuclear antigen	3.24				
	101431	BE185289	Hs.1076	small proline-rich protein 1B (cornifin)					7.90
	101448	NM_000424	Hs.195850	keratin 5 (epidermolysis bullosa simplex	8.31				
75	101462	AL035668	Hs.73853	bone morphogenetic protein 2				38.80	
	101466	BE262660	Hs.170197	glutamic-oxaloacetic transaminase 2, mit					4.01
	101484	AA053486	Hs.20315	interferon-induced protein with tetratri				12.00	
	101502	M26958		gb:Human parathyroid hormone-related pro	10.50				
	101505	AA307680	Hs.75692	asparagine synthetase					4.46
80	101526	NM_002197	Hs.154721	aconitase 1, soluble	4.02				
	101535	X57152	Hs.99853	fibrillarin					4.65
	101577	M34353	Hs.1041	v-ros avian UR2 sarcoma virus oncogene h				9.09	
	101649	AW959908	Hs.1690	heparin-binding growth factor binding pr	54.00				
	101663	NM_003528	Hs.2178	H2B histone family, member Q	5.59				
	101664	AA436989	Hs.121017	H2A histone family, member A	7.00				
85	101669	L24498	Hs.80409	growth arrest and DNA-damage-inducible,		7.60			



	101695	M69136	Hs.135626	chymase 1, mast cell	4.79			
	101724	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	15.21			
	101748	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen)	55.50			
5	101759	M80244	Hs.184601	solute carrier family 7 (cationic amino)			18.57	4.10
	101771	NM_002432	Hs.153837	myeloid cell nuclear differentiation ant				
	101804	M86699	Hs.169840	TTK protein kinase	4.50			
	101809	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	140.00			
	101833	AU076442	Hs.117938	collagen, type XVII, alpha 1	2.56			
10	101842	M93221	Hs.75182	mannose receptor, C type 1			12.80	
	101851	BE260964	Hs.82045	midkine (neurite growth-promoting factor				5.88
	102002	NM_002484	Hs.81469	nucleotide binding protein 1 (E.coli Min	7.80			
	102039	AL134223	Hs.306098	aldo-keto reductase family 1, member C1				4.35
	102072	U09410	Hs.78743	zinc finger protein 131 (clone pHZ-10)		7.40		
15	102083	T35901	Hs.75117	interleukin enhancer binding factor 2, 4				5.12
	102111	L36196	Hs.81884	sulfotransferase family, cytosolic, 2A,			12.00	
	102123	NM_001809	Hs.1594	centromere protein A (17kD)	6.20			
	102154	U17760	Hs.75517	laminin, beta 3 (niclin (125kD), kalinin	2.62			
	102193	AL036335	Hs.313	secreted phosphoprotein 1 (osteopontin,	5.85			
20	102217	AA829978	Hs.301613	JTV1 gene				6.18
	102224	NM_002810	Hs.148495	proteasome (prosome, macropain) 26S subu				4.49
	102234	AW163390	Hs.278554	heterochromatin-like protein 1				5.80
	102251	NM_004398	Hs.41706	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	4.50			
	102305	AL043202	Hs.90073	chromosome segregation 1 (yeast homolog)				5.15
25	102330	BE298063	Hs.77254	chromobox homolog 1 (Drosophila HP1 beta				4.17
	102340	U37055	Hs.278657	macrophage stimulating 1 (hepatocyte gro			9.33	
	102348	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	8.87			
	102368	U39817	Hs.36820	Bloom syndrome	15.91			
	102394	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma			19.20	
30	102404	NM_005429	Hs.79141	vascular endothelial growth factor C				14.00
	102537	U57094	Hs.50477	RAB27A, member RAS oncogene family			12.00	
	102581	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2				4.57
	102605	AI435128	Hs.181369	ubiquitin fusion degradation 1-like				3.98
	102610	U65011	Hs.30743	preferentially expressed antigen in mela	77.50			
35	102623	AW249285	Hs.37110	melanoma antigen, family A, 9	12.50			
	102642	AA205847	Hs.23016	G protein-coupled receptor			22.00	
	102654	AV649989	Hs.24385	Human hbc647 mRNA sequence		12.00		
	102659	BE245169	Hs.211610	CUG triplet repeat, RNA-binding protein			12.80	
	102669	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	6.50			
40	102672	U72066	Hs.29287	retinoblastoma-binding protein 8	8.50			
	102687	NM_007019	Hs.93002	ubiquitin carrier protein E2-C				9.24
	102696	BE540274	Hs.239	forkhead box M1				5.54
	102768	U82321		gb:Homo sapiens clone 14.9B mRNA sequenc		6.60		
45	102781	BE258778	Hs.108809	chaperonin containing TCP1, subunit 7 (e				3.78
	102784	U85658	Hs.61795	transcription factor AP-2 gamma (activat				4.26
	102824	U90916	Hs.82845	Homo sapiens cDNA: FLJ21930 fis, clone H			14.40	
	102829	NM_006183	Hs.80962	neurotensin	8.00			
	102888	AI346201	Hs.76118	ubiquitin carboxyl-terminal esterase L1				5.50
	102892	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin			6.70	
50	102913	NM_002275	Hs.80342	keratin 15	4.64			
	102935	BE561850	Hs.80506	small nuclear ribonucleoprotein polypept	2.93			
	102951	X15218	Hs.2969	v-ski avian sarcoma viral oncogene homol			11.40	
	102983	BE387202	Hs.118638	non-metastatic cells 1, protein (NM23A)				7.26
	103023	AW500470	Hs.117950	multifunctional polypeptide similar to S	3.01			
55	103036	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	27.90			
	103038	AA926960	Hs.334883	CD28 protein kinase 1				8.79
	103060	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin				4.27
	103099	AI693251	Hs.8248	NADH dehydrogenase (ubiquinone) Fe-S pro		9.80		
	103119	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	4.05			
60	103168	X53463	Hs.2704	glutathione peroxidase 2 (gastrointestin	3.07			
	103185	NM_006825	Hs.74368	transmembrane protein (63kD), endoplasm				5.62
	103192	M22440	Hs.170009	transforming growth factor, alpha		7.40		
	103223	BE275607	Hs.1708	chaperonin containing TCP1, subunit 3 (g				4.70
	103242	X76342	Hs.389	alcohol dehydrogenase 7 (class IV), mu o			100.00	
65	103316	X83301	Hs.324728	SMA5			9.80	
	103375	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	9.71			
	103376	AL036166	Hs.323378	coated vesicle membrane protein	14.00			
	103385	NM_007069	Hs.37189	similar to rat HREV107			11.00	
	103391	X94453	Hs.114366	pyrroline-5-carboxylate synthetase (glut	2.93			
70	103404	BE394784	Hs.78596	proteasome (prosome, macropain) subunit,				5.15
	103430	BE564090	Hs.20716	translocase of inner mitochondrial membr				3.98
	103446	X98834	Hs.79971	sal (Drosophila)-like 2			21.40	
	103476	Y07701	Hs.293007	aminopeptidase puromycin sensitive		13.00		
	103477	AJ011812	Hs.119018	transcription factor NRF			6.40	
75	103478	BE514982	Hs.38991	S100 calcium-binding protein A2	5.02			
	103515	Y10275	Hs.56407	phosphoserine phosphatase	10.50			
	103558	BE616547	Hs.2785	keratin 17	6.41			
	103580	AA328046	Hs.46405	polymerase (RNA) II (DNA directed) polyp				3.84
	103587	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	78.50			
80	103594	AI368680	Hs.816	SRY (sex determining region Y)-box 2	6.51			
	103636	NM_006235	Hs.2407	POU domain, class 2, associating factor	3.50			
	103768	AF086009		gb:Homo sapiens full length insert cDNA				4.48
	103841	AA314821	Hs.38178	hypothetical protein FLJ23468		8.00		
	103847	AF219946	Hs.102237	tubby super-family protein		10.40		
85	103913	AW967500	Hs.133543	ESTs			15.60	
	104094	AA418187	Hs.330515	ESTs			6.60	



5	104150	AL122044	Hs.331633	hypothetical protein DKFZp566N034		26.00	
	104257	BE560621	Hs.9222	estrogen receptor binding site associate	6.80		
	104261	AW248364	Hs.5409	RNA polymerase I subunit		3.98	
	104331	AB040450	Hs.279862	cdk inhibitor p21 binding protein	6.80		
	104415	BE410992	Hs.258730	heme-regulated initiation factor 2-alpha	10.29		
10	104558	R56678	Hs.88959	hypothetical protein MGC4816	4.21		
	104590	AW373062	Hs.83623	nuclear receptor subfamily 1, group I, m		15.79	
	104658	AA360954	Hs.27268	Homo sapiens cDNA: FLJ21933 fis, clone H		17.40	
	104660	BE298665	Hs.14846	Homo sapiens mRNA; cDNA DKFZp564D016 (fr	6.40		
	104689	AA420450	Hs.292911	ESTs, Highly similar to S60712 band-6-pr			6.55
15	104754	AI206234	Hs.155924	cAMP responsive element modulator		10.00	
	104758	BE560269	Hs.7010	NPD002 protein			4.47
	104971	BE311926	Hs.15830	hypothetical protein FLJ12691	2.87		
	105011	BE091926	Hs.16244	mitotic spindle coiled-coil related prot	3.83		
	105012	AF098158	Hs.9329	chromosome 20 open reading frame 1	2.86		
20	105026	AA809485	Hs.124219	hypothetical protein FLJ12934	11.00		
	105076	AI598252	Hs.37810	hypothetical protein MGC14833			5.01
	105132	AA148164	Hs.247280	HBV associated factor			3.99
	105143	AI368836	Hs.24808	ESTs, Weakly similar to I38022 hypotheti		11.00	
	105158	AW976357	Hs.234545	hypothetical protein NUF2R	16.00		
25	105175	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	4.32		
	105200	AA328102	Hs.24641	cytoskeleton associated protein 2	3.00		
	105264	AA227790		gb:zr57e08.s1 Soares_NhHMPu_S1 Homo sapi		10.00	
	105298	BE387790	Hs.26369	hypothetical protein FLJ20287	3.69		
	105409	AW505076	Hs.301855	DiGeorge syndrome critical region gene 8		9.20	
30	105460	AW296078	Hs.271721	Homo sapiens, clone IMAGE:4179986, mRNA,		7.80	
	105667	AA767526	Hs.22030	paired box gene 5 (B-cell lineage specif	4.12		
	105743	BE246502	Hs.9598	sema domain, immunoglobulin domain (Ig),	3.82		
	105782	H09748	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro		27.00	
	105848	AW954064	Hs.24951	ESTs		7.60	
35	105891	U55984	Hs.289088	heat shock 90kD protein 1, alpha			4.14
	106019	AF221993	Hs.46743	McKusick-Kaufman syndrome		16.80	
	106069	BE566623	Hs.29899	ESTs, Weakly similar to G02075 transcrip		23.40	
	106073	AL157441	Hs.17834	downstream neighbor of SON	9.50		
	106126	AA576953	Hs.22972	hypothetical protein FLJ13352	6.00		
40	106159	AK001301	Hs.3487	hypothetical protein FLJ10439			3.95
	106220	D61329	Hs.32196	mitochondrial ribosomal protein L36			6.04
	106260	AI097144	Hs.5250	ESTs, Weakly similar to ALU1_HUMAN ALU S		13.20	
	106300	Y10043	Hs.19114	high-mobility group (nonhistone chromoso			5.02
	106307	AA436174	Hs.37751	ESTs, Weakly similar to putative p150 [	6.60		
45	106318	AA025610	Hs.9605	cleavage and polyadenylation specific fa			5.04
	106341	AF191020	Hs.5243	hypothetical protein, estradiol-induced			7.25
	106440	AA449563	Hs.151393	glutamate-cysteine ligase, catalytic sub		13.80	
	106481	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	4.75		
	106586	AA243837	Hs.57787	ESTs		10.84	
50	106605	AW772298	Hs.21103	Homo sapiens mRNA; cDNA DKFZp564B076 (fr		45.60	
	106654	AW075485	Hs.286049	phosphoserine aminotransferase	28.00		
	106785	Y15227	Hs.20149	deleted in lymphocytic leukemia, 1	3.00		
	106813	C05766	Hs.181022	CGI-07 protein		11.40	
	106895	AK001826	Hs.25245	hypothetical protein FLJ11269		6.00	
55	106913	AI219346	Hs.86178	M-phase phosphoprotein 9	6.56		
	106919	AW043637	Hs.21766	ESTs, Weakly similar to ALU5_HUMAN ALU S			4.27
	107054	AI076459	Hs.15978	KIAA1272 protein		34.80	
	107059	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re	4.71		
	107098	AI823593	Hs.27688	ESTs		24.80	
60	107104	AU076640	Hs.15243	nucleolar protein 1 (120kD)			7.05
	107129	AC004770	Hs.4756	flap structure-specific endonuclease 1	2.60		
	107198	AV657225	Hs.9846	KIAA1040 protein		19.20	
	107203	D20426	Hs.41639	programmed cell death 2		7.60	
	107217	AL080235	Hs.35861	DKFZP586E1621 protein	9.50		
65	107284	NM_005629	Hs.187958	solute carrier family 6 (neurotransmitte	2.71		
	107318	T74445	Hs.5957	Homo sapiens clone 24416 mRNA sequence		8.71	
	107516	X57152	Hs.99853	fibrillarin			4.33
	107529	BE515065	Hs.296585	nucleolar protein (KKE/D repeat)			4.00
	107728	AA019551	Hs.294151	Homo sapiens, clone IMAGE:3603836, mRNA,	10.80		
70	107851	AA022953	Hs.61172	EST		8.00	
	107901	L42612	Hs.335952	keratin 6B	3.40		
	107922	BE153855	Hs.61460	Ig superfamily receptor LNIR	2.88		
	107932	AW392555	Hs.18878	hypothetical protein FLJ21620	7.50		
	108015	AW298357	Hs.49927	protein kinase NYD-SP15			23.40
75	108056	AA043675	Hs.62633	ESTs			12.80
	108075	AI867370	Hs.139709	hypothetical protein FLJ12572			12.80
	108187	BE245374	Hs.27842	hypothetical protein FLJ11210	7.00		
	108296	N31256	Hs.161623	ESTs	6.60		
	108305	AA071391		gb:zm61e06.r1 Stratagene fibroblast (937			11.80
80	108393	AA075211		gb:zm86a08.r1 Stratagene ovarian cancer			11.80
	108480	AL133092	Hs.68055	hypothetical protein DKFZp434I0428			20.80
	108554	AA084948		gb:zn13b09.s1 Stratagene hNT neuron (937	6.40		
	108573	AA086005		gb:z184c04.s1 Stratagene colon (937204)			25.40
	108584	AA088326	Hs.120905	Homo sapiens cDNA FLJ111448 fis, clone HE	9.60		
85	108597	AK000292	Hs.278732	hypothetical protein FLJ20285			14.60
	108695	AB029000	Hs.70823	KIAA1077 protein	3.00		
	108699	AA121514	Hs.70832	ESTs			10.00
	108700	AA121518	Hs.193540	ESTs, Moderately similar to 2109260A B c		11.00	
	108780	AU076442	Hs.117938	collagen, type XVII, alpha 1	11.21		



	108810	AW295647	Hs.71331	hypothetical protein MGC5350	8.50			
	108816	AA130884	Hs.270501	ESTs, Moderately similar to ALU2_HUMAN		7.40		
	108857	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	4.00			
5	108860	AA133334	Hs.129911	ESTs	6.09			
	108937	AL050107	Hs.24341	transcriptional co-activator with PDZ-bi	3.00			
	109010	NM_007240	Hs.44229	dual specificity phosphatase 12	2.69			
	109121	BE389387	Hs.49767	NADH dehydrogenase (ubiquinone) Fe-S pro			4.53	
	109166	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	10.58			
10	109227	AA766998	Hs.85874	Human DNA sequence from clone RP11-16L21		9.00		
	109415	U80736	Hs.110826	trinucleotide repeat containing 9		51.40		
	109418	AI866946	Hs.161707	ESTs			11.00	
	109454	AA232255	Hs.295232	ESTs, Moderately similar to A46010 X-li		17.60		
	109502	AW967069	Hs.211556	hypothetical protein MGC5487		9.49		
15	109543	AA564994	Hs.222851	ESTs	12.67			
	109648	H17800	Hs.71154	ESTs			10.40	
	109680	AB037734	Hs.4993	KIAA1313 protein		33.20		
	109700	F09609		gb:HSC33H092 normalized infant brain cDN			16.00	
	109704	AI743880	Hs.12876	ESTs		11.00		
20	109792	R49625		gb:yg61f03.s1 Soares infant brain 1N1B H			12.60	
	109981	BE546208	Hs.26090	hypothetical protein FLJ20272	4.00			
	109998	AL042201	Hs.21273	transcription factor NYD-sp10		7.80		
	110039	H11938	Hs.21907	histone acetyltransferase		7.00		
	110156	AA581322	Hs.4213	hypothetical protein MGC16207			4.24	
25	110500	AA907723	Hs.36962	ESTs	4.50			
	110551	AW450381	Hs.14529	ESTs		8.60		
	110561	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	3.06			
	110854	BE612992	Hs.27931	hypothetical protein FLJ10607 similar to		6.80		
	110886	AW274992	Hs.72249	three-PDZ containing protein similar to		8.80		
30	110916	BE178102	Hs.24349	ESTs		6.80		
	111003	N52980	Hs.83765	dihydrofolate reductase			16.80	
	111337	AA837396	Hs.263925	LIS1-interacting protein NUDE1, rat homo	2.54			
	111434	R01608	Hs.142736	ESTs			9.80	
	111439	AI476429	Hs.19238	ESTs			10.40	
35	111540	U82670	Hs.9786	zinc finger protein 275		15.40		
	111597	R11499	Hs.189716	ESTs			9.20	
	111895	T80581	Hs.12723	Homo sapiens clone 25153 mRNA sequence		6.80		
	111929	AF027208	Hs.112360	prominin (mouse)-like 1			14.67	
	112054	R43590		gb:yc85g02.s1 Soares infant brain 1N1B H		10.80		
40	112210	R49645	Hs.7004	ESTs			10.20	
	112244	AB029000	Hs.70823	KIAA1077 protein	2.99			
	112382	R59904		gb:yh07g12.s1 Soares infant brain 1N1B H		6.60		
	112392	R60763	Hs.193274	ESTs, Moderately similar to I57588 HSrel		7.10		
	112442	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regi	3.00			
45	112539	R70318	Hs.339730	ESTs			37.20	
	112772	AI992283	Hs.35437	ESTs, Moderately similar to I38026 MLN 6			14.60	
	112869	BE261750	Hs.4747	dyskeratosis congenita 1, dyskerin				4.83
	112935	R71449	Hs.268760	ESTs	2.73			
	112970	AA694010	Hs.6932	Homo sapiens clone 23809 mRNA sequence			12.00	
50	112973	AB033023	Hs.318127	hypothetical protein FLJ10201	11.50			
	112992	AL157425	Hs.133315	Homo sapiens mRNA; cDNA DKFZp761J1324 (f		10.89		
	113063	W15573	Hs.5027	ESTs, Weakly similar to A47582 B-cell gr	15.00			
	113073	N39342	Hs.103042	microtubule-associated protein 1B		15.31		
	113078	T40444	Hs.118354	CAT56 protein		7.00		
55	113238	R45467	Hs.189813	ESTs			41.20	
	113591	T91881	Hs.200597	KIAA0563 gene product			9.40	
	113702	T97307		gb:ye53h05.s1 Soares fetal liver spleen	25.00			
	113844	AI369275	Hs.243010	Homo sapiens cDNA FLJ14445 fis, clone HE			13.91	
	113984	R96696	Hs.35598	ESTs		7.80		
60	114073	R44953	Hs.22908	Homo sapiens mRNA; cDNA DKFZp434J1027 (f		7.20		
	114162	AF155661	Hs.22265	pyruvate dehydrogenase phosphatase	3.42			
	114208	AL049466	Hs.7859	ESTs		6.74		
	114251	H15261	Hs.21948	ESTs			33.20	
	114285	R44338	Hs.22974	ESTs			13.20	
65	114313	H18456	Hs.27946	ESTs			10.00	
	114339	AA782845	Hs.22790	ESTs		7.80		
	114407	BE539976	Hs.103305	Homo sapiens mRNA; cDNA DKFZp434B0425 (f				4.14
	114560	AI452469	Hs.165221	ESTs			9.80	
70	114699	AA127386		gb:zn90d09.r1 Stratagene lung carcinoma		7.60		
	114767	AI859865	Hs.154443	minichromosome maintenance deficient (S	3.21			
	114793	AA158245		gb:zo76c03.s1 Stratagene pancreas (93720		6.00		
	114833	AI417215	Hs.87159	hypothetical protein FLJ12577			11.40	
	115047	BE270930	Hs.82916	chaperonin containing TCP1, subunit 6A (				4.31
	115060	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3				4.03
75	115097	AA256213	Hs.72010	ESTs			35.40	
	115113	AA256460		gb:zr81a04.s1 Soares_NhHMPu_S1 Homo sapi			15.20	
	115123	AA256641	Hs.236894	ESTs, Highly similar to S02392 alpha-2-m				4.19
	115134	AW968073	Hs.194331	ESTs, Highly similar to A55713 inositol			12.40	
	115291	BE545072	Hs.122579	hypothetical protein FLJ10461	25.00			
80	115347	AA356792	Hs.334824	hypothetical protein FLJ14825		7.00		
	115414	AA662240	Hs.283099	AF15q14 protein	3.25			
	115522	BE614387	Hs.333893	c-Myc target JPO1	3.68			
	115536	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	10.50			
	115566	AI142336	Hs.43977	Human DNA sequence from clone RP11-196N1			24.40	
	115645	AI207410	Hs.69280	Homo sapiens, clone IMAGE:3636299, mRNA,	4.17			
85	115648	AW016811	Hs.234478	Homo sapiens cDNA: FLJ22648 fis, clone H		6.00		



	115652	BE093589	Hs.38178	hypothetical protein FLJ23468	3.81				
	115697	D31382	Hs.63325	transmembrane protease, serine 4	62.14				
	115793	AA424883	Hs.70333	hypothetical protein MGC10753				11.80	
5	115816	BE042915	Hs.287588	Homo sapiens cDNA FLJ13675 fis, clone PL				9.71	
	115892	AA291377	Hs.50831	ESTs			27.40		
	115906	AI767756	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	2.53				
	115909	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	11.82				
	115965	AA001732	Hs.173233	hypothetical protein FLJ10970				34.29	
10	115978	AL035864	Hs.69517	cDNA for differentially expressed CO16 g				8.23	
	115985	AA447709	Hs.268115	ESTs, Weakly similar to T08599 probable	3.00				
	116090	AI591147	Hs.61232	ESTs	5.17				
	116096	AA682382	Hs.59982	ESTs			8.20		
	116127	AF126743	Hs.279884	DNAJ domain-containing		10.60			
15	116157	BE439838	Hs.44298	mitochondrial ribosomal protein S17				5.82	
	116190	AI949095	Hs.67776	ESTs, Weakly similar to T22341 hypotheti				4.08	
	116278	NM_003686	Hs.47504	exonuclease 1	9.50				
	116335	AK001100	Hs.41690	desmocollin 3	3.67				
	116496	AW450694	Hs.21433	hypothetical protein DKFZp547J036		7.00			
20	116503	AI925316	Hs.212617	ESTs				12.60	
	116674	AI768015	Hs.92127	ESTs			32.00		
	116929	AA586922	Hs.80475	polymerase (RNA) II (DNA directed) polyp		7.60			
	116973	AI702054	Hs.166982	phosphatidylinositol glycan, class F		9.80			
	116993	AI417023	Hs.40478	ESTs				10.20	
25	117079	H92325		gb:ys85f05.s1 Soares retina N2b4HR Homo				15.20	
	117317	AI263517	Hs.43322	ESTs				13.40	
	117326	N23629	Hs.241420	Homo sapiens mRNA for KIAA1756 protein,				20.60	
	117396	W20128	Hs.296039	ESTs				10.60	
	117412	N32536	Hs.42645	ESTs				16.00	
30	117519	N32528	Hs.146286	kinesin family member 13A				9.11	
	117693	AW179019	Hs.112110	mitochondrial ribosomal protein L42				4.01	
	117721	N46100	Hs.93939	EST				19.80	
	117881	AF161470	Hs.260622	butyrate-induced transcript 1	2.71				
	117903	AA768283	Hs.47111	ESTs				17.80	
35	117992	AI015709	Hs.172089	Homo sapiens mRNA; cDNA DKFZp586i2022 (f				10.60	4.17
	118013	AI674126	Hs.94031	ESTs			8.82		
	118017	AI813444	Hs.42197	ESTs					
	118186	N22886	Hs.42380	ESTs		7.00			
	118325	AI888065	Hs.166184	intersectin 2				13.80	
40	118367	N64269	Hs.48946	EST			6.14		
	118368	N64339	Hs.48956	gap junction protein, beta 6 (connexin 3	3.14				
	118472	AI157545	Hs.42179	bromodomain and PHD finger containing, 3			12.40		
	118709	AA232970	Hs.293774	ESTs				12.20	
	119025	BE003760	Hs.55209	Homo sapiens mRNA; cDNA DKFZp434K0514 (f	4.50				
45	119027	AF086161	Hs.114611	hypothetical protein FLJ11808	3.22				
	119052	R10889		gb:yf38d02.s1 Soares fetal liver spleen		9.60			
	119164	AF221993	Hs.46743	McKusick-Kaufman syndrome			6.60		
	119186	AI979147	Hs.101265	hypothetical protein FLJ22593				10.80	
	119243	T12603		gb:CHR90123 Chromosome 9 exon II Homo sa				9.44	
50	119490	AA195276	Hs.263858	ESTs, Moderately similar to B34087 hypot				11.80	
	119499	AI918906	Hs.55080	ESTs			14.80		
	119599	W45552		gb:zc26d03.s1 Soares_senescent_fibroblas			12.60		
	119780	NM_016625	Hs.191381	hypothetical protein	17.00				
	119845	W79123	Hs.58561	G protein-coupled receptor 87	13.50				
55	119941	AA699485	Hs.58896	ESTs			8.00		
	119994	AA642402	Hs.59142	ESTs	7.73				
	120102	W67353	Hs.170218	KIAA0251 protein				39.60	
	120104	AK000123	Hs.180479	hypothetical protein FLJ20116	2.91				
	120294	AK000059	Hs.153881	Homo sapiens NY-REN-62 antigen mRNA, par			8.20		
60	120486	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	8.73				
	120599	AA804448	Hs.104463	ESTs		7.00			
	120699	AI683243	Hs.97258	ESTs, Moderately similar to S29539 ribos				10.00	
	120715	AA292700		gb:zs59a06.s1 NCL_CGAP_GCB1 Homo sapiens		9.40			
	120821	Y19062	Hs.96870	staufer (Drosophila, RNA-binding protein				13.80	
65	120859	AA826434	Hs.1619	achaete-scute complex (Drosophila) homol		9.00			
	120880	AA360240	Hs.97019	EST		15.60			
	120983	AA398209	Hs.97587	EST			27.66		
	121034	AL389951	Hs.271623	nucleoporin 50kD			20.80		
	121121	AA399371	Hs.189095	similar to SALL1 (sal (Drosophila)-like		22.80			
70	121313	AA402713	Hs.97872	ESTs				10.00	
	121369	AW450737	Hs.128791	CGI-09 protein	25.71				
	121376	AA448103	Hs.187958	solute carrier family 6 (neurotransmitte				5.42	
	121476	AA412311	Hs.97903	ESTs		8.30			
	121509	AA868939	Hs.97888	ESTs		8.59			
75	121553	AA412488	Hs.48820	TATA box binding protein (TBP)-associat	18.50				
	121753	AK000552	Hs.323518	WD repeat domain 5	7.00				
	121838	AA425680	Hs.98441	ESTs				10.40	
	121857	BE387162	Hs.280858	ESTs, Highly similar to A35661 DNA excis	6.00				
	121991	AA430058	Hs.98649	EST				12.20	
80	122089	AW016543	Hs.98682	hypothetical protein FKSG32			8.60		
	122105	AW241685	Hs.98699	ESTs			6.14		
	122163	AA435702	Hs.98829	EST				10.40	
	122318	AA429743		gb:zv60b05.r1 Soares_testis_NHT Homo sap				18.20	
	122335	AA443258	Hs.241551	chloride channel, calcium activated, fam	13.50				
85	122338	AA443311	Hs.98998	ESTs	4.80				
	122414	AI313473	Hs.99087	ESTs, Weakly similar to S47073 finger pr		8.00			



	122512	AF053305	Hs.98658	budding uninhibited by benzimidazoles 1	8.80		
	122516	AA449352	Hs.99217	ESTs		9.40	
	122702	AI220089	Hs.99439	ESTs	9.20		
5	122852	AI580056	Hs.98992	ESTs		10.40	
	122925	AW268962	Hs.111335	ESTs	6.80		
	123005	AW369771	Hs.52620	integrin, beta 8		12.60	
	123044	AK001035	Hs.130881	B-cell CLL/lymphoma 11A (zinc finger pro			5.35
	123160	AA488687	Hs.284235	ESTs, Weakly similar to I38022 hypothe		6.06	
10	123315	AA496369		gb:zv37d10.s1 Soares ovary tumor NbHOT H		12.40	
	123329	Z47542	Hs.179312	small nuclear RNA activating complex, po		11.80	
	123497	AA765256	Hs.135191	ESTs, Weakly similar to unnamed protein	12.00		
	123518	AL035414	Hs.21068	hypothetical protein		13.00	
	123519	AW015887	Hs.112574	ESTs	12.20		
15	123614	AK000492	Hs.98806	hypothetical protein		7.80	
	123616	AA680003	Hs.109363	Homo sapiens cDNA: FLJ23603 fis, clone L		10.60	
	123673	BE550112	Hs.158549	ESTs, Weakly similar to T2D3_HUMAN TRANS	23.00		
	123727	AI083986	Hs.282977	hypothetical protein FLJ13490	7.00		
	123731	AA609839		gb:ae62f01.s1 Stratagene lung carcinoma		9.80	
20	123752	AA227714	Hs.179703	KIAA0129 gene product	3.50		
	123900	AA621223	Hs.112953	EST		12.80	
	124006	AI147155	Hs.270016	ESTs	97.00		
	124059	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypothe	3.02		
	124069	AF134160	Hs.7327	claudin 1		27.80	
25	124191	T96509	Hs.248549	ESTs, Moderately similar to S65657 alpha		35.80	
	124273	AA457211	Hs.8858	bromodomain adjacent to zinc finger doma	7.20		
	124297	AL080215	Hs.102301	Homo sapiens mRNA; cDNA DKFZp586J0323 (f		11.00	
	124305	AW963221		gb:EST375294 MAGE resequences, MAGH Homo		16.00	
	124676	AI360119.comp	Hs.181013	phosphoglycerate mutase 1 (brain)		6.08	
30	124874	BE550182	Hs.127826	RalGEF-like protein 3, mouse homolog		21.00	
	124904	AK000483	Hs.93872	KIAA1682 protein	9.40		
	124969	AI650360	Hs.100256	ESTs		10.80	
	125000	T58615	Hs.110640	ESTs		9.80	
	125201	AA693960	Hs.103158	ESTs, Weakly similar to T33296 hypothe	7.60		
35	125266	W90022	Hs.186809	ESTs, Highly similar to LCT2_HUMAN LEUKO	6.59		
	125299	T32982	Hs.102720	ESTs		9.57	
	125356	AI057052	Hs.133554	ESTs, Weakly similar to Z195_HUMAN ZINC		14.00	
	125370	AA256743	Hs.134158	Homo sapiens, Similar to KIAA0092 gene p	8.20		
40	125418	AA777690	Hs.188501	ESTs		13.20	
	125433	AL162066	Hs.54320	hypothetical protein DKFZp762D096	21.40		
	125437	AI609449	Hs.140197	ESTs	6.96		
	125446	BE219987	Hs.166982	phosphatidylinositol glycan, class F	8.80		
	125711	AA305800	Hs.5672	hypothetical protein AF140225		11.20	
	125756	BE174587	Hs.289721	growth arrest specific transcript 5		4.31	
45	125757	AI274906	Hs.166835	ESTs, Highly similar to 1814460A p53-ass		15.60	
	125769	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	3.20		
	125839	AW836261	Hs.337717	ESTs	8.20		
	125850	W85858	Hs.99804	ESTs	2.65		
	125875	H14480		gb:ym18b09.r1 Soares infant brain 1NIB H	7.40		
50	125924	BE272506	Hs.82109	syndecan 1		4.23	
	125972	AI927475	Hs.35406	ESTs, Highly similar to unnamed protein		3.98	
	126034	H60340		gb:yr39b04.r1 Soares fetal liver spleen		10.60	
	126327	AA432266	Hs.44648	ESTs	11.60		
	126345	N49713		gb:yv23f06.s1 Soares fetal liver spleen	6.67		
55	126435	AW614529	Hs.285847	CGI-19 protein		10.60	
	126487	AA283809	Hs.184601	solute carrier family 7 (cationic amino		4.38	
	126521	AI475110	Hs.203933	ESTs	6.60		
	126522	W31912		gb:zc76d03.s1 Pancreatic Islet Homo sapi		14.80	
	126543	AL035864	Hs.69517	cDNA for differentially expressed CO16 g		4.01	
60	126567	AA058394	Hs.57887	ESTs, Weakly similar to KIAA0758 protein	7.80		
	126605	AA676910		gb:zj65h07.s1 Soares_fetal_liver_spleen_		11.60	
	126627	AA497044	Hs.20887	hypothetical protein FLJ10392		14.60	
	126628	N49776	Hs.170994	hypothetical protein MGC10946	8.00		
	126737	AW976516	Hs.283707	Homo sapiens cDNA: FLJ21354 fis, clone C	2.92		
65	126795	AW975076	Hs.172589	nuclear phosphoprotein similar to S. cer	7.50		
	126802	AW805510	Hs.97056	hypothetical protein FLJ21634	11.60		
	126892	AF121856	Hs.284291	sorting nexin 6	3.50		
	126928	AA480902	Hs.137401	ESTs		22.83	
70	126979	AA210954		gb:zq89h10.r1 Stratagene hNT neuron (937		11.80	
	126986	AI279892	Hs.46801	sorting nexin 14		11.60	
	126992	AI809521		gb:wf30e03.x1 Soares_NFL_T_GBC_S1 Homo s		20.80	
	127066	R25066		gb:yq42c07.r1 Soares infant brain 1NIB H		27.60	
	127099	AA347668		gb:EST54026 Fetal heart II Homo sapiens		21.60	
	127139	AA830233	Hs.293585	ESTs		11.20	
75	127209	AA305023	Hs.81964	SEC24 (S. cerevisiae) related gene famil	3.10		
	127221	BE062109	Hs.241551	chloride channel, calcium activated, fam	2.76		
	127225	AA315933	Hs.120879	ESTs		16.80	
	127313	AK002014	Hs.47546	Homo sapiens cDNA FLJ11458 fis, clone HE	14.00		
	127444	AW978474	Hs.7560	Homo sapiens mRNA for KIAA1729 protein,		13.60	
80	127500	AW971353	Hs.162115	ESTs	11.20		
	127524	AI243596	Hs.94830	ESTs, Moderately similar to T03094 A-kin	7.80		
	127540	N45572	Hs.105362	Homo sapiens, clone MGC:18257, mRNA, com	3.53		
	127599	AA613204	Hs.150399	ESTs		13.80	
	127609	X80031	Hs.530	collagen, type IV, alpha 3 (Goodpasture		28.00	
85	127662	W80755	Hs.8294	KIAA0196 gene product		19.80	
	127668	AI343257	Hs.139993	ESTs		11.20	



	127746	AI239495	Hs.120189	ESTs			14.18
	127812	AA741368	Hs.291434	ESTs	4.50		
	127817	AA836641	Hs.163085	ESTs			24.60
5	127959	AI302471	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L			9.20
	127960	AI613226	Hs.41569	phosphatidic acid phosphatase type 2A			16.83
	127969	F06498	Hs.93748	Homo sapiens cDNA FLJ14676 fis, clone NT	13.60		
	128015	Z21169	Hs.334659	hypothetical protein MGC14139	7.00		
	128027	AI433721	Hs.164153	ESTs			37.40
10	128077	AI310330	Hs.128720	ESTs			9.60
	128166	NM_006147	Hs.11801	interferon regulatory factor 6			9.24
	128226	AI284940	Hs.289082	GM2 ganglioside activator protein	19.00		
	128305	AI954968	Hs.279009	matrix Gla protein			10.40
	128341	AA191420	Hs.185030	ESTs	9.00		
15	128527	AA504583	Hs.101047	transcription factor 3 (E2A immunoglobul			4.30
	128539	R46163	Hs.258618	ESTs	12.60		
	128568	H12912	Hs.274691	adenylate kinase 3			4.56
	128572	AA933022	Hs.256583	interleukin enhancer binding factor 3, 9			10.00
	128777	AI878918	Hs.10526	cysteine and glycine-rich protein 2		16.80	
20	128781	N71826	Hs.105465	small nuclear ribonucleoprotein polypept			4.48
	128796	AJ000152	Hs.105924	defensin, beta 2	8.12		
	128920	AA622037	Hs.166468	programmed cell death 5			4.62
	128924	BE279383	Hs.26557	plakophilin 3			4.04
	128971	H05132	Hs.107510	ESTs	12.60		
25	129008	AL079648	Hs.301088	ESTs	8.80		
	129041	BE382756	Hs.169902	solute carrier family 2 (facilitated glu			6.05
	129075	BE250162	Hs.83765	dihydrofolate reductase	2.59		
	129105	AI769160	Hs.108681	Homo sapiens brain tumor associated prot		6.67	
	129189	AB023179	Hs.9059	KIAA0962 protein	8.00		
30	129229	AF013758	Hs.109643	polyadenylate binding protein-interactin	4.00		
	129241	AI878857	Hs.109706	hematological and neurological expressed			4.06
	129300	W94197	Hs.110165	ribosomal protein L26 homolog	2.55		
	129404	AI267700	Hs.317584	ESTs	18.00		
	129457	X61959	Hs.207776	aspartylglucosaminidase	6.50		
35	129466	L42583	Hs.334309	keratin 6A	12.94		
	129494	AI148976	Hs.112062	ESTs			11.00
	129605	AF061812	Hs.115947	keratin 16 (focal non-epidermolytic palm			4.46
	129641	AI911527	Hs.11805	ESTs			12.00
	129665	AW163331	Hs.118778	KDEL (Lys-Asp-Glu-Leu) endoplasmic retic			4.70
40	129703	BE388665	Hs.179999	Homo sapiens, clone IMAGE:3457003, mRNA			4.02
	129720	AA156214	Hs.12152	APMCF1 protein			5.71
	129748	M16707	Hs.123053	H4 histone, family 2	3.50		
	129890	AI868872	Hs.282804	hypothetical protein FLJ22704			4.21
	129896	BE295568	Hs.13225	UDP-Gal:betaGlcNAc beta 1,4- galactosylt	2.56		
45	129945	BE514376	Hs.165998	PAI-1 mRNA-binding protein			4.03
	130010	AA301116	Hs.142838	nucleolar phosphoprotein Nopp34		7.00	
	130026	T40480	Hs.332112	EST	6.40		
	130080	X14850	Hs.147097	H2A histone family, member X			4.65
	130149	AW067805	Hs.172665	methylenetetrahydrofolate dehydrogenase	2.74		
50	130285	AA063546	Hs.75981	ubiquitin specific protease 14 (IRNA-gua		7.40	
	130441	U63630	Hs.155637	protein kinase, DNA-activated, catalytic			3.91
	130482	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	4.87		
	130500	AB007913	Hs.158291	KIAA0444 protein			9.60
	130524	U89995	Hs.159234	forkhead box E1 (thyroid transcription f		13.40	
55	130541	X05608	Hs.211584	neurofilament, light polypeptide (68kD)		8.20	
	130553	AF062649	Hs.252587	pituitary tumor-transforming 1			6.06
	130567	AA383092	Hs.1608	replication protein A3 (14kD)		7.00	
	130577	M69241	Hs.162	insulin-like growth factor binding prote	3.04		
	130627	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	3.87		
60	130648	AI458165	Hs.17296	hypothetical protein MGC2376			16.20
	130697	L29472	Hs.1802	major histocompatibility complex, class			17.80
	130744	H59696	Hs.18747	POP7 (processing of precursor, S. cerevi			5.28
	130800	AI187292	Hs.19574	hypothetical protein MGC5469			4.43
	130867	NM_001072	Hs.284239	UDP glycosyltransferase 1 family, polype	16.84		
65	130869	J03626	Hs.2057	uridine monophosphate synthetase (protat			4.92
	130925	AF093419	Hs.169378	multiple PDZ domain protein			9.60
	130994	W17044	Hs.327337	ESTs	12.40		
	131028	AI879165	Hs.2227	CCAAT/enhancer binding protein (C/EBP),	10.21		
70	131031	NM_001650	Hs.288650	aquaporin 4			9.80
	131041	T15767	Hs.22452	Homo sapiens mRNA for KIAA1737 protein,			9.60
	131058	W28545	Hs.101514	hypothetical protein FLJ10342			17.00
	131090	AI143139	Hs.2288	visinin-like 1	2.74		
	131112	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp566A1046 (f		8.80	
	131148	AW953575	Hs.303125	p53-induced protein PIGPC1	3.12		
75	131185	BE280074	Hs.23960	cyclin B1	3.07		
	131200	BE540516	Hs.293732	hypothetical protein MGC3195	3.07		
	131219	W25005	Hs.24395	small inducible cytokine subfamily B (Cy	2.87		
	131257	AW339037	Hs.24908	ESTs			14.67
	131375	AW293165	Hs.143134	ESTs		19.20	
80	131460	NM_003729	Hs.27076	RNA 3'-terminal phosphate cyclase	3.50		
	131476	AI521663	Hs.334644	hypothetical protein FLJ14668	15.00		
	131510	BE245374	Hs.27842	hypothetical protein FLJ11210		7.80	
	131646	BE302464	Hs.30057	MRS2 (S. cerevisiae)-like, magnesium hom		7.00	
	131786	BE000971	Hs.306083	Novel human gene mapping to chromosome 22	2.65		
85	131839	AB014533	Hs.33010	KIAA0633 protein			35.20
	131843	AA192315	Hs.184062	putative Rab5-interacting protein			4.11



	131877	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	19.00		
	131885	BE502341	Hs.3402	ESTs	6.48		
	131921	AA456093	Hs.34720	ESTs		8.40	
5	131945	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	56.00		
	131958	NM_014062	Hs.3566	ART-4 protein			3.82
	131965	W79283	Hs.35962	ESTs	3.03		
	132000	AW247017	Hs.36978	melanoma antigen, family A, 3		9.80	
	132040	NM_001196	Hs.315689	Homo sapiens cDNA: FLJ22373 fis, clone H	3.30		
10	132109	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagon	21.00		
	132114	NM_006152	Hs.40202	lymphoid-restricted membrane protein		8.40	
	132162	AA315805	Hs.94560	desmoglein 2			12.25
	132164	AI752235	Hs.41270	procollagen-lysine, 2-oxoglutarate 5-dio	2.70		
	132180	NM_004460	Hs.418	fibroblast activation protein, alpha	2.71		
15	132181	AW961231	Hs.16773	Homo sapiens clone TCCCA00427 mRNA sequ	3.83		
	132182	NM_014210	Hs.70499	ecotropic viral integration site 2A			13.20
	132231	AA662910	Hs.42635	hypothetical protein DKFZp434K2435	9.50		
	132277	AK001745	Hs.184628	hypothetical protein FLJ10883	4.50		
	132328	NM_014787	Hs.44896	DnaJ (Hsp40) homolog, subfamily B, membe			9.20
20	132394	AK001680	Hs.30488	DKFZP434F091 protein			19.80
	132424	AA417878	Hs.48401	ESTs, Moderately similar to ALU8_HUMAN A		8.60	
	132528	T78736	Hs.50758	SMC4 (structural maintenance of chromoso		27.40	
	132543	BE568452	Hs.5101	protein regulator of cytokinesis 1	4.38		
	132544	L19778	Hs.51011	H2A histone family, member P		7.00	
25	132550	AW969253	Hs.170195	bone morphogenetic protein 7 (osteogenic	2.64		
	132552	BE621985	Hs.296922	thiopurine S-methyltransferase			15.83
	132581	AK000631	Hs.52256	hypothetical protein FLJ20624		6.60	
	132617	AF037335	Hs.5338	carbonic anhydrase XII	4.95		
	132638	AI796870	Hs.54277	DNA segment on chromosome X (unique) 992		8.20	
30	132653	Z15008	Hs.54451	laminin, gamma 2 (nicein (100kD), kalini	4.38		
	132669	W38586	Hs.293981	guanine nucleotide binding protein (G pr			4.36
	132710	W74001	Hs.55279	serine (or cysteine) proteinase inhibito	4.60		
	132771	Y10275	Hs.56407	phosphoserine phosphatase	3.71		
	132799	W73311	Hs.169407	SAC2 (suppressor of actin mutations 2,			9.48
35	132833	U78525	Hs.57783	eukaryotic translation initiation factor			5.83
	132892	AW834050	Hs.9973	tensin			12.00
	132906	BE613337	Hs.234896	geminin	3.09		
	132959	AW014195	Hs.61472	ESTs, Weakly similar to YAE6_YEAST HYPOT			3.87
40	132962	AA576635	Hs.6153	CGI-48 protein	3.50		
	132990	X77343	Hs.334334	transcription factor AP-2 alpha (activat	6.18		
	132994	AA112748	Hs.279905	clone HQ0310 PRO0310p1	3.19		
	133000	AL042444	Hs.62402	p21/Cdc42/Rac1-activated kinase 1 (yeast	2.96		
	133050	X73424	Hs.63788	propionyl Coenzyme A carboxylase, beta p	2.55		
45	133083	BE244588	Hs.6456	chaperonin containing TCP1, subunit 2 (b			4.00
	133086	L17131	Hs.139800	high-mobility group (nonhistone chromoso			8.96
	133134	AF198620	Hs.65648	RNA binding motif protein 8A			4.28
	133155	M58583	Hs.662	cerebellin 1 precursor			10.80
	133181	X91662	Hs.66744	twist (Drosophila) homolog (acrocephalos	3.00		
	133204	BE267696	Hs.254105	enolase 1, (alpha)			4.63
50	133412	U41493	Hs.73112	guanine nucleotide binding protein (G pr		12.50	
	133421	AF134160	Hs.7327	claudin 1	2.85		
	133451	AW970026	Hs.73818	ubiquinol-cytochrome c reductase hinge p			4.66
	133453	AI659306	Hs.73826	protein tyrosine phosphatase, non-recept		6.80	
	133504	NM_004415	Hs.74316	desmoplakin (DPI, DPII)	6.14		
55	133506	BE562958	Hs.74346	hypothetical protein MGC14353			4.55
	133615	M62843	Hs.75236	ELAV (embryonic lethal, abnormal vision,			17.80
	133627	NM_002047	Hs.75280	glycyl-tRNA synthetase			4.85
	133649	U25849	Hs.75393	acid phosphatase 1, soluble			6.34
	133669	NM_006925	Hs.166975	splicing factor, arginine/serine-rich 5			14.00
60	133749	L20852	Hs.10018	solute carrier family 20 (phosphate tran		6.11	
	133776	BE268649	Hs.177766	ADP-ribosyltransferase (NAD+; poly (ADP-			4.91
	133865	AB011155	Hs.170290	discs, large (Drosophila) homolog 5	3.07		
	133946	AJ001258	Hs.173878	NIPSNAP, C. elegans, homolog 1			4.60
	133973	N55540	Hs.78026	ESTs, Weakly similar to similar to ankyr			13.00
65	134047	BE262529	Hs.78771	phosphoglycerate kinase 1			3.85
	134098	BE513171	Hs.79086	mitochondrial ribosomal protein L3	2.56		
	134107	NM_005629	Hs.187958	solute carrier family 6 (neurotransmitte		8.20	
	134112	AW449809	Hs.79150	chaperonin containing TCP1, subunit 4 (d			4.08
	134158	U15174	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	31.00		
70	134160	T98152	Hs.79432	fibrillin 2 (congenital contractural ara		24.60	
	134168	AA398908	Hs.181634	Homo sapiens cDNA: FLJ23602 fis, clone L			6.71
	134185	AA285136	Hs.301914	neuronal specific transcription factor D			14.74
	134201	L35035	Hs.79886	ribose 5-phosphate isomerase A (ribose 5		8.40	
	134272	X76040	Hs.278614	protease, serine, 15	4.50		
75	134276	BE083936	Hs.80976	antigen identified by monoclonal antibod		9.00	
	134353	AL138201	Hs.82120	nuclear receptor subfamily 4, group A, m			16.40
	134367	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	2.80		
	134380	AU077143	Hs.179565	minichromosome maintenance deficient (S.	4.68		
	134423	H53497	Hs.83006	CGI-139 protein			3.84
	134469	AA279661	Hs.83753	small nuclear ribonucleoprotein polypept			5.81
80	134470	X54942	Hs.83758	CDC28 protein kinase 2			4.21
	134498	AW246273	Hs.84131	threonyl-tRNA synthetase			7.30
	134502	BE148534	Hs.84168	UV-B repressed sequence, HUR 7		13.60	
	134510	NM_002757	Hs.250870	mitogen-activated protein kinase kinase			9.70
	134548	N95406	Hs.333495	Deleted in split-hand/split-foot 1 regio			4.63
85	134654	AK001741	Hs.8739	hypothetical protein FLJ10879	6.00		



## WO 02/086443

## PCT/US02/12476

5	134724	AF045239	Hs.321576	ring finger protein 22		12.00
	134743	AA044163	Hs.89463	potassium large conductance calcium-acti	4.00	
	134781	AA374372	Hs.89626	parathyroid hormone-like hormone		25.20
	134806	AD001528	Hs.89718	spermine synthase		4.58
	134853	BE268326	Hs.90280	5-aminimidazole-4-carboxamide ribonucle		4.79
	134859	D26488	Hs.90315	KIAA0007 protein		6.20
	134891	R51083	Hs.90787	ESTs		7.40
	134960	BE246400	Hs.285176	acetyl-Coenzyme A transporter	4.00	
10	134993	BE409809	Hs.301005	purine-rich element binding protein B		4.48
	135047	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	9.50	
	135080	AI761180	Hs.94211	rcd1 (required for cell differentiation,	5.00	
	135103	NM_003428	Hs.9450	zinc finger protein 84 (HPF2)		11.00
	135145	AW014729	Hs.95262	nuclear factor related to kappa B bindin		4.01
15	135184	U13222	Hs.96028	forkhead box D1		7.00
	135242	AI583187	Hs.9700	cyclin E1	13.50	
	135286	AW023482	Hs.97849	ESTs	6.46	
	135289	AW372569	Hs.9788	hypothetical protein MGC10924 similar to		8.80
	135355	AK001652	Hs.99423	ATP-dependent RNA helicase	10.00	
20	135371	NM_006025	Hs.997	protease, serine, 22	8.00	
	135393	L11244	Hs.99886	complement component 4-binding protein,		14.60

TABLE 5B shows the accession numbers for those primekeys lacking unigenelD's for Table 5A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number  
 CAT number: Gene cluster number  
 Accession: Genbank accession numbers

Pkey	CAT number	Accessions
35	117079	1621717_1 H92325 T97125
	124305	242183_1 AW963221 AA344870 AA344871 H93331
	101502	18202_6 M26958
	109792	754958_1 R49625 F10674
40	126034	1598157_1 H60340 N91637
	102768	44641_1 U82321 H66077
	126345	1653833_1 N49713 N49819 W03810
	127066	1703458_1 R25066 R20144 R20145 Z43845
	127099	244301_1 AA347668 AW956810 Z44271 F07065 F07064 R13506
	119243	1774795_1 T12603 T12604
45	125875	1566433_1 H14480 N98295
	112054	1538292_1 R43590 F10439
	128979	171411_1 AA210954 AA211007
	126992	880655_1 AI809521 H12174 Z42556
	122318	292419_1 AA429743 AA442754
50	114699	135322_1 AA127386 R15644 AA127404
	114793	150742_1 AA158245 AA158235
	108305	111550_1 AA071391 AA069892 AA069891
	108393	113411_1 AA075211 AA075245 AA075126 AA074946
	100867	tigr_HT4586 U14622
55	123731	genbank_AA609839 AA609839
	109700	genbank_F09609 F09609
	120715	genbank_AA292700 AA292700
	113702	genbank_T97307 T97307
	115113	genbank_AA256460 AA256460
60	101045	entrez_J05614 J05614
	108554	genbank_AA084948 AA084948
	108573	genbank_AA086005 AA086005
	119052	149538_1 R10889 R10888
	126522	416020_1 W31912 AI167491
65	126605	439280_1 AA676910 AA778853 AA778865 W86800
	103768	46922_1 W42667 AI580740 AI690440 AI561350 AW467906 AW151450 AI825927 AI041716 AI885600 AI742213 AW248624 AI955498 AA033947
		AA845593 AI623711 N68583 C00064 AA193567 AW083868 AW163216 AA191595 AA522778 AI628008 AI915518 AA843508 AI926195
		AA176265 AW167963 AA992115 W93647 AW103572 AI862994 AI342059 AA911719 AA176155 AA024712 AA069988 AA205591 AI591107
		AI199673 AI811766 AI275832 AI422233 AI191852 AI096682 AI580124 AI683612 AA582453 AA927559 AA486415 T32414 AI084978 H44849
70		H44848 H20477 T91695 W47039 AA070055 AA024795 AA328855 AA379248 AA379330 AA385580 W25920 W03588 AA448359 AA093881
		AW362477 AA089997 AI350265 W93479 N99688 AA932257 AW351469 H68590 AA663402 AA069771 AW087986 AI858420 AA600214
		AI970774 AI857712 AI683081 AI885584 AW131150 AI567981 AW002714 AW189973 AW075495 AW168303 AA953714 AW516881 AI357375
		AI566663 AW512676 AI570580 AI023690 AA448216 AI079853 AI422707 AA779516 AW026972 AW130082 AW162307 AW438646 AA709332
		AW192394 AI167350 AI217879 AI129152 AA719509 AI350480 AA663418 AI003634 AW118546 AA180261 AA442833 AI268625 AA888881
75		AI038759 AA846723 AI248770 AA993694 AI280335 AI885107 AW518649 AA641563 AA995835 AA582521 AI276744 AA436478 AI017360
		AI620763 AI859887 N73926 AI076327 AI741615 AI160617 AW172819 AI492005 AA677429 AA996334 AI693771 AI950039 AI245629 AI288515
		AI866186 T93293 AA173262 AA599779 AI680092 AW439316 AI084555 AI272672 AI583507 AW473219 AW738132 AW473283 AI367492
		AA995410 AI689624 AA206353 AI033095 AI040382 AA873630 AI221074 AI934840 AI418680 AA844306 R94503 AA773520 AA843169
		AA219425 AA629658 AI811719 AW411275 AI590981 W37907 AI591178 AI684051 AA983238 AA669347 AA976239 AA704570 AI628339
80		AI884391 AI241580 AI003539 AW176687 AA009650 N34566 AI333493 AI186070 AA070827 AA411683 AI280884 AA872023 AA207255
		AA021576 N71953 AI885888 AW076039 T15777 AI537673 AW248048 H09554 W93480 W47001 AW079114 AA063160 AA757453 R60788
		AI859431 H20478 AA218882 AA757465 AA100995 AI864135 AI934209 AA070503 H47008 AA219646 W61039 W93907 AW385050 W37967
		W78028 AA189007 AA479136 R93650 AA442312 T30287 AA847628 AA180262 AA009649 C03892 AW149464 AA310963 AA219693
		AA069747 R29207 AA094784 AA293615 AA447848 AI984167 N90393 C05097 N56499 AW292351 AW149681 AW473258 AA629322 AI004409
85		AW105577 AI954937 AI811070 AA902422 AW514437 AA535460 AA916877 AW517122 AA974657 AA975649 AW517130 AW517129 F31737
		W07688 AA193645 AA378994 AA489273 F32267 W39303 AA021181 N86810 AA406524 AA062553 AA436801 H08985 H15979 N40310



AA436789 AA232172 AW360778 W25862 R60282 AA436530 AA378894 AA187461 AI940535 AA604210 AA088514 AA360421 N88243 N84281  
 AA209340 N56174 N88374 AA191088 AW247691 AA249013 AA093111 AA972536 AW298594 AA375893 T12139 W28186 AW243849  
 AI288629 AA843996 W15260 AI188286 AW248079 R15836

119599 genbank\_W45552 W45552  
 112382 genbank\_R59904 R59904  
 105264 genbank\_AA227934 AA227934  
 100071 entrez\_A28102 A28102  
 123315 714071\_1 AA496369 AA496646

Table 6A shows 99 genes up-regulated nonsmokers with lung cancer relative to smokers with lung cancer. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Pkey: Unique Eos probeset identifier number  
 ExAccon: Exemplar Accession number, Genbank accession number  
 UnigenelD: Unigene number  
 Unigene Title: Unigene gene title  
 R1: average of AI for samples from non-smokers with adenocarcinoma divided by the 90th percentile of AI for samples from smokers with adenocarcinoma  
 R2: average of AI for samples from non-smokers with squamous cell carcinoma divided by the 90th percentile of AI for samples from smokers with squamous cell carcinoma

Pkey	ExAccon	UnigenelD	Unigene Title	R1	R2
100971	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte		3.64
101174	L17330	Hs.280	pre-T/NK cell associated protein	15.00	
101296	Y12490	Hs.85092	thyroid hormone receptor interactor 11		2.46
101304	AA001021	Hs.6685	thyroid hormone receptor interactor 8		12.00
101806	AA586894	Hs.112408	S100 calcium-binding protein A7 (psoriasis)		2.68
101972	S82472		gb:beta-pol=DNA polymerase beta (exon a)		2.11
102274	U30930	Hs.158540	UDP glycosyltransferase 8 (UDP-galactose)	7.50	
102394	NM_003816	Hs.2442	a disintegrin and metalloproteinase domain	7.50	
102832	U92015		gb:Human clone 143789 defective mariner	13.50	
103010	X52509	Hs.161640	tyrosine aminotransferase	9.50	
103439	X98266		gb:H.sapiens mRNA for ligase like protein		2.50
103563	L02911	Hs.150402	activin A receptor, type I	9.00	
103857	AI076795	Hs.45033	lacrimal proline rich protein		3.94
104239	AB002367	Hs.21355	doublecortin and CaM kinase-like 1	13.50	
104590	AW373062	Hs.83623	nuclear receptor subfamily 1, group I, member 1		12.66
104907	AA055829	Hs.196701	ESTs, Weakly similar to ALU1_HUMAN ALU	16.50	
106131	BE514788	Hs.296244	SNARE protein		2.17
106672	H47233	Hs.30643	ESTs	7.00	
106872	T56887	Hs.18282	KIAA1134 protein	11.50	
106960	AA156238	Hs.32501	ESTs		2.38
106971	Z43846	Hs.194478	Homo sapiens mRNA; cDNA DKFp434O1572 (f)	9.50	
107982	AA035375	Hs.57887	ESTs, Weakly similar to KIAA0758 protein		2.95
108562	AA100796		gb:zm26c06.s1 Stratagene pancreas (93720)	16.50	
108599	AB018549	Hs.69328	MD-2 protein	13.00	
108663	BE219231	Hs.292653	ESTs, Weakly similar to T26845 hypothetical		2.40
109247	AA314907	Hs.85950	ESTs	7.00	
109630	R44607	Hs.22672	ESTs		5.00
110193	AI004874	Hs.310764	Homo sapiens mRNA; cDNA DKFp434M082 (f)	12.50	
110234	H24458	Hs.32085	EST	16.50	
110644	R94207	Hs.268989	ESTs, Highly similar to type II CALM/AF1	8.00	
110886	AW274992	Hs.72249	three-PDZ containing protein similar to	17.00	
111057	T79639	Hs.14629	ESTs	16.50	
111950	AF071594	Hs.110457	Wolf-Hirschhorn syndrome candidate 1	11.00	
112291	R53972	Hs.26026	ESTs		3.00
112956	Z43784	Hs.75893	ankyrin 3, node of Ranvier (ankyrin G)		2.79
113009	T23699	Hs.7246	ESTs		4.50
113060	BE564162	Hs.250820	hypothetical protein FLJ14827	9.79	
113073	N39342	Hs.103042	microtubule-associated protein 1B	32.50	
113074	AK001335	Hs.31137	protein tyrosine phosphatase, receptor type 1		3.82
113121	T48011	Hs.8764	EST		2.21
113125	AA968672	Hs.8929	hypothetical protein FLJ11362	19.50	
113757	AA703095	Hs.18631	ESTs		2.65
113848	W52854	Hs.27099	hypothetical protein FLJ23293 similar to	6.00	
113884	AI333076	Hs.28529	chromosome 12 open reading frame 2		6.00
113936	W17056	Hs.83623	nuclear receptor subfamily 1, group I, member 1		4.63
114875	AA235609	Hs.236443	Homo sapiens mRNA; cDNA DKFp564N1063 (f)		7.00
114987	AA251016	Hs.87808	EST		6.00
115460	AW958439	Hs.38613	ESTs		2.27
115722	W91892	Hs.59609	ESTs		9.00
116261	AA481788	Hs.190150	ESTs	9.50	
116830	H61037	Hs.70404	ESTs, Weakly similar to ALU2_HUMAN ALU	8.50	
116970	AB023179	Hs.9059	KIAA0962 protein	7.50	
117178	H98675	Hs.269034	ESTs		2.68
117757	AF088019	Hs.46732	EST	7.50	
118283	AA287747	Hs.173012	ESTs, Weakly similar to A46010 X-linked	16.50	
118384	AF217525	Hs.49002	Down syndrome cell adhesion molecule		2.50
118657	AI822106	Hs.49902	ESTs		2.39
120328	AA923278	Hs.290905	ESTs, Weakly similar to protease [H.sapiens]		3.50
120404	AB023230	Hs.96427	KIAA1013 protein	7.00	
120524	AA261852	Hs.192905	ESTs	6.00	
120688	AW207555	Hs.97093	Homo sapiens cDNA: FLJ23004 f1s, clone L	17.92	



	121558	AA412497	gb:zt95g12.s1 Soares_testis_NHT Homo sap		2.95
	121676	H56037	Hs.108146 ESTs	10.00	
	121936	AI024600	Hs.98612 ESTs	15.00	
5	121938	AA428659	Hs.98610 ESTs	14.00	
	122177	AA435789	Hs.98833 EST	8.93	
	123442	AA299652	Hs.111496 Homo sapiens cDNA FLJ11643 fis, clone HE	13.04	
	123551	AA608837	gb:af03h12.s1 Soares_testis_NHT Homo sap	11.50	
	123756	AA609971	Hs.112795 EST	11.00	
10	123861	AA620840	gb:af89g01.s1 Soares_testis_NHT Homo sap		2.50
	124371	N24924	Hs.188601 ESTs	6.50	
	127477	BE328720	Hs.280651 ESTs		4.33
	127591	AI190540	Hs.131092 ESTs		3.02
	128252	AA455924	Hs.192228 ESTs	7.00	
15	128426	AI265784	Hs.145197 ESTs		2.08
	128925	R67419	Hs.21851 Homo sapiens cDNA FLJ12900 fis, clone NT		2.11
	128945	AI990506	Hs.8077 Homo sapiens mRNA; cDNA DKFZp547E184 (fr	10.00	
	129105	AI769160	Hs.108681 Homo sapiens brain tumor associated prot	15.50	
	129235	AW977238	Hs.126084 KIAA1055 protein		4.25
20	129506	AB020684	Hs.11217 KIAA0877 protein	6.50	
	129595	U09550	Hs.1154 oviductal glycoprotein 1, 120kD (mucin 9		10.00
	130160	AA305688	Hs.267695 UDP-Gal:betaGlcNAc beta 1,3-galactosyltr	20.00	
	130340	D82326	Hs.239106 solute carrier family 3 (cystine, dibasi	11.50	
	131220	AB023194	Hs.300855 KIAA0977 protein	17.50	
25	131430	AI879148	Hs.26770 fatty acid binding protein 7, brain	6.10	
	132114	NM_006152	Hs.40202 lymphoid-restricted membrane protein		6.15
	132458	AA935315	Hs.48965 Homo sapiens cDNA: FLJ21693 fis, clone C		5.58
	132647	NM_006927	Hs.54432 sialyltransferase 4B (beta-galactosidase	7.50	
	132655	D49372	Hs.54460 small inducible cytokine subfamily A (Cy		2.53
30	132682	AI077500	Hs.54900 serologically defined colon cancer antig		2.50
	132747	AA345241	Hs.55950 ESTs, Weakly similar to KIAA1330 protein		2.83
	132812	R50333	Hs.92186 Leman coiled-coil protein		3.82
	133337	AF085983	Hs.293676 ESTs		5.00
	133876	AL134906	Hs.771 phosphorylase, glycogen; liver (Hers dis		3.00
35	134119	AW157837	Hs.79226 fasciculation and elongation protein zet		2.06
	134464	AA302983	Hs.239720 CCR4-NOT transcription complex, subunit		2.27
	134542	M14156	Hs.85112 insulin-like growth factor 1 (somatomedi		11.50
	135002	AA448542	Hs.251677 G antigen 7B	87.00	
40	135305	AA203555	Hs.98288 Homo sapiens cDNA FLJ14903 fis, clone PL		6.50

TABLE 6B show the accession numbers for those primekeys lacking unigenelD's for Table 6A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number  
CAT number: Gene cluster number  
Accession: Genbank accession numbers

Pkey	CAT number	Accessions
108562	36375_1	AA100796 AF020589 AA074629 AA075946 AA100849 AA085347 AA126309 AA079311 AA079323 AA085274
103439	35330_1	X98266 N41124
123551	genbank_AA608837	AA608837
123861	genbank_AA620840	AA620840
102832	entrez_U92015	U92015
101972	entrez_S82472	S82472
121558	genbank_AA412497	AA412497



Table 7A shows 98 genes down-regulated in non-smokers with lung cancer relative to smokers with lung cancer. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

5	Pkey:	Unique Eos probeset identifier number				
	ExAccn:	Exemplar Accession number, Genbank accession number				
	UnigenelD:	Unigene number				
	Unigene Title:	Unigene gene title				
10	R1:	90th percentile of AI for samples from smokers with adenocarcinoma divided by the average of AI for samples from non-smokers with adenocarcinoma.				
	R2:	90th percentile of AI for samples from smokers with squamous cell carcinoma divided by the average of AI for samples from non-smokers with squamous cell carcinoma.				
	Pkey	ExAccn	UnigenelD	Unigene Title	R1	R2
15	100187	D17793	Hs.78183	aldo-keto reductase family 1, member C3		164.10
	100380	D82343	Hs.18551	neuroblastoma (nerve tissue) protein		77.40
	100576	X00356	Hs.37058	calcitonin/calcitonin-related polypeptid	102.40	
	100971	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte	463.80	
	101046	K01160		(NONE)	672.00	
20	101066	AW970254	Hs.889	Charol-Leyden crystal protein	66.00	
	101175	U82671	Hs.36980	melanoma antigen, family A, 2		77.20
	101497	W05150	Hs.37034	homeo box A5	62.80	
	101663	NM_003528	Hs.2178	H2B histone family, member Q	78.00	
	101677	NM_000715	Hs.1012	complement component 4-binding protein,	186.20	
25	101745	M88700	Hs.150403	dopa decarboxylase (aromatic L-amino aci	80.08	
	101941	S77583		gb:HERVK10/HUMMTV reverse transcriptase	99.20	
	102125	NM_006456	Hs.288215	sialyltransferase		103.10
	102242	U27185	Hs.82547	retinoic acid receptor responder (tazaro	67.00	
30	102340	U37055	Hs.278657	macrophage stimulating 1 (hepatocyte gro	71.60	
	102369	U39840	Hs.299867	hepatocyte nuclear factor 3, alpha		69.70
	102457	NM_001394	Hs.2359	dual specificity phosphatase 4	153.00	
	102669	U71207	Hs.29279	eyes absent (Drosophila) homolog 2		65.70
	102796	AL079646	Hs.107019	sympleskin; Huntingtin interacting protei		58.80
	102829	NM_006183	Hs.80962	neurotensin		268.80
35	103207	X72790		gb:Human endogenous retrovirus mRNA for	70.00	
	103242	X76342	Hs.389	alcohol dehydrogenase 7 (class IV), mu o		212.10
	103260	X78416	Hs.3155	casein, alpha		130.70
	103351	X89211		gb:H.sapiens DNA for endogenous retrovir	64.60	
40	104212	AB002298	Hs.173035	KIAA0300 protein	66.80	
	104252	AF002246	Hs.210863	cell adhesion molecule with homology to	63.80	
	104258	AF007216	Hs.5462	solute carrier family 4, sodium bicarbon	94.40	
	105024	AA126311	Hs.9879	ESTs	68.20	
	106260	AI097144	Hs.5250	ESTs, Weakly similar to ALU1_HUMAN ALU S		74.60
45	106440	AA449563	Hs.151393	glutamate-cysteine ligase, catalytic sub		71.10
	106566	BE298210		gb:601118016F1 NIH_MGC_17 Homo sapiens c	73.20	
	106605	AW772298	Hs.21103	Homo sapiens mRNA; cDNA DKFZp564B076 (fr	83.80	
	106614	AA648459	Hs.335951	hypothetical protein AF301222		62.30
	106654	AW075485	Hs.286049	phosphoserine aminotransferase		202.40
50	106999	H93281	Hs.10710	hypothetical protein FLJ20417		89.60
	108700	AA121518	Hs.193540	ESTs, Moderately similar to 2109260A B c		66.40
	108810	AW295647	Hs.71331	hypothetical protein MGC5350		95.50
	108857	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act		63.40
	109597	AA989362	Hs.293780	ESTs	85.00	
55	109691	T65568	Hs.12860	ESTs		58.70
	109704	AI743880	Hs.12876	ESTs		60.60
	110942	R63503	Hs.28419	ESTs	76.40	
	111722	R23924	Hs.23596	EST	74.60	
	112891	T03927	Hs.293147	ESTs, Moderately similar to A46010 X-II	64.80	
60	112992	AL157425	Hs.133315	Homo sapiens mRNA; cDNA DKFZp761J1324 (f		76.70
	113073	N39342	Hs.103042	microtubule-associated protein 1B		120.20
	114251	H15261	Hs.21948	ESTs	127.20	
	115230	AA278300	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L	174.00	
	115291	BE545072	Hs.122579	hypothetical protein FLJ10461		91.00
65	115815	AW905328	Hs.180842	ribosomal protein L13	66.40	
	115909	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH		226.60
	115965	AA001732	Hs.173233	hypothetical protein FLJ10970	82.80	
	116107	AL133916	Hs.172572	hypothetical protein FLJ20093		361.60
	116552	D20508	Hs.164649	hypothetical protein DKFZp434H247	69.00	
70	116571	D45652		gb:HUMGS02848 Human adult lung 3' direct	64.20	
	118466	N66741		gb:y233g08.s1 Morton Fetal Cochlea Homo		63.50
	120484	AA253170	Hs.96473	EST	81.60	
	120983	AA398209	Hs.97587	EST		81.10
	121034	AL389951	Hs.271623	nucleoporin 50kD		66.20
75	121423	AW973352	Hs.290585	ESTs	64.40	
	122553	AA451884	Hs.190121	ESTs		60.40
	122946	AI718702	Hs.308026	major histocompatibility complex, class	188.60	
	123130	AA487200		gb:ab19f02.s1 Stratagene lung (937210) H		80.20
	124472	N52517	Hs.102670	EST	71.00	
80	124526	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci		104.90
	125489	H49193	Hs.124984	ESTs, Moderately similar to ALU7_HUMAN A		72.00
	125731	R61771	Hs.26912	ESTs		69.90
	125747	NM_002884	Hs.865	RAP1A, member of RAS oncogene family	69.00	
	126020	H79863	Hs.114243	ESTs		62.40
	126547	U47732	Hs.84072	transmembrane 4 superfamily member 3		62.80
85	126966	R38438	Hs.182575	solute carrier family 15 (H+/peptide tra		60.10



	127472	AA761378	Hs.192013	ESTs	70.20	
	127610	AA960867	Hs.150271	ESTs, Highly similar to unnamed protein	64.00	
	127742	AW293496	Hs.180138	ESTs	85.20	
5	127987	AI022103	Hs.124511	ESTs	96.60	
	128233	AW889132	Hs.11916	ribokinase		78.90
	128420	AA650274	Hs.41296	fibronectin leucine rich transmembrane p		106.90
	128766	AW160432	Hs.296460	craniofacial development protein 1	66.80	
	129014	AW935187	Hs.170162	KIAA1357 protein		58.53
10	129215	AB040930	Hs.126085	KIAA1497 protein	64.20	
	130090	H97878	Hs.132390	zinc finger protein 36 (KOX 18)	63.80	
	130385	AW067800	Hs.155223	stanniocalcin 2		139.60
	130732	AW890487	Hs.63984	cadherin 13, H-cadherin (heart)		64.60
	131025	AB040900	Hs.6189	KIAA1467 protein	64.40	
15	131241	BE501914	Hs.24654	Homo sapiens cDNA FLJ11640 fis, clone HE	76.20	
	131775	AB014548	Hs.31921	KIAA0648 protein	97.80	
	132240	AB018324	Hs.42676	KIAA0781 protein		71.00
	132856	NM_001448	Hs.58367	glypican 4		88.40
	132977	AA093322	Hs.301404	RNA binding motif protein 3	133.20	
20	133749	L20852	Hs.10018	solute carrier family 20 (phosphate tran		59.30
	133818	AI110684	Hs.7645	fibrinogen, B beta polypeptide	341.00	
	134264	AF149297	Hs.8087	NAG-5 prtein		64.30
	134265	M83772	Hs.80876	flavin containing monooxygenase 3		232.53
	134346	X84002	Hs.82037	TATA box binding protein (TBP)-associate	66.00	
25	134395	AA456539	Hs.8262	lysosomal-associated membrane protein 2		75.80
	135047	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su		108.30
	135056	N75765	Hs.93765	lipoma HMGIC fusion partner	71.40	
	135309	AI564123	Hs.42500	ADP-ribosylation factor-like 5	70.40	

30 TABLE 7B shows the accession numbers for those primekeys lacking unigenelD's for Table 7A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

35 Pkey: Unique Eos probeset identifier number  
CAT number: Gene cluster number  
Accession: Genbank accession numbers

Pkey	CAT number	Accessions
40 103207	30635_4	X72790
106566	120358_1	BE298210 AI672315 AW086489 BE298417 AA455921 AA902537 BE327124 R14963 AA085210 AW274273 AI333584 AI369742 AI039658 AI885095 AI476470 AI287650 AI885299 AI985381 AW592624 AW340136 AI266556 AA456390 AI310815 AA484951
45 116571	genbank_D45652	D45652
118466	genbank_N66741	N66741
101046	entrez_K01160 K01160	
101941	entrez_S77583 S77583	
103351	entrez_X89211 X89211	
50 123130	genbank_AA487200	AA487200



Table 8A shows 1720 genes either up or down-regulated in lung tumors or chronically diseased lung relative to a broad collection of over 40 distinct normal body tissues. Chronically diseased lung samples represent chronic non-malignant lung diseases such as fibrosis, emphysema, and bronchitis. These genes were selected from 39494 probesets on the Eos/Affymetrix Hu02 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Pkey: Unique Eos probeset identifier number  
 ExAccn: Exemplar Accession number, Genbank accession number  
 UnigenelD: Unigene number  
 Unigene Title: Unigene gene title  
 R1: 70th percentile of AI for lung tumors divided by 90th percentile of AI for normal lung  
 R2: 70th percentile of AI for chronically diseased lung divided by 90th percentile of AI for normal lung

Pkey	ExAccn	UnigenelD	Unigene Title	R1	R2
300097	AI916973	Hs.213603	ESTs	5.46	4.69
300117	AW189787	Hs.147474	ESTs	0.58	0.56
300197	AI686661	Hs.218286	ESTs	4.26	5.44
300201	AI308300		gb:ta90c06.x1 NCI_CGAP_Bm20 Homo sapien	0.62	0.83
300225	AI989963	Hs.197505	ESTs	1.68	1.75
300247	AW274682	Hs.161394	ESTs	1.08	2.28
300256	AI469095	Hs.298241	Transmembrane protease, serine 3	0.86	1.00
300337	AI707881	Hs.202090	ESTs	5.80	9.09
300362	Z42308		gb:HSC0FB121 normalized infant brain cDN	4.18	12.78
300374	AI859947	Hs.314158	ESTs	2.99	4.38
300387	AW270150	Hs.254516	ESTs	1.50	2.53
300440	AI421541	Hs.146164	ESTs	3.98	5.25
300441	R10367	Hs.307921	EST, Weakly similar to Z232_HUMAN ZINC F	3.18	6.80
300449	AI362967	Hs.132221	hypothetical protein FLJ12401	0.43	0.62
300469	AW135830	Hs.233955	hypothetical protein FLJ20401	0.16	0.83
300552	X85711	Hs.21838	hypothetical protein FLJ11191	4.10	9.75
300627	W27363		gb:ab37d01.r1 Stratagene HeLa cell s3 93	4.60	12.60
300630	AW118822	Hs.128757	ESTs	2.91	5.86
300716	AI216113	Hs.126280	hypothetical protein FLJ23393	1.00	0.92
300738	AI623332	Hs.130541	KIAA1542 protein	1.82	1.71
300777	AA235361	Hs.96840	KIAA1527 protein	4.48	8.22
300790	AI492471	Hs.188270	ESTs	1.29	1.18
300832	AI688147	Hs.220615	ESTs, Weakly similar to T03829 transcrip	5.51	8.56
300836	Z44942	Hs.22958	calcium channel alpha2-delta3 subunit	4.90	6.34
300838	AI582897	Hs.192570	hypothetical protein FLJ22028	1.70	2.81
300878	AW449802	Hs.285901	Homo sapiens cDNA FLJ20428 fis, clone KA	4.56	7.91
300897	AI890356	Hs.127804	ESTs, Weakly similar to T17233 hypotheri	2.23	1.58
300926	AA504860		gb:ab03a10.s1 Stratagene fetal retina 93	2.13	3.50
300960	AI041019	Hs.152454	ESTs	2.74	4.46
300961	AW204069	Hs.312716	ESTs, Weakly similar to unnamed protein	1.00	1.00
300962	AA593373	Hs.293744	ESTs	1.46	1.51
300967	AA565209	Hs.269439	ESTs	0.39	1.30
300987	AW450840	Hs.148590	ESTs, Weakly similar to AF208846 1 BM-00	1.49	1.08
300988	AI927208	Hs.208952	ESTs	0.16	0.37
301050	AW136973	Hs.288516	ESTs, Weakly similar to S69890 mitogen i	3.23	1.94
301098	AA677570	Hs.185918	ESTs	6.76	14.28
301157	AA729905	Hs.231916	ESTs	3.16	8.85
301162	AI142118	Hs.129004	ESTs	1.68	7.18
301170	AA737594	Hs.247606	ESTs	4.40	6.42
301192	AI808751	Hs.121188	ESTs	6.38	11.59
301193	AA758115	Hs.128350	ESTs, Weakly similar to JC5423 2-hydroxy	4.35	7.78
301267	AW297762	Hs.255690	ESTs	1.56	1.61
301281	AA843986	Hs.190586	ESTs	2.19	1.78
301341	AI819198	Hs.208229	ESTs	0.76	0.76
301382	AA912839	Hs.163369	ESTs	1.00	1.81
301407	AW450466	Hs.126830	ESTs	1.48	1.51
301452	AA975688	Hs.159955	ESTs	0.51	1.46
301483	AW272467	Hs.254655	Untitled	2.40	5.02
301494	AI678034	Hs.131099	ESTs	2.79	3.41
301521	AI733621	Hs.133011	zinc finger protein 117 (HPF9)	0.67	0.67
301531	AI077462	Hs.134084	ESTs	2.52	3.76
301580	AI878959	Hs.73737	splicing factor, arginine/serine-rich 1	7.41	11.92
301676	Z43570	Hs.27453	ESTs, Moderately similar to G01251 Rar p	8.31	10.70
301690	F05865	Hs.108323	ubiquitin-conjugating enzyme E2E 2 (homo	2.70	4.22
301718	F07744	Hs.7987	DKFZP434F162 protein	4.20	8.78
301799	AA384252	Hs.286132	D15F37 (pseudogene)	5.93	7.04
301804	AA581004	Hs.62180	anillin (Drosophila Scraps homolog), act	1.70	0.76
301822	X17033	Hs.271986	integrin, alpha 2 (CD49B, alpha 2 subuni	1.58	1.36
301846	R20002	Hs.6823	hypothetical protein FLJ10430	1.00	1.00
301868	T71508	Hs.13861	ESTs, Weakly similar to pH sensitive max	2.88	5.49
301882	T78054		gb:yc97g09.r1 Soares infant brain 1NIB H	2.28	3.80
301905	AI991127	Hs.117202	ESTs	1.00	1.00
301948	AA344647	Hs.116724	aldo-keto reductase family 1, member B11	5.28	2.28
301960	AW070252	Hs.27973	KIAA0874 protein	5.38	6.48
302011	T91418	Hs.125156	transcriptional adaptor 2 (ADA2, yeast,	3.03	3.42
302016	N40834	Hs.23495	hypothetical protein FLJ11252	1.00	1.25
302041	NM_001501	Hs.129715	gonadotropin-releasing hormone 2	0.71	0.99
302072	AJ238381	Hs.132576	paired box gene 9	1.60	1.71
302094	AI286176	Hs.6786	ESTs	0.52	1.20
302095	AW044300	Hs.137506	Homo sapiens BAC clone RP11-120J2 from 7	2.75	4.93
302148	AW269618	Hs.23244	ESTs	3.04	3.87



	302155	AI088485	Hs.144759	ESTs	0.45	1.15
	302201	AJ006276	Hs.159003	transient receptor potential channel 6	0.33	0.84
	302202	AF097159	Hs.159140	UDP-Gal:betaGlcNAc beta 1,4- galactosylt	0.52	0.94
5	302206	AI937193	Hs.41143	phosphoinositide-specific phospholipase	2.76	3.65
	302209	AF047445	Hs.159297	killer cell lectin-like receptor subfam1	1.00	1.00
	302235	AL049987	Hs.166361	Homo sapiens mRNA; cDNA DKFZp564F112 (fr	1.68	1.50
	302290	AL117607	Hs.175563	Homo sapiens mRNA; cDNA DKFZp564N0763 (f	1.00	2.11
	302328	AA354849	Hs.23240	Homo sapiens cDNA FLJ13496 fis, clone PL	9.38	13.08
10	302346	AL039101	Hs.194625	dynein, cytoplasmic, light intermediate	3.27	7.24
	302360	AJ010901	Hs.198267	mucin 4, tracheobronchial	2.54	1.88
	302384	Y08982	Hs.202676	synaptonemal complex protein 2	1.00	0.91
	302406	U86751	Hs.211956	CD3-epsilon-associated protein; antisens	2.63	2.67
	302409	AF155156	Hs.218028	adaptor-related protein complex 4, epsil	5.82	9.34
	302423	AB028977	Hs.225974	KIAA1054 protein	3.66	3.18
15	302432	AL080068	Hs.272534	Homo sapiens mRNA; cDNA DKFZp564J062 (fr	2.44	6.77
	302435	AF092047	Hs.227277	sine oculis homeobox (Drosophila) homolo	0.44	0.84
	302437	AB024730	Hs.227473	UDP-N-acetylglucosamine:a-1,3-D-mannosid	4.18	5.64
	302455	AA356923	Hs.240770	nuclear cap binding protein subunit 2, 2	1.85	0.92
	302472	AA317451	Hs.6335	SWI/SNF related, matrix associated, acti	2.04	2.13
20	302476	AF182294	Hs.241578	U6 snRNA-associated Sm-like protein LSm8	1.44	1.89
	302489	T80660	Hs.230424	Homo sapiens cDNA FLJ13540 fis, clone PL	0.51	1.10
	302490	AA885502	Hs.187032	ESTs	2.64	4.87
	302562	AJ005585	Hs.48956	gap junction protein, beta 6 (connexin 3	5.34	2.68
25	302566	AA085996	Hs.248572	hypothetical protein FLJ22965	1.00	1.21
	302630	AB029488	Hs.272100	SMS3 protein	0.52	1.24
	302634	AB032953	Hs.173560	odd Oz/ten-m homolog 2 (Drosophila, mous	1.00	1.00
	302638	AA463798	Hs.102696	MCT-1 protein	1.58	1.02
	302647	X57723	Hs.198273	NADH dehydrogenase (ubiquinone) 1 beta s	2.72	6.85
	302655	AJ227892	Hs.146274	ESTs	1.00	4.32
30	302656	AW293005	Hs.70704	Homo sapiens, clone IMAGE:2823731, mRNA,	2.97	0.93
	302668	AA580691	Hs.180789	S164 protein	0.80	0.95
	302679	H65022		gb:yu66g11.1 r1 Weizmann Olfactory Epithel	1.68	5.04
	302680	AW192334	Hs.38218	ESTs	2.70	7.98
35	302697	AJ001408		gb:Homo sapiens mRNA for immunoglobulin	4.25	8.13
	302705	U09060		gb:Human immunoglobulin heavy chain, V-r	3.91	8.68
	302711	L08442		gb:Human autonomously replicating sequen	2.20	2.73
	302719	W69724	Hs.288959	hypothetical protein FLJ20920	0.54	1.02
	302742	L12069		gb:Homo sapiens (clone WR4.10VH) anti-th	4.28	11.57
40	302755	AW384815	Hs.149208	KIAA1555 protein	1.57	2.38
	302771	H98476	Hs.42522	ESTs	2.94	4.68
	302789	AJ245067		gb:Homo sapiens mRNA for immunoglobulin	3.49	6.31
	302795	AJ245313	Hs.272838	hypothetical protein FLJ10494	0.80	2.74
	302802	Y08250		gb:H.sapiens mRNA for variable region of	1.13	0.77
45	302803	AA442824	Hs.293961	ESTs, Moderately similar to putative DNA	3.14	10.68
	302812	N31301	Hs.152664	hypothetical protein FLJ20051	3.04	8.24
	302847	X98940		gb:H.sapiens rearranged Ig heavy chain (	1.80	1.92
	302885	AL137763	Hs.132127	hypothetical protein LOC57822	1.00	1.00
	302943	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheti	0.53	0.67
50	302977	AW263124	Hs.315111	hypothetical protein FLJ12894	2.45	2.62
	303006	AF078950	Hs.24139	Homo sapiens cDNA: FLJ23137 fis, clone L	4.88	8.61
	303011	AF090405		gb:Homo sapiens clone 2A1 scFV antibody	1.41	1.86
	303013	F07898	Hs.288968	RAB22A, member RAS oncogene family	1.51	1.19
	303061	AF151882	Hs.27693	peptidylprolyl isomerase (cyclophilin)-I	0.72	0.76
55	303077	AF163305		gb:H.sapiens T-cell receptor mRNA	1.17	3.90
	303090	AA443259	Hs.146286	kinesin family member 13A	4.08	6.46
	303091	AF192913	Hs.130683	zinc finger protein 180 (HHZ168)	2.50	4.37
	303094	AF195513	Hs.278953	Pur-gamma	5.38	8.38
	303095	AF202051	Hs.134079	NM23-H8	3.26	4.08
60	303131	AW081061	Hs.103180	DC2 protein	2.02	1.83
	303195	AA082211	Hs.233936	myosin, light polypeptide, regulatory, n	1.32	3.95
	303196	AA082298	Hs.59710	ESTs	0.77	0.53
	303216	AA581439	Hs.152328	ESTs	0.24	0.63
	303222	AA333538	Hs.204501	hypothetical protein FLJ10534	3.56	6.22
65	303234	AA132255	Hs.143951	ESTs	2.28	3.17
	303251	AW340037	Hs.115897	protocadherin 12	0.38	1.02
	303295	AA205625	Hs.208067	ESTs	2.30	1.00
	303297	T80072	Hs.13423	Homo sapiens clone 24468 mRNA sequence	1.86	4.48
	303316	AF033122	Hs.14125	p53 regulated PA26 nuclear protein	0.10	0.80
70	303467	AA398801	Hs.323397	ESTs	4.54	9.65
	303506	AA340805	Hs.105887	ESTs, Weakly similar to Homolog of rat Z	0.09	0.04
	303552	AA359799	Hs.224662	ESTs, Weakly similar to unnamed protein	1.00	1.72
	303598	AA382814		gb:EST96097 Testis I Homo sapiens cDNA 5	4.96	9.14
75	303637	AF056083	Hs.24879	phosphatidic acid phosphatase type 2C	2.06	2.02
	303655	AA504702	Hs.258802	ATPase, (Na+)/K+ transporting, beta 4 po	1.00	1.24
	303756	AI738488	Hs.115838	ESTs	1.08	1.43
	303856	AA968589	Hs.180532	glucose phosphate isomerase	1.76	1.31
	303893	N88597	Hs.113503	karyopherin (importin) beta 3	2.30	2.57
	303907	AW467774	Hs.171880	polymerase (RNA) II (DNA directed) polyp	3.10	5.79
80	303946	AW474196	Hs.306637	Homo sapiens cDNA FLJ12363 fis, clone MA	5.06	11.86
	303978	AW513315		gb:xo43c12.x1 NCI_CGAP_U11 Homo sapiens	5.14	7.31
	303981	AW513804	Hs.278834	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.83	4.06
	303990	AW515465		gb:xu71a11.x1 NCI_CGAP_Kid8 Homo sapiens	1.15	2.35
	303998	AW516449		gb:xt68f05.x1 NCI_CGAP_U12 Homo sapiens	2.20	9.35
85	303999	AW516611		gb:xp70b11.x1 NCI_CGAP_Ov39 Homo sapiens	4.85	6.28
	304006	AW517947		gb:xt66h02.x1 NCI_CGAP_U12 Homo sapiens	3.21	4.07



	304008	AW518198	Hs.3297	ribosomal protein S27a	6.50	11.08
	304009	AW518206	Hs.181165	eukaryotic translation elongation factor	1.88	3.27
	304024	T03036		gb:FB21B7 Fetal brain, Stratagene Homo s	2.15	3.55
5	304026	T03160		gb:FB26F2 Fetal brain, Stratagene Homo s	5.88	11.80
	304028	T03266		gb:FB7C1 Fetal brain, Stratagene Homo sa	5.59	13.46
	304036	T16855	Hs.244621	ribosomal protein S14	6.55	14.43
	304046	T54803		gb:yb42d06.s1 Stratagene fetal spleen (9	6.18	12.19
	304061	T61521		gb:yb73g01.s1 Stratagene ovary (937217)	2.64	8.23
10	304063	T62536		gb:yc04c12.s1 Stratagene lung (937210) H	0.53	1.61
	304097	R25376	Hs.177592	ribosomal protein, large, P1	6.49	11.67
	304114	R78946		gb:yl87g02.s1 Soares placenta Nb2HP Homo	2.90	4.18
	304122	H28966		gb:ym31a06.s1 Soares infant brain 1NIB H	1.00	2.76
	304155	H68696		gb:yr78b06.s1 Soares fetal liver spleen	0.79	1.18
15	304203	N56929		gb:yy82d08.s1 Soares_multiple_sclerosis_	4.28	11.34
	304234	W81608		gb:zd88h06.s1 Soares_fetal_heart_NbHH19W	6.47	11.03
	304267	AA064862	Hs.73742	ribosomal protein, large, P0	1.34	1.16
	304270	AA069711	Hs.297753	vimentin	3.40	5.40
	304287	AA079286	Hs.78466	proteasome (prosome, macropain) 26S sub	2.93	4.42
20	304348	AA179868		gb:zp38g12.s1 Stratagene muscle 937209 H	3.98	10.96
	304415	AA290747	Hs.169476	glyceraldehyde-3-phosphate dehydrogenase	3.32	5.99
	304430	AA347682		gb:EST54044 Fetal heart II Homo sapiens	1.00	1.00
	304456	AA411240		gb:zv26g05.s1 Soares_NhHMPu_S1 Homo sapi	1.42	3.33
	304521	AA464716		gb:zx82c11.s1 Soares ovary tumor NbHOT H	2.18	1.15
25	304526	AA476427		gb:zx02c05.s1 Soares_total_fetus_Nb2HF8_	5.38	14.11
	304542	AA482602	Hs.169476	glyceraldehyde-3-phosphate dehydrogenase	4.16	8.23
	304546	AA486074	Hs.297681	serine (or cysteine) proteinase inhibitor	0.55	1.20
	304607	AA513322		gb:nh85e08.s1 NCI_CGAP_Br1.1 Homo sapien	1.95	2.10
	304640	AA524440	Hs.111334	ferritin, light polypeptide	2.10	2.83
30	304650	AA527489	Hs.3463	ribosomal protein S23	3.33	12.62
	304735	AA576453		gb:nm75h11.s1 NCI_CGAP_Co9 Homo sapiens	1.33	0.88
	304760	AA580401		gb:nn13g09.s1 NCI_CGAP_Co12 Homo sapiens	3.68	8.14
	304849	AA588157	Hs.13801	KIAA1685 protein	2.77	3.70
	304917	AA602685	Hs.284136	PRO2047 protein	7.16	11.01
35	304921	AA603092	Hs.297753	vimentin	2.47	4.24
	304966	AA613893	Hs.282435	ESTs	6.78	11.66
	304987	AA618044	Hs.300697	immunoglobulin heavy constant gamma 3 (G	0.90	1.23
	305016	AA626876		gb:zu89h06.s1 Soares_testis_NHT Homo sap	6.46	10.17
	305034	AA630128		gb:ab99c04.s1 Stratagene lung (937210) H	1.00	1.00
40	305072	AA641012		gb:nr72a12.s1 NCI_CGAP_Pr24 Homo sapiens	5.68	11.59
	305111	AA644187	Hs.303405	ESTs	1.48	1.37
	305148	AA654070		gb:nt01g08.s1 NCI_CGAP_Lym3 Homo sapiens	1.76	4.61
	305159	AA659166	Hs.275668	EST, Weakly similar to EF1D_HUMAN ELONG	1.00	2.15
	305190	AA665955		gb:ag57d12.s1 Gessler Wilms tumor Homo s	5.31	8.14
45	305232	AA670052	Hs.169476	glyceraldehyde-3-phosphate dehydrogenase	0.78	1.18
	305235	AA670480		gb:ag37e01.s1 Jla bone marrow stroma Hom	3.11	8.66
	305245	AA676695	Hs.81328	nuclear factor of kappa light polypeptid	4.38	7.53
	305312	AA700201		gb:zj44f07.s1 Soares_fetal_liver_spleen_	2.13	2.66
	305322	AA701597	Hs.163019	EST	1.20	1.40
50	305394	AA720942	Hs.300697	immunoglobulin heavy constant gamma 3 (G	1.16	0.68
	305413	AA724659		gb:al10f08.s1 Soares_parathyroid_tumor_N	5.86	9.87
	305447	AA737856		gb:nx10c08.s1 NCI_CGAP_GC3 Homo sapiens	2.21	2.86
	305476	AA745664	Hs.287445	hypothetical protein FLJ11726	3.36	6.54
	305483	AA748030	Hs.303512	EST	1.00	2.02
55	305528	AA769156		gb:nz12e05.s1 NCI_CGAP_GC31 Homo sapiens	6.44	9.10
	305612	AA782347	Hs.272572	hemoglobin, alpha 2	0.19	0.79
	305614	AA782866		gb:aj09h02.s1 Soares_parathyroid_tumor_N	1.00	1.00
	305616	AA782884	Hs.275865	ribosomal protein S18	7.57	10.20
	305637	AA806124		gb:oe29a12.s1 NCI_CGAP_Pr25 Homo sapiens	4.78	12.42
60	305639	AA806138		gb:oe29c12.s1 NCI_CGAP_Pr25 Homo sapiens	0.89	0.70
	305650	AA807709		gb:nw31e04.s1 NCI_CGAP_GC80 Homo sapiens	4.49	8.71
	305690	AA813477		gb:al67a05.s1 Soares_testis_NHT Homo sap	4.91	9.40
	305726	AA828156	Hs.73742	ribosomal protein, large, P0	0.19	0.81
	305728	AA828209		gb:of34a02.s1 NCI_CGAP_Kid6 Homo sapiens	5.12	9.29
65	305759	AA835353		gb:ak72b06.s1 Barstead spleen HPLRB2 Hom	1.66	4.11
	305792	AA845256		gb:ak84a08.s1 Barstead spleen HPLRB2 Hom	2.34	4.25
	305864	AA864374	Hs.73742	ribosomal protein, large, P0	0.30	1.40
	305901	AA872968		gb:oh63h08.s1 NCI_CGAP_Kid5 Homo sapiens	2.10	5.21
	305910	AA875981		gb:nx21h02.s1 NCI_CGAP_GC3 Homo sapiens	0.32	1.01
70	306015	AA897116		gb:am08b07.s1 Soares_NFL_T_GBC_S1 Homo s	1.56	1.12
	306017	AA897221	Hs.109058	ribosomal protein S6 kinase, 90kD, polyp	5.21	7.90
	306020	AA897630	Hs.130027	EST	1.96	6.59
	306063	AA906316		gb:ok03g03.s1 Soares_NFL_T_GBC_S1 Homo s	7.38	20.69
	306065	AA906725		gb:ok78g02.s1 NCI_CGAP_GC4 Homo sapiens	7.19	13.48
75	306104	AA910956		gb:ok85h11.s1 NCI_CGAP_Kid3 Homo sapiens	6.50	9.13
	306109	AA911861		gb:og21a07.s1 NCI_CGAP_PNS1 Homo sapiens	4.21	5.25
	306148	AA917409	Hs.288036	tRNA Isopentenylpyrophosphate transferas	2.20	2.70
	306242	AA932805		gb:oo60g04.s1 NCI_CGAP_Lu5 Homo sapiens	2.84	5.35
	306288	AA936900		gb:ois53h05.s1 NCI_CGAP_HN3 Homo sapiens	1.60	1.12
80	306325	AA953072	Hs.210546	interleukin 21 receptor	1.65	2.26
	306353	AA961382	Hs.275865	ribosomal protein S18	3.78	6.32
	306375	AA968650	Hs.276018	EST, Moderately similar to JC4662 ribos	4.30	5.74
	306396	AA970223		gb:op09d05.s1 NCI_CGAP_Kid6 Homo sapiens	0.95	2.45
	306428	AA975110	Hs.191228	hypothetical protein FLJ20284	3.19	4.10
	306442	AA976899		gb:og35e09.s1 NCI_CGAP_GC4 Homo sapiens	4.67	7.44
85	306446	AA977348		gb:og72e12.s1 NCI_CGAP_Kid6 Homo sapiens	3.92	6.27



5	306458	AA978186		gb:op33c06.s1 Soares_NFL_T_GBC_S1 Homo s	3.35	5.77
	306467	AA983508	Hs.163593	ribosomal protein L18a	3.72	5.37
	306510	AA988546		gb:or84d07.s1 NCI_CGAP_Lu5 Homo sapiens	1.00	1.00
	306555	AA994304	Hs.276083	EST, Weakly similar to RL23_HUMAN 60S R	6.61	10.91
	306557	AA994530		gb:ou57e08.s1 NCI_CGAP_Br2 Homo sapiens	16.20	31.83
10	306572	AA995686		gb:os25c12.s1 NCI_CGAP_Kid5 Homo sapiens	2.51	6.52
	306582	AA996248		gb:os18c10.s1 NCI_CGAP_Kid5 Homo sapiens	1.42	3.13
	306598	AI000320	Hs.169476	glyceraldehyde-3-phosphate dehydrogenase	4.91	8.68
	306605	AI000497	Hs.119500	ribosomal protein, large P2	1.96	8.60
	306656	AI004024		gb:ou11b07.x1 Soares_NFL_T_GBC_S1 Homo s	0.11	0.45
15	306676	AI005603	Hs.284136	PRO2047 protein	9.56	17.28
	306686	AI015615		gb:ov29f10.x1 Soares_testis_NHT Homo sap	1.86	3.60
	306702	AI022565	Hs.307670	EST	1.47	1.19
	306728	AI027359	Hs.272572	hemoglobin, alpha 2	1.28	2.83
	306751	AI032589		gb:ow70h12.s1 Soares_fetal_liver_spleen_	3.91	5.21
20	306767	AI038963	Hs.249118	ESTs	3.33	6.06
	306892	AI092465		gb:qa75h12.x1 Soares_fetal_heart_NbHH19W	3.77	7.46
	306897	AI093967		gb:qa33c06.s1 Soares_NhHMPu_S1 Homo sapi	2.12	2.85
	306956	AI125111		gb:am66f03.s1 Barstead spleen HPLRB2 Hom	6.10	10.52
	306958	AI125152		gb:am55e09.x1 Johnston frontal cortex Ho	1.72	1.56
25	307035	AI142774	Hs.119122	ribosomal protein L13a	2.00	4.70
	307041	AI144243		gb:qb85b12.x1 Soares_fetal_heart_NbHH19W	9.12	12.56
	307091	AI167439		gb:ox70h06.s1 Soares_NhHMPu_S1 Homo sapi	4.88	8.52
	307181	AI189251		gb:qc99g06.x1 Soares_pregnant_uterus_NbH	3.55	6.44
	307297	AI205798	Hs.111334	ferritin, light polypeptide	2.46	4.65
30	307317	AI208303	Hs.147333	EST	5.64	10.13
	307327	AI214142	Hs.246381	CD68 antigen	3.18	5.15
	307382	AI223158	Hs.147885	ESTs	2.02	3.73
	307410	AI241715	Hs.77039	ribosomal protein S3A	0.72	0.48
	307415	AI242118		gb:qh92b02.x1 Soares_NFL_T_GBC_S1 Homo s	2.38	3.51
35	307423	AI243206	Hs.179573	collagen, type I, alpha 2	2.60	5.44
	307426	AI243364		gb:qh30g11.x1 Soares_NFL_T_GBC_S1 Homo s	3.18	7.67
	307517	AI275055		gb:ql72d03.x1 Soares_NhHMPu_S1 Homo sapi	1.00	1.00
	307551	AI281556		gb:qu52f11.x1 NCI_CGAP_Lym6 Homo sapiens	3.40	11.20
	307561	AI282207		gb:qp65a12.x1 Soares_fetal_lung_NbHL19W	4.74	15.51
40	307608	AI290295		gb:qm01f02.x1 Soares_NhHMPu_S1 Homo sapi	3.50	7.19
	307657	AI306428	Hs.298262	ribosomal protein S19	1.76	2.44
	307691	AI318285		gb:tb17b01.x1 NCI_CGAP_Ov37 Homo sapiens	1.59	1.31
	307701	AI318583	Hs.276672	EST, Weakly similar to RL6_HUMAN 60S RI	1.90	2.13
	307718	AI333406	Hs.83753	small nuclear ribonucleoprotein polypept	0.45	0.99
45	307730	AI336092		gb:qt43b07.x1 Soares_fetal_lung_NbHL19W	1.51	0.99
	307760	AI342387		gb:ql27f07.x1 Soares_pregnant_uterus_NbH	1.00	1.00
	307764	AI342731		gb:qp026a07.x1 NCI_CGAP_Lu5 Homo sapiens	4.52	12.58
	307783	AI347274		gb:tc05d02.x1 NCI_CGAP_Co16 Homo sapiens	1.42	1.00
	307796	AI350556		gb:qt18f09.x1 NCI_CGAP_GC4 Homo sapiens	6.57	9.61
50	307807	AI351799		gb:qt09d02.x1 NCI_CGAP_GC4 Homo sapiens	3.38	7.68
	307808	AI351826		gb:qt09g03.x1 NCI_CGAP_GC4 Homo sapiens	0.33	0.86
	307820	AI355761		gb:qt94a11.x1 NCI_CGAP_Co14 Homo sapiens	7.94	21.57
	307830	AI358722	Hs.276737	EST, Weakly similar to R5HU22 ribosomal	2.05	3.32
	307852	AI365541		gb:qz08g05.x1 NCI_CGAP_CLL1 Homo sapiens	3.18	5.21
55	307902	AI380462		gb:tg02h05.x1 NCI_CGAP_CLL1 Homo sapiens	3.13	4.99
	307997	AI434512	Hs.181165	eukaryotic translation elongation factor	1.00	3.01
	308002	AI435240	Hs.283442	ESTs	5.86	12.64
	308011	AI439473		gb:ti60a08.x1 NCI_CGAP_Lym12 Homo sapien	3.79	5.83
	308023	AI452732	Hs.251577	hemoglobin, alpha 1	0.38	0.88
60	308041	AI458824	Hs.169476	glyceraldehyde-3-phosphate dehydrogenase	4.36	6.06
	308059	AI468938	Hs.276877	EST, Weakly similar to RL10_HUMAN 60S R	1.80	1.98
	308085	AI474135	Hs.181165	eukaryotic translation elongation factor	3.38	4.14
	308101	AI475950	Hs.181165	eukaryotic translation elongation factor	1.30	3.87
	308106	AI476803		gb:lj77e12.x1 Soares_NSF_F8_9W_OT_PA_P_S2.38		8.72
65	308122	AI480123	Hs.309411	EST	2.70	3.86
	308154	AI500600		gb:tn93d08.x1 NCI_CGAP_Ui2 Homo sapiens	0.66	1.33
	308171	AI523632	Hs.298766	ESTs, Weakly similar to schlafen4 [M.mu	2.48	4.86
	308211	AI557029	Hs.278572	anaplastic lymphoma kinase (Ki-1)	2.43	2.14
	308213	AI557041		gb:PT2.1_12_E04.r tumor2 Homo sapiens cD	3.34	3.79
70	308216	AI557135		gb:PT2.1_13_H06.r tumor2 Homo sapiens cD	4.61	4.78
	308219	AI557246		gb:PT2.1_15_D07.r tumor2 Homo sapiens cD	4.87	7.94
	308271	AI567844	Hs.252259	ribosomal protein S3	2.40	6.35
	308319	AI583983	Hs.181165	eukaryotic translation elongation factor	2.45	3.33
	308362	AI613519	Hs.105749	KIAA0553 protein	1.24	1.41
75	308413	AI636253	Hs.196511	ESTs	3.16	4.82
	308450	AI660860	Hs.96840	KIAA1527 protein	1.79	2.68
	308464	AI672425	Hs.277117	EST, Moderately similar to I38055 myosi	4.87	8.27
	308588	AI718299		gb:as51g12.x1 Barstead aorta HPLRB6 Homo	3.90	5.64
	308599	AI719893		gb:as47d07.x1 Barstead aorta HPLRB6 Homo	3.32	5.12
80	308615	AI738593	Hs.101774	hypothetical protein FLJ23045	3.11	2.36
	308643	AI745040		gb:tr19a12.x1 NCI_CGAP_Ov23 Homo sapiens	3.98	3.69
	308673	AI760864		gb:wi09c10.x1 NCI_CGAP_CLL1 Homo sapiens	0.82	0.99
	308697	AI767143		gb:wi97a07.x1 NCI_CGAP_Kid12 Homo sapien	2.76	5.59
	308762	AI807405	Hs.259408	ESTs	3.17	6.30
85	308778	AI811109		gb:tr04c11.x1 NCI_CGAP_Ov23 Homo sapiens	1.00	1.00
	308782	AI811767	Hs.2186	eukaryotic translation elongation factor	2.94	5.15
	308808	AI818289		gb:wk52c01.x1 NCI_CGAP_Pr22 Homo sapiens	4.41	8.34
	308823	AI824118	Hs.217493	annexin A2	1.85	1.92
	308875	AI832332		gb:at48g03.x1 Barstead colon HPLRB7 Homo	2.52	3.80



5	308879	AI832763	Hs.75968	thymosin, beta 4, X chromosome	3.38	7.96
	308886	AI833240		gb:al76d10.x1 Barstead colon HPLRB7 Homo	3.06	2.65
	308898	AI858845		gb:wl32d10.x1 NCI_CGAP_Ut1 Homo sapiens	2.45	3.44
	308934	AI865023	Hs.177	phosphatidylinositol glycan, class H	4.14	6.76
	308966	AI870704		gb:wl47h01.x1 NCI_CGAP_Ut1 Homo sapiens	1.00	1.00
10	308979	AI873111		gb:wl52h05.x1 NCI_CGAP_Brn25 Homo sapien	7.15	11.10
	309045	AI910902		gb:lq39f01.x1 NCI_CGAP_Ut1 Homo sapiens	0.61	0.59
	309051	AI911975		gb:wd78d01.x1 NCI_CGAP_Lu24 Homo sapiens	1.78	4.42
	309069	AI917366	Hs.78202	SWI/SNF related, matrix associated, act	3.27	5.88
	309083	AI922426	Hs.119598	ribosomal protein L3	2.39	3.34
15	309105	AI925503	Hs.265884	ESTs	5.54	17.78
	309122	AI928178		gb:wo95a11.x1 NCI_CGAP_Kid11 Homo sapien	1.00	2.92
	309128	AI928816	Hs.180842	ribosomal protein L13	1.38	5.55
	309164	AI937761		gb:wp84b09.x1 NCI_CGAP_Brn25 Homo sapien	2.43	3.11
	309177	AI951118		gb:wx63g05.x1 NCI_CGAP_Br18 Homo sapiens	0.81	0.97
20	309288	AI991525	Hs.299426	ESTs	4.86	7.46
	309299	AW003478		gb:wq66c06.x1 NCI_CGAP_GC6 Homo sapiens	4.36	9.43
	309303	AW004823		gb:ws93a08.x1 NCI_CGAP_Co3 Homo sapiens	2.88	7.54
	309411	AW085201	Hs.244144	EST	4.30	7.14
	309437	AW090702	Hs.278242	tubulin, alpha, ubiquitous	2.49	3.11
25	309459	AW117645	Hs.65114	keratin 18	2.88	4.55
	309476	AW129368		gb:xe14b05.x1 NCI_CGAP_Ut4 Homo sapiens	2.08	6.60
	309499	AW136325	Hs.279771	Homo sapiens clone PP1596 unknown mRNA	2.82	3.55
	309529	AW150807	Hs.181357	laminin receptor 1 (67kD, ribosomal pro	4.78	3.95
	309532	AW151119		gb:xg33e10.x1 NCI_CGAP_Ut1 Homo sapiens	1.18	4.40
30	309626	AW192004	Hs.297681	serine (or cysteine) proteinase inhibit	4.46	12.06
	309641	AW194230	Hs.253100	EST, Moderately similar to GHU Ig gamm	1.47	1.39
	309675	AW205681	Hs.253506	EST, Moderately similar to ATPN_HUMAN A	5.68	15.20
	309693	AW237221	Hs.181357	laminin receptor 1 (67kD, ribosomal prot	1.00	1.00
	309695	AW238011	Hs.295605	mannosidase, alpha, class 2A, member 2	5.45	9.61
35	309700	AW241170	Hs.179661	tubulin, beta polypeptide	1.41	1.25
	309747	AW264889		gb:xq36h02.x1 NCI_CGAP_Lu28 Homo sapiens	5.00	8.35
	309769	AW272346		gb:xs13c10.x1 NCI_CGAP_Kid11 Homo sapien	5.76	11.90
	309782	AW275156	Hs.156110	immunoglobulin kappa constant	0.42	0.69
	309783	AW275401	Hs.254798	EST	1.00	4.11
40	309799	AW276964		gb:xp58h01.x1 NCI_CGAP_Ov39 Homo sapiens	1.68	1.44
	309866	AW299916		gb:xs44c01.x1 NCI_CGAP_Kid11 Homo sapien	3.02	5.04
	309903	AW339071	Hs.300697	immunoglobulin heavy constant gamma 3 (G	1.05	1.18
	309923	AW340684		gb:hd05g08.x1 Soares_NFL_T_GBC_S1 Homo s	2.30	3.67
	309928	AW341418		gb:hd08c03.x1 Soares_NFL_T_GBC_S1 Homo s	7.41	13.71
45	309931	AW341683		gb:hd13d01.x1 Soares_NFL_T_GBC_S1 Homo s	1.20	12.70
	309933	AW341936		gb:hb73f10.x1 NCI_CGAP_Ut2 Homo sapiens	4.90	18.29
	309964	AW449111	Hs.257111	hypothetical protein MGC3265	1.99	3.07
	310002	AI439096	Hs.323079	Homo sapiens mRNA; cDNA DKFZp564P116 (fr	0.20	0.47
	310096	AW136822	Hs.172824	ESTs, Weakly similar to B48013 proline-r	1.51	1.22
50	310098	AI685841	Hs.161354	ESTs	0.31	0.76
	310109	AI203094	Hs.148633	ESTs	2.06	5.83
	310112	AW197233	Hs.147253	ESTs	2.92	3.55
	310115	AI611317	Hs.223796	ESTs	1.25	0.84
	310121	AW195642	Hs.148901	ESTs	1.00	2.71
55	310146	AI206614	Hs.197422	ESTs	9.50	15.31
	310193	AI627653	Hs.147562	ESTs	2.85	4.18
	310255	AW450439	Hs.153378	ESTs	4.26	10.63
	310261	AI240483	Hs.201217	ESTs	3.28	4.40
	310264	AI915771	Hs.74170	metallothionein 1E (functional)	0.26	0.86
60	310275	AI242102	Hs.213636	ESTs	5.43	8.19
	310282	AI243332	Hs.156055	ESTs	3.15	8.06
	310290	AW013815	Hs.149103	ESTs	2.19	3.12
	310333	AI253200	Hs.145402	ESTs	1.17	1.91
	310346	AI261340	Hs.145517	ESTs	4.81	9.95
65	310385	AI263392	Hs.156151	ESTs	5.96	7.79
	310443	AW119018	Hs.164231	ESTs	2.90	4.63
	310444	AW196632	Hs.252956	ESTs	0.85	1.01
	310446	AI275715	Hs.145926	ESTs	2.18	3.85
	310468	AI984074	Hs.196398	ESTs	3.39	5.19
70	310477	AI948801	Hs.171073	ESTs	1.00	1.00
	310512	AW275603	Hs.200712	ESTs	3.87	8.12
	310514	AI681145	Hs.160724	ESTs	3.30	7.33
	310524	AW082270	Hs.12496	ESTs, Highly similar to AC004836 1 simil	0.72	1.44
	310547	AI302654	Hs.208024	ESTs	3.26	3.46
75	310584	AI653007	Hs.156304	ESTs	2.39	4.08
	310608	AI962234	Hs.196102	ESTs	5.60	6.49
	310624	AI341594		gb:Human endogenous retrovirus H proteas	4.91	9.09
	310636	AI814373	Hs.164175	ESTs	1.85	1.71
	310648	AI347863	Hs.156672	ESTs	0.17	0.69
80	310694	AI654370	Hs.157752	Homo sapiens mRNA full length insert cDN	5.40	13.22
	310695	AI472124	Hs.157757	ESTs	4.82	6.27
	310714	AI418446	Hs.157882	ESTs	1.76	3.51
	310722	AI989803	Hs.157289	ESTs	1.14	6.85
	310756	AI916560	Hs.158707	ESTs	8.46	13.01
85	310764	AI376769	Hs.167172	ESTs	4.76	7.37
	310848	AI459554	Hs.161286	ESTs	2.84	1.96
	310851	AW291714	Hs.221703	ESTs	1.00	2.32
	310854	AI421677	Hs.161332	ESTs	6.37	7.94
	310858	AI871000	Hs.161330	ESTs	6.07	9.84



	310864	AI924558	Hs.161399	ESTs	0.87	0.78
	310875	T47764	Hs.132917	ESTs	1.00	3.63
	310896	AW157731	Hs.270982	ESTs, Moderately similar to ALU7_HUMAN A	7.07	16.68
5	310922	AW195634	Hs.170401	ESTs	1.00	1.00
	310955	AI560210	Hs.263912	ESTs	10.08	17.66
	310957	AW190974	Hs.196918	ESTs	2.18	3.18
	311000	AI521830	Hs.171050	ESTs	3.06	6.64
	311012	AW298070	Hs.241097	ESTs	1.23	3.77
10	311034	AI564023	Hs.311389	ESTs, Moderately similar to PT0375 natur	2.44	2.09
	311074	AW290922	Hs.199848	ESTs	6.04	14.19
	311134	AI990849	Hs.196971	ESTs	3.54	6.96
	311174	AW450552	Hs.205457	perixin	0.65	0.95
	311187	AI638374	Hs.224189	ESTs	2.46	2.78
15	311220	AI656040	Hs.196532	ESTs	1.10	2.52
	311230	AI989808	Hs.197663	ESTs	1.41	1.75
	311236	AI653378	Hs.197674	ESTs	2.18	2.11
	311242	AW016812	Hs.200266	ESTs	0.63	5.11
	311258	AI671221	Hs.199887	ESTs	1.00	1.41
20	311277	AW072813	Hs.270868	ESTs, Moderately similar to ALU4_HUMAN A	2.56	1.94
	311294	AA826425	Hs.291829	ESTs	1.04	2.69
	311308	F12664	Hs.49000	ESTs	1.96	6.70
	311351	AI682303	Hs.201274	ESTs	4.77	9.38
	311390	AW392997	Hs.202280	ESTs	2.80	6.06
25	311405	AW290961	Hs.201815	ESTs	3.80	11.66
	311409	AI698839		gb:wd31f02.x1 Soares_NFL_T_GBC_S1 Homo s	3.84	6.94
	311420	AI936291	Hs.209867	ESTs	5.30	12.56
	311443	AI791521	Hs.192206	ESTs	4.39	6.09
	311467	AI934909	Hs.175377	ESTs	1.00	1.04
30	311479	AI933672	Hs.211399	ESTs	2.76	5.61
	311488	R57390	Hs.301064	arfaptin 1	2.50	5.73
	311495	AW300077	Hs.221358	ESTs	3.63	6.09
	311511	AW444568	Hs.210303	ESTs	2.00	2.87
	311534	AW130351	Hs.243549	ESTs	0.31	1.33
35	311537	AI805121	Hs.211828	ESTs	3.69	5.85
	311543	AI681360	Hs.201259	ESTs	1.73	1.34
	311551	AW449774	Hs.296380	POM (POM121 rat homolog) and ZP3 fusion	3.31	6.12
	311557	AI819230	Hs.211238	interleukin-1 homolog 1	1.00	1.00
	311558	Z44432	Hs.63128	KIAA1292 protein	2.25	3.41
40	311559	AW008271	Hs.265848	similar to rat myomegalin	2.68	5.90
	311563	AI922143	Hs.211334	ESTs	2.39	3.32
	311586	AI827834	Hs.211227	ESTs	2.47	3.85
	311616	AW450675	Hs.212709	ESTs	1.00	1.00
	311621	AI924307	Hs.213464	ESTs	4.16	6.74
45	311635	AI928456	Hs.213081	ESTs	2.17	3.76
	311668	AW193674	Hs.240044	ESTs	2.60	3.12
	311672	R11807	Hs.20914	hypothetical protein FLJ23056	2.79	5.18
	311683	AW183738	Hs.232644	ESTs	0.19	0.96
	311700	R49601	Hs.171495	retinoic acid receptor, beta	6.28	8.83
50	311714	AW131785	Hs.246831	ESTs, Weakly similar to CLKG_HUMAN VOLTA	5.00	8.17
	311735	AW294416	Hs.144687	Homo sapiens cDNA FLJ12981 fis, clone NT	0.96	0.72
	311743	T99079	Hs.191194	ESTs	1.00	1.95
	311783	AI682478	Hs.13528	hypothetical protein FLJ14054	0.16	0.77
	311785	AI056769	Hs.133512	ESTs	1.34	3.97
55	311799	AA780791	Hs.14014	ESTs, Weakly similar to KIAA0973 protein	8.52	13.32
	311819	AW265275	Hs.254325	ESTs	3.58	3.91
	311823	AI089422	Hs.131297	ESTs	1.40	1.72
	311877	AA349893	Hs.85339	G protein-coupled receptor 39	0.95	0.91
	311886	AA522738	Hs.132554	ESTs	0.88	0.87
60	311896	AW206447		gb:U1-H-BI1-afg-g-02-0-U1.s1 NCI_CGAP_Su	1.66	1.13
	311910	N28365	Hs.22579	Homo sapiens clone CDABP0036 mRNA sequen	1.66	2.30
	311923	T60843	Hs.189679	ESTs	0.42	2.63
	311933	AI597963	Hs.118726	ESTs	1.88	3.02
	311959	T67262	Hs.124733	ESTs	2.02	2.33
65	311960	AW440133	Hs.189690	ESTs	3.87	6.62
	311967	AI382726	Hs.182434	ESTs	5.80	8.14
	311975	AA804374	Hs.272203	Homo sapiens cDNA FLJ20843 fis, clone AD	0.98	3.26
	312005	T78450	Hs.13941	ESTs	0.12	1.39
70	312028	T78886	Hs.284450	ESTs	3.78	4.92
	312046	AI580018	Hs.268591	ESTs	4.11	7.32
	312056	T83748	Hs.268594	ESTs	2.36	3.08
	312064	AA676713	Hs.191155	ESTs	3.34	5.28
	312088	AW303760	Hs.13685	ESTs	1.60	1.15
	312093	T91809	Hs.121296	ESTs	0.68	0.85
75	312094	Z78390		gb:HSZ78390 Human fetal brain S. Meier-E	3.05	4.48
	312097	AI352096	Hs.112180	zinc finger protein 148 (pHZ-52)	4.52	9.70
	312118	T85332	Hs.178294	ESTs	2.40	2.60
	312128	AI052609	Hs.17631	Homo sapiens cDNA FLJ20118 fis, clone CO	2.39	3.53
	312147	T89855	Hs.195648	ESTs	0.67	1.03
80	312175	AA953383	Hs.127554	ESTs	5.85	10.60
	312179	AI052572	Hs.269864	ESTs	2.41	3.32
	312201	AI928365	Hs.91139	solute carrier family 1 (neuronal/epithe	0.24	0.89
	312207	H90213	Hs.191330	ESTs	2.20	4.55
	312220	N74613		gb:za55a07.s1 Soares fetal liver spleen	4.28	11.13
85	312252	AI128388	Hs.143655	ESTs	1.64	1.57
	312304	AA491949	Hs.269392	ESTs	0.12	2.47



	312318	AW235092	Hs.143981	ESTs	3.46	5.69
	312319	AA216698	Hs.180780	TEFA protein	5.78	4.46
	312321	R66210	Hs.186937	ESTs	0.44	1.74
5	312331	AA825512	Hs.289101	glucose regulated protein, 58kD	3.73	5.96
	312339	AA524394	Hs.165544	ESTs	3.07	0.95
	312363	AI675558	Hs.181867	ESTs	10.08	16.73
	312375	AI375096	Hs.172405	cell division cycle 27	2.78	3.71
	312376	R52089	Hs.172717	ESTs	1.00	1.00
10	312389	AI863140		gb:tz43h12.x1 NCI_CGAP_Brn52 Homo sapien	2.37	3.98
	312437	AA995028		gb:RC4-BT0629-120200-011-b10 BT0629 Homo	4.06	5.41
	312440	AI051133	Hs.133315	Homo sapiens mRNA; cDNA DKFZp761J1324 (f	1.00	1.00
	312451	R59989	Hs.176539	ESTs	4.96	10.04
	312458	AI167637	Hs.146924	ESTs	1.11	1.00
15	312507	AI168177	Hs.143653	ESTs	5.89	8.24
	312520	AI742591	Hs.205392	ESTs	3.30	8.92
	312548	AI566228	Hs.159426	hypothetical protein PRO2121	1.38	1.65
	312564	H21520	Hs.35088	ESTs	0.40	0.77
	312583	AI193122	Hs.124141	ESTs	0.13	0.94
20	312599	AI865073	Hs.125720	ESTs	3.75	5.29
	312602	AA046451	Hs.165200	ESTs	6.78	12.93
	312645	H52121	Hs.193007	ESTs	0.38	1.13
	312666	AI240582	Hs.214678	ESTs	0.98	2.03
	312689	AW450461	Hs.203965	ESTs	0.21	0.61
25	312817	H75459	Hs.233425	ESTs	1.51	0.85
	312846	AW152104	Hs.200879	ESTs	8.93	13.78
	312873	AI690071	Hs.283552	ESTs, Weakly similar to unnamed protein	4.20	6.23
	312893	AI016204	Hs.172922	ESTs	2.67	3.15
	312902	AW292797	Hs.130316	ESTs, Weakly similar to T2D3_HUMAN TRANS	1.19	0.71
30	312925	N90868	Hs.271695	ESTs	2.50	4.25
	312936	AI681581	Hs.121525	ESTs	1.00	1.17
	312975	AI640506	Hs.293119	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.30	4.80
	312978	N24887	Hs.292500	ESTs	0.80	1.05
	312980	AA497043	Hs.115685	ESTs	3.12	3.60
35	312984	N25871	Hs.177337	ESTs	2.03	2.13
	313000	AI147412	Hs.146657	ESTs	5.52	8.42
	313029	AA731520	Hs.170504	ESTs	0.96	1.39
	313039	AI419290	Hs.149990	ESTs, Weakly similar to unnamed protein	6.48	13.20
40	313049	AW293055	Hs.119357	ESTs	6.44	10.73
	313056	AI651930	Hs.135684	ESTs	1.51	2.04
	313058	D81015	Hs.125382	ESTs	0.25	1.50
	313070	AI422023	Hs.161338	ESTs	8.56	11.60
	313097	AI676164	Hs.204339	ESTs	3.72	4.56
	313130	AW449171	Hs.168677	ESTs	3.28	5.06
45	313136	N59284	Hs.288010	ESTs	0.49	1.36
	313153	AI240838	Hs.132750	ESTs	5.36	5.52
	313210	N74077	Hs.197043	ESTs	0.30	0.66
	313236	AW238169	Hs.83513	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.16	8.76
	313239	W19632	Hs.124170	ESTs	1.00	3.87
50	313265	N93466	Hs.121764	ESTs, Weakly similar to testicular tekti	0.74	2.06
	313267	AI770008	Hs.129583	ESTs	0.23	1.30
	313275	AI027604	Hs.159650	ESTs	6.68	9.57
	313290	AI753247	Hs.29643	Homo sapiens cDNA FLJ13103 fis, clone NT	1.34	1.07
	313292	AI362991	Hs.202121	ESTs, Weakly similar to env protein [H.s	2.00	4.32
55	313325	AI420611	Hs.127832	ESTs	1.20	2.27
	313357	AW074848	Hs.201501	ESTs	4.02	5.33
	313393	AI674685	Hs.200141	ESTs	1.36	2.84
	313399	AW376889	Hs.194097	ESTs	2.58	5.26
	313414	AI241540	Hs.132933	ESTs	6.57	15.07
60	313417	AA741151	Hs.137323	ESTs	0.63	3.01
	313457	AA576052	Hs.193223	Homo sapiens cDNA FLJ11646 fis, clone HE	2.78	4.70
	313499	AI261390	Hs.146085	KIAA1345 protein	0.91	2.37
	313516	AA029058	Hs.135145	ESTs	3.41	7.08
	313556	AA628517	Hs.118502	ESTs	0.23	0.70
65	313569	AI273419	Hs.135146	hypothetical protein FLJ13984	1.88	1.00
	313570	AA041455	Hs.209312	ESTs	0.73	2.27
	313638	AI753075	Hs.104627	Homo sapiens cDNA FLJ10158 fis, clone HE	1.00	1.72
	313662	AA740151	Hs.130425	ESTs	0.20	1.42
	313671	W49823	Hs.104613	RP42 homolog	1.00	1.00
70	313672	AW468891	Hs.122948	ESTs	3.46	5.80
	313690	AI493591	Hs.78146	platelet/endothelial cell adhesion molec	0.51	0.97
	313711	AA398070	Hs.133471	ESTs	0.18	1.01
	313723	AA070412		gb:zm68c10.s1 Stratagene neuroepithelium	1.08	1.03
	313726	AI744687	Hs.257806	ESTs	2.13	2.99
75	313774	AW136836	Hs.144583	ESTs	1.38	1.19
	313784	AA910514	Hs.134905	ESTs	3.88	5.78
	313790	AW078569	Hs.177043	ESTs	0.22	2.06
	313832	AW271022	Hs.133294	ESTs	1.15	0.91
	313834	AW418779	Hs.114889	ESTs	0.68	3.14
80	313835	AI538438	Hs.159087	ESTs	5.74	8.88
	313852	H18633	Hs.123641	protein tyrosine phosphatase, receptor t	0.16	1.14
	313854	AW470806	Hs.275002	ESTs	2.09	4.06
	313865	AA731470	Hs.163839	ESTs	3.41	4.09
	313871	AW471088	Hs.145950	ESTs	5.28	6.83
85	313883	AI949384		gb:nu76d01.s1 NCI_CGAP_Alv1 Homo sapiens	2.90	10.91
	313915	AI969390	Hs.163443	Homo sapiens cDNA FLJ11576 fis, clone HE	1.00	1.00



	313926	AW473830	Hs.171442	ESTs	3.40	4.11
	313948	AW452823	Hs.135268	ESTs	5.77	9.15
	313978	AI870175	Hs.13957	ESTs	0.46	0.75
5	313983	AI829133	Hs.226780	ESTs	4.10	6.40
	314035	AA164199	Hs.270152	ESTs	5.88	7.90
	314037	AW300048	Hs.275272	ESTs	1.00	3.79
	314040	AA166970	Hs.118748	ESTs	7.60	11.33
	314067	AW293538	Hs.51743	KIAA1340 protein	1.86	1.21
10	314103	AI028477	Hs.132775	ESTs	2.90	5.29
	314107	AA806113	Hs.189025	ESTs	2.00	1.66
	314113	AA218986	Hs.118854	ESTs	0.91	4.17
	314124	AW118745	Hs.9460	Homo sapiens mRNA; cDNA DKFZp547C244 (fr	2.53	3.32
	314126	AA226431		gb:nc18b12.s1 NCL_CGAP_Pr1 Homo sapiens	3.13	5.08
15	314128	AA935633	Hs.194628	ESTs	2.90	6.35
	314151	AA236183	Hs.202430	ESTs	4.15	6.45
	314184	AW081795	Hs.233465	ESTs	3.44	4.65
	314192	AW290975	Hs.118923	ESTs	1.00	1.23
	314244	AL036450	Hs.103238	ESTs	2.88	3.67
20	314253	AA278679	Hs.189510	ESTs	4.98	7.16
	314262	AW086215	Hs.246096	ESTs	0.38	1.94
	314320	AA811598	Hs.275809	ESTs	3.34	5.66
	314332	AL037551	Hs.95612	ESTs	2.85	2.09
	314335	AA287443	Hs.142570	Homo sapiens clone 24629 mRNA sequence	4.35	4.78
25	314340	AW304350	Hs.130879	ESTs, Moderately similar to putative p15	0.77	0.86
	314351	AA292275	Hs.193746	ESTs	3.07	3.77
	314376	AI628633	Hs.324679	ESTs	4.10	6.11
	314443	AA827125	Hs.192043	ESTs	6.20	13.67
	314458	AI217440	Hs.143873	ESTs	0.58	2.49
30	314466	AA767818	Hs.122707	ESTs	2.53	2.62
	314478	AI521173	Hs.125507	DEAD-box protein	3.94	5.65
	314482	AL043807	Hs.134182	ESTs	1.30	1.44
	314506	AA833655	Hs.208668	Homo sapiens cDNA FLJ14056 fis, clone HE	3.28	3.47
	314519	R42554	Hs.210862	T-box, brain, 1	3.12	6.16
35	314529	AL046412	Hs.202151	ESTs	3.43	6.87
	314546	AW007211	Hs.16131	hypothetical protein FLJ12876	1.38	1.00
	314562	AI564127	Hs.143493	ESTs	2.29	5.27
	314579	AW197442	Hs.116998	ESTs	3.87	5.75
	314580	AW451832	Hs.255938	ESTs, Moderately similar to KIAA1200 pro	0.10	0.71
40	314585	AA918474	Hs.216363	ESTs	1.08	1.40
	314589	AW384790	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT	1.00	1.00
	314592	AA435761	Hs.192148	ESTs	0.90	2.60
	314603	AA418024	Hs.270670	ESTs	4.56	6.29
	314604	AA946582	Hs.8700	deleted in liver cancer 1	3.42	3.92
45	314606	AA418241	Hs.188767	ESTs	2.97	4.55
	314648	AA878419		gb:EST391378 MAGE resequences, MAGP Homo1.42	1.36	1.36
	314699	AI038719	Hs.132801	ESTs	3.66	4.97
	314701	AI754634	Hs.131987	ESTs	0.03	0.90
	314710	AI669131	Hs.290989	EST	3.40	7.52
50	314750	AI095005	Hs.135174	ESTs	2.80	6.54
	314767	AW135412	Hs.164002	ESTs	3.20	4.26
	314801	AA481027	Hs.109045	hypothetical protein FLJ10498	1.00	1.00
	314817	AI694139	Hs.192855	ESTs	0.91	0.99
	314835	AI281370	Hs.76064	ribosomal protein L27a	5.75	7.44
55	314852	AI903735		gb:MR-BT035-200199-031 BT035 Homo sapien	1.68	4.34
	314853	AA729232	Hs.153279	ESTs	0.60	1.85
	314940	AW452768	Hs.162045	ESTs	10.10	16.20
	314941	AA515902	Hs.130650	ESTs	0.31	1.02
	314943	AI476797	Hs.184572	cell division cycle 2, G1 to S and G2 to	2.18	0.37
60	314955	AA521382	Hs.192534	ESTs	2.59	3.90
	314973	AW273128	Hs.300268	ESTs	1.05	1.25
	315004	AA527941	Hs.325351	EST	5.64	13.63
	315006	AI538613	Hs.298241	Transmembrane protease, serine 3	0.52	1.78
	315033	AI493046	Hs.146133	ESTs	2.46	1.00
65	315035	AI569476	Hs.177135	ESTs	0.34	1.33
	315056	AI202703	Hs.152414	ESTs	2.10	2.64
	315069	AI821517	Hs.105866	ESTs	1.00	1.30
	315071	AA552690	Hs.152423	Homo sapiens cDNA: FLJ21274 fis, clone C	1.78	1.00
	315073	AW452948	Hs.257631	ESTs	1.17	1.52
70	315078	AA568548	Hs.190616	ESTs	3.00	3.79
	315080	AA744550	Hs.136345	ESTs	1.00	1.00
	315120	AA564991	Hs.269477	ESTs	0.64	1.44
	315175	AI025842	Hs.152530	ESTs	0.61	1.91
	315193	AI241331	Hs.131765	ESTs	1.06	0.97
75	315196	AA972756	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	0.48	1.96
	315200	AI808235	Hs.307686	EST	3.76	9.40
	315254	AI474433	Hs.179566	ESTs	5.37	9.36
	315353	AW452608	Hs.279610	hypothetical protein FLJ10493	1.00	1.30
	315397	AA218940	Hs.137516	filagelin-like 1	3.38	2.24
80	315403	AW362980	Hs.163924	ESTs	2.04	5.23
	315431	AA622104	Hs.184838	ESTs	2.36	8.04
	315454	AI239473		gb:qh36f02.x1 Soares_NFL_T_GBC_S1 Homo s	3.46	7.64
	315455	AW393391	Hs.156919	ESTs	3.78	5.76
	315473	AI681671	Hs.312671	ESTs, Moderately similar to OVCA1	0.89	2.15
85	315483	AW512763	Hs.222024	transcription factor BMAL2	2.32	1.96
	315526	AI193048	Hs.128685	ESTs	1.67	1.78



	315530	AI200852	Hs.127780	ESTs	1.05	1.01
	315541	AI168233	Hs.123159	sperm associated antigen 4	0.85	0.56
	315552	AW445034	Hs.256578	ESTs	1.00	2.22
5	315562	AA737415	Hs.152826	ESTs	2.66	2.48
	315577	AW513545	Hs.17283	hypothetical protein FLJ10890	2.20	2.25
	315587	AI268399	Hs.140489	ESTs	1.00	1.04
	315589	AW072387	Hs.158258	Homo sapiens mRNA; cDNA DKFZp434B1272 (f	0.14	1.05
	315623	AA364078	Hs.258189	ESTs	7.44	12.56
10	315634	AA837085	Hs.220585	ESTs	0.50	1.40
	315668	AA912347	Hs.136585	ESTs	0.43	1.22
	315677	AI932662	Hs.164073	ESTs	0.60	1.39
	315706	AW440742	Hs.155556	hypothetical protein FLJ20202	2.18	3.77
	315707	AI418055	Hs.161160	ESTs	2.88	2.63
15	315730	H25899	Hs.201591	ESTs	0.11	0.60
	315745	AI821759	Hs.191856	ESTs	3.50	7.25
	315791	AA678177		gb:z115a05.s1 Soares_fetal_liver_spleen_	1.78	2.63
	315801	AA827752	Hs.266134	ESTs	4.31	6.23
	315820	AI652022	Hs.258785	ESTs	2.35	3.01
20	315878	AA683336	Hs.189046	ESTs	2.12	2.64
	315905	AI821911	Hs.209452	ESTs	1.03	1.97
	315923	AI052789	Hs.133263	ESTs	2.63	5.06
	315954	AW276810	Hs.254859	ESTs, Moderately similar to ALU5_HUMAN A	1.21	0.85
	315978	AA830893	Hs.119769	ESTs	3.09	3.41
25	316001	AI248584	Hs.190745	Homo sapiens cDNA: FLJ21326 fis, clone C	2.20	6.82
	316011	AW516953	Hs.201372	ESTs	0.35	1.63
	316012	AA764950	Hs.119898	ESTs	6.56	8.13
	316040	AI983409	Hs.189226	ESTs	5.69	10.69
	316048	AI720759	Hs.224971	ESTs	2.84	10.45
30	316076	AW297895	Hs.116424	ESTs	0.30	1.05
	316124	AI308862	Hs.167028	ESTs	1.00	1.43
	316151	AI806016	Hs.156520	ESTs	5.80	9.03
	316187	AW518299	Hs.192253	ESTs	1.20	3.96
	316204	AA731509	Hs.120257	ESTs	4.92	6.94
35	316232	AW297853	Hs.251203	ESTs	1.48	1.60
	316275	AI671041	Hs.292611	ESTs, Moderately similar to ALU1_HUMAN A	5.86	12.14
	316291	AW375974	Hs.156704	ESTs	2.73	2.69
	316303	AA740994	Hs.209609	ESTs	1.53	1.26
	316344	AA744518	Hs.120610	ESTs	3.66	8.34
40	316346	AI028478	Hs.157447	ESTs	3.51	6.69
	316365	AI627845	Hs.210776	ESTs	2.50	4.33
	316380	AI393378	Hs.164496	ESTs	1.16	2.16
	316470	AA809902	Hs.243813	ESTs	5.40	10.34
	316509	AA767310	Hs.291766	ESTs	2.46	2.89
45	316514	AA768037	Hs.291671	ESTs	4.70	6.04
	316519	AI929097		gb:cd10c11.s1 NCI_CGAP_GCB1 Homo sapiens	4.41	9.70
	316609	AW292520	Hs.122082	ESTs	1.00	2.89
	316633	AI125586	Hs.127955	ESTs	2.61	3.72
	316700	AW172316	Hs.252961	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.46	4.64
50	316711	AI743721	Hs.285316	ESTs, Moderately similar to ALU7_HUMAN A	4.45	6.95
	316713	AI090671	Hs.134807	hypothetical protein FLJ12057	0.30	2.40
	316715	AI440266	Hs.170673	ESTs, Weakly similar to AF126780 1 retin	0.20	1.45
	316787	AW369770	Hs.130351	ESTs	4.05	5.53
	316809	AA825839	Hs.202238	ESTs	2.25	3.82
55	316811	AA922060	Hs.132471	ESTs	1.00	1.32
	316812	AW135045	Hs.232001	ESTs	3.28	4.70
	316818	AA827176	Hs.124316	ESTs	0.67	1.81
	316824	AA837416	Hs.124299	ESTs	3.53	6.00
	316827	AI380429	Hs.172445	ESTs	0.72	1.56
60	316891	AW298119	Hs.202536	ESTs	1.64	2.97
	316951	AA134365	Hs.57548	ESTs	1.45	1.08
	316970	AA860172	Hs.132406	ESTs	1.00	1.53
	316971	AA860212	Hs.170991	ESTs	1.08	1.96
	316990	AA861611	Hs.130643	ESTs	5.44	10.04
65	317001	AI627917	Hs.233694	hypothetical protein FLJ11350	3.56	4.37
	317008	AW051597	Hs.143707	ESTs	0.69	1.37
	317051	AA873253	Hs.126233	ESTs	6.18	12.72
	317128	AA971374	Hs.125674	ESTs	1.87	2.66
70	317129	H12523	Hs.78521	Homo sapiens cDNA: FLJ21193 fis, clone C	4.12	6.64
	317137	AW341567	Hs.125710	ESTs	2.82	5.12
	317196	AI348258	Hs.153412	ESTs	1.98	2.51
	317212	AI866468	Hs.148294	ESTs	1.86	2.83
	317223	AW297920	Hs.130054	ESTs	0.83	1.57
75	317224	D56760	Hs.93029	sparc/osteoneclin, cwcv and kazal-like d	2.74	0.86
	317266	AA906289	Hs.203614	ESTs	1.00	1.00
	317282	AI807444	Hs.176101	ESTs	2.60	4.21
	317285	AW370882	Hs.222080	ESTs	1.96	3.49
	317302	AA908709	Hs.135564	ESTs	7.16	8.32
	317304	AW449899	Hs.130184	ESTs	1.38	2.28
80	317320	AA927151	Hs.130452	ESTs	3.58	8.13
	317413	AW341701	Hs.126622	ESTs	2.08	4.92
	317417	AA918420	Hs.145378	ESTs	3.06	4.79
	317452	AA972965	Hs.135568	ESTs	4.22	9.21
	317519	AI859695	Hs.126860	ESTs	1.88	4.15
85	317521	AI824338	Hs.126891	ESTs	3.12	4.55
	317529	AI916517	Hs.126865	ESTs	2.73	3.34



	317570	AI733361	Hs.127122	ESTs	1.00	2.43
	317571	AA938663	Hs.199828	ESTs	5.20	11.95
	317598	AW206035	Hs.192123	ESTs	0.33	1.56
5	317627	AI346110	Hs.132553	ESTs	1.50	1.39
	317650	AI733310	Hs.127346	ESTs	0.48	1.46
	317659	AA961216	Hs.127785	ESTs	4.18	7.14
	317674	AW294909	Hs.132208	ESTs	2.92	3.20
	317686	AA969051	Hs.187319	ESTs	1.00	1.01
10	317692	AI307659	Hs.174794	ESTs	5.33	9.59
	317701	AI674774	Hs.128014	ESTs	1.00	1.00
	317711	AI733015	Hs.272189	ESTs	5.13	7.81
	317722	AI733373	Hs.128119	ESTs	2.50	6.03
	317756	AA973667	Hs.128320	ESTs	1.59	1.30
15	317777	AI143525	Hs.47313	KIAA0258 gene product	1.00	2.48
	317799	AI498273	Hs.128808	ESTs	1.78	2.11
	317803	AA983251	Hs.128899	ESTs	0.80	1.06
	317821	AI368158	Hs.70983	PTPL1-associated RhoGAP 1	0.17	0.68
	317848	AI820575	Hs.129086	Homo sapiens cDNA FLJ12007 fis, clone HE	5.30	8.16
20	317850	N29974	Hs.152982	hypothetical protein FLJ13117	1.30	2.28
	317861	AW341064	Hs.129119	ESTs	2.18	5.93
	317865	AI298794	Hs.129130	ESTs	4.48	8.20
	317869	AW295184	Hs.129142	deoxyribonuclease II beta	0.44	0.99
	317881	AI827248	Hs.224398	Homo sapiens cDNA FLJ11469 fis, clone HE	4.06	2.23
25	317890	AI915599	Hs.129225	ESTs	4.68	7.48
	317899	AI952430	Hs.150614	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.14	3.37
	317986	AI005163	Hs.201378	ESTs, Weakly similar to T12545 hypotheti	0.28	1.66
	318001	AW235697	Hs.130980	ESTs	5.12	9.97
	318016	AI016694	Hs.256921	ESTs	1.86	4.50
30	318023	AW243058	Hs.131155	ESTs	2.92	5.22
	318054	AW449270	Hs.232140	ESTs	3.92	6.37
	318068	AI024540	Hs.131574	ESTs	1.21	1.27
	318117	AI208304	Hs.250114	ESTs	0.86	1.17
	318187	AI792585	Hs.133272	ESTs, Weakly similar to ALUC_HUMAN !!!!	5.90	6.98
35	318223	AI077540	Hs.134090	ESTs	1.05	0.90
	318240	AI085377	Hs.143610	ESTs	3.10	2.40
	318255	AI082692	Hs.134662	ESTs	0.02	1.05
	318266	AI554341	Hs.271443	ESTs	6.12	10.55
	318330	AI093840	Hs.143758	ESTs	4.98	7.90
40	318369	AI493501	Hs.170974	ESTs	2.46	5.62
	318428	AI949409	Hs.194591	ESTs	0.77	0.45
	318458	AI149783	Hs.158438	ESTs	3.54	4.92
	318467	AI151395	Hs.144834	ESTs	4.56	5.62
	318473	AI939339	Hs.146883	ESTs	2.08	4.05
45	318476	AI693927	Hs.265165	ESTs	4.22	8.07
	318487	AI167877	Hs.143716	ESTs	1.47	1.05
	318488	AI217431	Hs.144709	ESTs	1.40	4.14
	318491	T26477	Hs.22883	ESTs, Weakly similar to ALU8_HUMAN ALU S	1.84	1.90
	318499	T25451		gb:PTH188 HTCCL1 Homo sapiens cDNA 5/3	2.58	5.20
50	318537	AA377908	Hs.13254	ESTs	3.26	4.18
	318538	N28625	Hs.74034	Homo sapiens clone 24651 mRNA sequence	0.35	1.07
	318547	R20578	Hs.90431	ESTs	3.22	4.60
	318552	R18364	Hs.90363	ESTs	4.87	9.06
	318575	R55102	Hs.107761	ESTs, Weakly similar to unnamed protein	1.91	1.98
55	318580	T34571	Hs.49007	poly(A) polymerase alpha	2.74	6.22
	318587	AA779704	Hs.168830	Homo sapiens cDNA FLJ12136 fis, clone MA	0.85	2.46
	318596	AI470235	Hs.172698	EST	4.88	4.93
	318622	T48325	Hs.237658	apolipoprotein A-II	4.80	12.51
	318629	N25163	Hs.8861	ESTs	0.39	1.04
60	318637	AA243539	Hs.9196	hypothetical protein	1.72	3.57
	318648	T77141	Hs.184411	albumin	6.27	9.91
	318650	AA393302	Hs.176626	hypothetical protein EDAG-1	3.96	8.84
	318671	AA188823	Hs.299254	Homo sapiens cDNA: FLJ23597 fis, clone L	1.53	0.81
	318679	T58115	Hs.10336	ESTs	1.00	2.19
65	318711	AI936475	Hs.101282	Homo sapiens cDNA: FLJ21238 fis, clone C	3.05	3.18
	318725	AI962487	Hs.242990	ESTs	1.08	2.46
	318728	Z30201	Hs.291289	ESTs, Weakly similar to ALU1_HUMAN ALU S	0.77	1.33
	318740	NM_002543	Hs.77729	oxidised low density lipoprotein (lectin	0.25	1.49
	318776	R24963	Hs.23766	ESTs	1.00	3.01
70	318784	H00148	Hs.5181	proliferation-associated 2G4, 38kD	2.70	3.86
	318816	F07873	Hs.21273	ESTs	3.90	7.13
	318865	H10818		gb:ym04f10.r1 Soares infant brain 1N1B H	2.25	3.56
	318879	R56332	Hs.18268	adenylate kinase 5	1.78	5.00
	318881	Z43224	Hs.124952	ESTs	4.79	14.13
75	318894	F08138	Hs.7387	DKFZP564B116 protein	5.31	7.00
	318901	AW368520	Hs.301528	L-kynurenine/alpha-aminoadipate aminotra	1.03	0.91
	318925	Z43577	Hs.21470	ESTs	2.23	3.80
	318936	AI219221	Hs.308298	ESTs	1.86	7.16
	318982	Z44140	Hs.269622	ESTs	5.84	9.79
80	318986	Z44186	Hs.169161	ESTs, Highly similar to MAON_HUMAN NADP-	1.00	1.00
	319041	Z44720	Hs.98365	ESTs, Weakly similar to weak similarity	3.38	6.11
	319103	H05896	Hs.4993	KIAA1313 protein	1.00	1.07
	319170	R13678	Hs.285306	putative selenocysteine lyase	3.79	5.03
	319196	F07953	Hs.16085	putative G-protein coupled receptor	1.00	2.98
85	319199	F07361	Hs.13306	ESTs	3.53	5.66
	319242	F11472	Hs.12839	ESTs	5.87	7.26



	319263	T65331	Hs.81360	Homo sapiens cDNA: FLJ21927 fis, clone H	1.81	1.57
	319267	F11802	Hs.6818	ESTs	1.10	4.72
	319270	R13474	Hs.290263	ESTs	4.80	10.40
5	319279	T65094	Hs.12677	CGI-147 protein	1.50	2.11
	319282	AA461358	Hs.12876	ESTs	1.00	1.00
	319289	W07304	Hs.79059	transforming growth factor, beta recepto	0.18	0.68
	319291	W86578	Hs.285243	hypothetical protein FLJ22029	0.26	0.62
	319293	F12119	Hs.12583	ESTs	3.13	4.50
10	319312	Z45481		gb:HSC2QE041 normalized infant brain cDN	1.10	1.00
	319370	H54254	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A	0.16	0.73
	319391	R06304	Hs.13911	ESTs	1.26	2.43
	319396	H67130	Hs.301743	ESTs	0.70	0.76
	319398	AA359754	Hs.191196	ESTs	2.45	3.59
15	319407	R05329		gb:ye91b04.r1 Soares fetal liver spleen	2.00	3.54
	319425	T82930		gb:yd39f07.r1 Soares fetal liver spleen	4.28	8.81
	319433	R06050	Hs.191198	ESTs	6.15	14.13
	319437	AA282420	Hs.111991	ESTs, Weakly similar to Y48A5A.1 [C.eleg	3.26	5.68
	319466	AI809937	Hs.116417	ESTs	1.76	5.65
20	319471	R06546	Hs.19717	ESTs	4.29	4.84
	319480	R06933	Hs.184221	ESTs	1.00	1.00
	319484	T91772		gb:yd52a10.s1 Soares fetal liver spleen	2.81	4.88
	319486	AI382429	Hs.250799	ESTs	2.08	2.82
	319508	T99898	Hs.270104	ESTs, Moderately similar to ALU8_HUMAN A	2.80	4.39
	319523	T69499	Hs.191184	ESTs	1.55	3.25
25	319545	R83716	Hs.14355	Homo sapiens cDNA FLJ13207 fis, clone NT	1.65	1.19
	319546	R09692		gb:yf23b12.r1 Soares fetal liver spleen	5.11	8.54
	319552	AA096106	Hs.20403	ESTs	1.89	3.36
	319582	T82998	Hs.250154	hypothetical protein FLJ12973	3.48	4.82
30	319586	D78808	Hs.283683	chromosome 8 open reading frame 4	0.26	0.82
	319604	R11679	Hs.297753	vimentin	1.68	3.41
	319609	AW247514	Hs.12293	hypothetical protein FLJ21103	3.06	4.24
	319611	H14957		gb:ym19c10.r1 Soares infant brain 1NIB H	2.76	4.24
	319653	AA770183	Hs.173515	uncharacterized hypothalamus protein HTO	2.51	3.55
35	319657	R19897	Hs.106604	ESTs	5.32	7.68
	319658	R13432	Hs.167481	syntrophin, gamma 1	3.35	5.00
	319661	H08035	Hs.21398	ESTs, Moderately similar to A Chain A, H	5.18	12.55
	319662	H06382	Hs.21400	ESTs	1.58	1.56
	319708	R15372	Hs.22664	ESTs	1.00	1.22
40	319742	T77668	Hs.21162	ESTs	2.48	3.13
	319748	R18178	Hs.295866	Homo sapiens mRNA; cDNA DKFZp434N1923 (f	3.02	4.85
	319772	R76633	Hs.22646	ESTs	4.36	11.61
	319788	AA321932	Hs.117414	KIAA1320 protein	2.56	3.68
	319805	R92857	Hs.271350	likely ortholog of mouse polydom	4.63	6.56
45	319812	N74880	Hs.264330	N-acylsphingosine amidohydrolase (acid c	0.63	1.32
	319834	AA071267		gb:zm61g01.r1 Stratagene fibroblast (937	0.30	0.94
	319878	T78517	Hs.13941	ESTs	3.99	6.44
	319882	AA258981	Hs.291392	ESTs	5.09	7.36
	319912	T77559	Hs.94109	Homo sapiens cDNA FLJ13634 fis, clone PL	3.24	3.21
50	319935	H79460	Hs.271722	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.40	9.42
	319944	T79248	Hs.133510	ESTs	3.31	5.39
	319947	AA160967	Hs.14479	Homo sapiens cDNA FLJ14199 fis, clone NT	2.90	4.95
	319962	H06350	Hs.135056	Human DNA sequence from clone RP5-850E9	1.81	1.57
	320007	AA336314		gb:EST40943 Endometrial tumor Homo sapie	3.42	6.29
55	320018	T83263		gb:yd40h09.r1 Soares fetal liver spleen	2.77	5.14
	320030	H63789	Hs.296288	ESTs, Weakly similar to KIAA0638 protein	4.10	6.69
	320032	AI699772	Hs.292664	ESTs, Weakly similar to A46010 X-linked	3.27	3.27
	320040	AA233671	Hs.87164	hypothetical protein FLJ14001	1.81	1.64
	320047	T86564	Hs.302256	EST	3.38	7.36
60	320063	AA074108	Hs.120844	FOXJ2 forkhead factor	5.90	16.73
	320096	H58138	Hs.117915	ESTs	2.08	4.47
	320099	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis	1.00	1.00
	320112	T92107	Hs.188489	ESTs	2.27	2.06
	320140	H94179	Hs.119023	SMC2 (structural maintenance of chromoso	1.00	1.00
65	320188	AW419200	Hs.172318	ESTs	1.26	1.00
	320193	AA831259	Hs.17132	ESTs	2.58	6.23
	320195	R62203	Hs.24321	Homo sapiens cDNA FLJ12028 fis, clone HE	2.85	4.53
	320199	R78659	Hs.29792	ESTs	0.40	0.94
	320203	AL049227	Hs.124776	Homo sapiens mRNA; cDNA DKFZp564N1116 (f	0.84	1.18
70	320219	AA327564	Hs.127011	tubulointerstitial nephritis antigen	1.00	1.17
	320220	AF054910	Hs.127111	teklin 2 (testicular)	0.18	1.09
	320225	AF058989	Hs.128231	G antigen, family B, 1 (prostate associa	5.26	13.75
	320231	H03139	Hs.24683	ESTs	1.59	1.93
	320260	NM_003608	Hs.131924	G protein-coupled receptor 65	1.38	4.56
75	320267	AL049337	Hs.132571	Homo sapiens mRNA; cDNA DKFZp564P016 (fr	1.00	1.92
	320268	H06019	Hs.151293	Homo sapiens cDNA FLJ10664 fis, clone NT	5.58	5.70
	320322	AF077374	Hs.139322	small proline-rich protein 3	1.41	1.01
	320325	AI167978	Hs.139851	caveolin 2	0.05	0.67
	320330	AF026004	Hs.141660	chloride channel 2	2.17	1.26
80	320339	H10807	Hs.281434	Homo sapiens cDNA FLJ14028 fis, clone HE	1.81	2.32
	320388	H16065	Hs.31286	ESTs	1.00	3.22
	320402	R22291	Hs.23368	Homo sapiens clone FLC0578 PRO2852 mRNA,	1.41	1.36
	320413	AA203711	Hs.173269	ESTs	2.31	3.61
	320432	R62786	Hs.124136	ESTs	11.25	20.78
	320436	AA253352	Hs.293663	ESTs	2.22	3.49
85	320438	W24548	Hs.5669	ESTs	3.53	8.14



	320448	AI240233	Hs.80887	v-yes-1 Yamaguchi sarcoma viral related	1.42	3.46
	320451	R26944	Hs.180777	Homo sapiens mRNA; cDNA DKFZp564M0264 (f	0.87	0.81
	320484	AA094436	Hs.296267	folliculin-like 1	0.65	1.18
5	320499	R32555	Hs.24321	Homo sapiens cDNA FLJ12028 fis, clone HE	3.44	7.15
	320514	AB007978	Hs.158278	KIAA0509 protein	6.44	13.62
	320521	N31464	Hs.24743	hypothetical protein FLJ20171	1.48	1.04
	320526	AW374205	Hs.111314	ESTs	3.66	7.87
	320527	R34672	Hs.324522	ESTs	3.16	5.63
10	320536	AA331732	Hs.137224	ESTs	2.83	5.83
	320556	AF054177	Hs.14570	hypothetical protein FLJ22530	1.28	1.00
	320564	AF056209	Hs.159396	peptidylglycine alpha-amidating monooxyg	1.22	0.81
	320587	Z44524	Hs.167456	Homo sapiens mRNA full length insert cDN	1.84	2.44
	320635	R54159	Hs.80506	small nuclear ribonucleoprotein polypept	1.00	6.25
15	320639	AA243258	Hs.7395	hypothetical protein FLJ23182	2.60	2.30
	320648	N48521	Hs.26549	Homo sapiens mRNA for KIAA1708 protein,	1.00	1.53
	320651	AA489268	Hs.111334	ferritin, light polypeptide	0.14	0.79
	320664	AI904216	Hs.91251	hypothetical protein FLJ11198	5.02	8.84
	320676	AA132650	Hs.300511	ESTs	3.63	5.37
	320683	R59291	Hs.26638	ESTs, Weakly similar to unnamed protein	0.37	1.31
20	320689	AA334609	Hs.171929	ESTs, Weakly similar to A54849 collagen	1.27	1.02
	320696	AW135016	Hs.172780	ESTs	3.53	4.60
	320714	AI445591		gb:yyq04a10.r1 Soares fetal liver spleen	1.06	0.85
	320727	U96044	Hs.181125	immunoglobulin lambda locus	1.35	1.49
25	320771	AI793266	Hs.117176	poly(A)-binding protein, nuclear 1	0.04	0.82
	320794	AA281993	Hs.91226	ESTs	2.96	4.33
	320822	AF100780	Hs.194679	WNT1 inducible signaling pathway protein	0.10	0.79
	320824	AF120274	Hs.194689	arlemn	1.16	1.11
	320830	AJ132445	Hs.266416	claudin 14	1.06	1.75
30	320843	AA317372	Hs.34744	Homo sapiens mRNA; cDNA DKFZp547C136 (fr	1.36	1.47
	320849	D60031	Hs.34771	ESTs	5.30	7.49
	320853	AI473796	Hs.135904	ESTs	1.00	1.00
	320896	AB002155	Hs.271580	uropalakin 1B	5.90	2.55
	320921	R94038	Hs.199538	inhibin, beta C	2.20	1.17
35	320927	AI205786	Hs.213923	ESTs	0.18	1.46
	320957	AI878933	Hs.92023	core histone macroH2A2.2	1.67	2.18
	320997	H22544		gb:yn69f11.r1 Soares adult brain N2b5HB5	3.26	3.62
	321045	W88483	Hs.293650	ESTs	2.25	4.55
40	321046	H27794	Hs.269055	ESTs	2.69	4.25
	321052	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	2.14	2.56
	321059	AI092824	Hs.126465	ESTs	1.69	0.53
	321062	R87955	Hs.241411	Homo sapiens mRNA full length insert cDN	2.76	5.20
	321067	AF131782	Hs.241438	Homo sapiens clone 24941 mRNA sequence	4.79	7.41
45	321102	AA018306		gb:ze40d08.r1 Soares retina N2b4HR Homo	1.79	4.27
	321130	H43750	Hs.125494	ESTs	1.00	3.14
	321142	AI817933	Hs.298351	ASPL protein	8.73	15.36
	321155	AA336635	Hs.99598	hypothetical protein MGC5338	3.04	5.03
	321158	AA700289		gb:yu76f11.r1 Soares fetal liver spleen	4.62	8.39
	321170	N53742	Hs.172982	ESTs	2.21	4.46
50	321199	AW385512		gb:yy56d10.s1 Soares_multiple_sclerosis_	5.69	8.01
	321206	H54178	Hs.226469	Homo sapiens cDNA FLJ12417 fis, clone MA	4.00	7.32
	321225	AL080073	Hs.251414	Homo sapiens mRNA; cDNA DKFZp564B1462 (f	4.17	4.63
	321236	AW371941	Hs.18192	Ser/Arg-related nuclear matrix protein (	1.00	1.00
	321244	AF068654		gb:Homo sapiens isolate AN.1 immunoglobu	2.18	9.13
55	321270	R83560		gb:yyv76c06.s1 Soares fetal liver spleen	3.80	5.26
	321317	AI937060	Hs.6298	KIAA1151 protein	1.81	1.65
	321318	AB033041	Hs.137507	KIAA1215 protein	1.00	1.00
	321325	AB033100	Hs.300646	KIAA protein (similar to mouse paladin)	0.44	0.93
	321342	AA127984	Hs.222024	transcription factor BMAL2	4.94	4.93
60	321356	R93443	Hs.271770	ESTs	3.10	4.66
	321418	AI739161	Hs.161075	ESTs	2.28	2.54
	321420	AI368667	Hs.132743	ESTs	1.13	0.97
	321430	U05890		gb:H.sapiens (DIG3) mRNA for immunoglobu	2.42	3.35
	321453	N50080	Hs.82845	Homo sapiens cDNA: FLJ21930 fis, clone H	1.60	3.11
65	321467	X13075		gb:Human 2a12 mRNA for kappa-immunoglobu	0.42	0.72
	321468	AA514198	Hs.38540	ESTs	2.46	6.50
	321491	H70665	Hs.292549	ESTs	1.00	1.25
	321498	AW295517	Hs.255436	ESTs	3.19	6.24
	321504	W02356	Hs.268980	ESTs	2.28	3.86
70	321510	AA703650	Hs.255748	ESTs	2.14	3.94
	321513	H84972	Hs.108551	ESTs	2.78	5.37
	321516	AI382803	Hs.159235	ESTs	3.06	7.19
	321565	AI525773	Hs.266514	hypothetical protein FLJ11342	4.89	7.82
	321577	H84260		gb:ys90g04.r1 Soares retina N2b5HR Homo	1.00	1.73
75	321581	AA019964	Hs.28803	ESTs	4.88	6.73
	321582	AA143755	Hs.21858	trinucleotide repeat containing 3	1.00	2.08
	321587	H95531		gb:ys76e02.r1 Soares retina N2b4HR Homo	2.26	4.52
	321626	AA295430	Hs.96322	hypothetical protein FLJ23560	1.95	3.83
	321628	H87064	Hs.161051	ESTs, Moderately similar to ALU6_HUMAN A	0.47	1.02
80	321642	AW085917	Hs.247084	ESTs	1.52	1.38
	321669	H95404	Hs.294110	ESTs	2.17	2.45
	321687	AA625149		gb:af70c12.r1 Soares_NhHMPu_S1 Homo sapi	4.31	6.95
	321688	H97646	Hs.123158	Homo sapiens cDNA FLJ12830 fis, clone NT	2.82	3.28
	321693	AA700017	Hs.173737	ras-related C3 botulinum toxin substrate	0.51	1.08
85	321700	N55160	Hs.167260	ESTs	4.57	7.46
	321701	AW390923	Hs.42568	ESTs	1.00	1.00



	321709	N25847	Hs.108923	RAB38, member RAS oncogene family	1.00	1.00
	321710	N35682	Hs.259743	ESTs	2.97	5.26
	321775	AI694875	Hs.202312	Homo sapiens clone N11 Ntera2D1 teratoca	1.00	1.00
5	321777	AI637993	Hs.202312	Homo sapiens clone N11 Ntera2D1 teratoca	1.68	0.45
	321779	N42729	Hs.163835	ESTs	0.90	0.90
	321829	D81993	Hs.8966	tumor endothelial marker 8	2.69	3.89
	321846	AA281594	Hs.87902	ESTs	5.11	7.64
	321879	AL109670	Hs.302809	ESTs	6.49	9.58
10	321883	AA426494	Hs.46901	KIAA1462 protein	0.28	0.95
	321899	N55158	Hs.29468	ESTs	0.39	0.95
	321911	AF026944	Hs.293797	ESTs	6.20	10.76
	321949	R49202	Hs.181694	EST	4.62	10.51
	321955	AI651866	Hs.195689	ESTs	2.89	5.47
	321956	AL110177	Hs.132882	ESTs	0.32	1.25
15	321987	AL133612	Hs.272759	KIAA1457 protein	1.00	1.83
	321991	AL133627	Hs.158923	Homo sapiens mRNA; cDNA DKFZp434K0722 (f	4.00	6.47
	322002	AA328801	Hs.84522	ESTs	2.10	3.48
	322035	AL137517	Hs.306201	hypothetical protein DKFZp564O1278	1.00	1.90
20	322044	AW340926		gb:xy51b10.x1 NCI_CGAP_Lu34.1 Homo sapie	3.20	9.67
	322057	N92197	Hs.154679	synaptotagmin 1	1.55	1.07
	322060	AI341937		gb:ql10e03.x1 NCI_CGAP_GC4 Homo sapiens	4.59	7.68
	322070	U80769	Hs.210322	Homo sapiens mRNA for KIAA1766 protein,	2.78	4.52
	322083	AF074982	Hs.226031	ESTs, Highly similar to KIAA0535 protein	3.10	5.52
25	322091	AI819863	Hs.106243	ESTs	1.59	1.75
	322125	R93901		gb:yq16c12.r1 Soares fetal liver spleen	2.06	5.27
	322130	R98978	Hs.117767	ESTs	10.12	16.49
	322147	AF085919	Hs.114176	ESTs	0.94	0.64
	322166	AF085958		gb:yr88b03.r1 Soares fetal liver spleen	4.09	6.67
30	322173	H52567		gb:y185d04.r1 Soares_pineal_gland_N3HPG	3.46	4.85
	322178	H56535		gb:y188g03.r1 Soares_pineal_gland_N3HPG	0.44	2.54
	322179	H92891		gb:y194c02.s1 Soares_pineal_gland_N3HPG	4.52	7.50
	322186	H67346	Hs.269187	ESTs	0.15	0.98
	322196	W87895	Hs.211516	ESTs	2.20	5.04
35	322212	AF087995	Hs.134877	ESTs	3.42	4.84
	322221	AI890619	Hs.179562	nucleosome assembly protein 1-like 1	0.82	2.14
	322277	AI640193	Hs.226389	ESTs	3.62	3.98
	322278	AF086283		gb:zd46f01.r1 Soares_fetal_heart_NbHH19W	1.00	1.00
40	322284	AI792140	Hs.49265	ESTs	0.66	2.76
	322288	AL037273	Hs.7886	pellino (Drosophila) homolog 1	0.71	0.70
	322320	AF086419		gb:zd78d03.r1 Soares_fetal_heart_NbHH19W	2.02	2.76
	322336	AA308526	Hs.76152	decorin	2.92	4.44
	322339	W17348		gb:zb18c07.x5 Soares_fetal_lung_NbHL19W	8.50	11.56
	322366	AW404274	Hs.122492	hypothetical protein	0.61	1.34
45	322372	W25624	Hs.153943	ESTs	7.37	12.07
	322374	AI394663	Hs.122116	ESTs, Moderately similar to Ostf2 [M.musc	4.78	10.50
	322378	AF064819	Hs.201877	DESC1 protein	1.00	1.00
	322388	AI815730	Hs.247474	hypothetical protein FLJ21032	7.09	8.49
	322416	AA223183	Hs.298442	adaptor-related protein complex 3, mu 1	3.20	5.80
50	322419	AA248987	Hs.14084	ring finger protein 7	1.64	1.57
	322425	W37943	Hs.34892	KIAA1323 protein	0.83	1.00
	322431	AA069222	Hs.141892	ESTs	3.96	5.22
	322450	AA040131	Hs.25144	ESTs	5.18	12.67
55	322465	AA137152	Hs.286049	phosphoserine aminotransferase	3.41	2.23
	322467	AF116826	Hs.180340	putative protein-tyrosine kinase	1.00	1.30
	322473	AA744286	Hs.266935	tRNA selenocysteine associated protein	1.75	2.03
	322509	T52172	Hs.302213	ESTs	1.00	2.27
	322523	W80398	Hs.193197	ESTs	2.75	5.49
	322527	AF147359		gb:Homo sapiens full length insert cDNA	1.25	1.27
60	322560	AI916847	Hs.270947	ESTs	4.57	8.81
	322566	W87285	Hs.269587	ESTs	1.00	1.42
	322585	AA837622		gb:zh69c01.r1 Soares_fetal_liver_spleen_	4.18	6.94
	322635	AA679084		gb:zh90h08.r1 Soares_fetal_liver_spleen_	2.40	4.85
	322641	AA007352	Hs.256042	ESTs	2.94	4.64
65	322653	AI828854	Hs.258538	striatin, calmodulin-binding protein	0.48	0.38
	322664	AA011522		gb:zl03g07.r1 Soares_fetal_liver_spleen_	1.92	2.18
	322687	AI110759		gb:AF074666 Human fetal liver cDNA libra	4.14	6.75
	322692	AA018117	Hs.60843	potassium voltage-gated channel, shaker-	3.50	5.00
70	322694	AI110872	Hs.279812	PRO0327 protein	1.80	1.72
	322708	AF113674	Hs.283773	clone FLB1727	1.00	3.43
	322712	AA021328	Hs.23607	hypothetical protein FLJ11109	3.28	3.86
	322766	AW068805	Hs.288467	Homo sapiens cDNA FLJ12280 fis, clone MA	1.63	1.53
	322770	AA045796	Hs.122682	ESTs	1.53	1.06
	322794	AI608591	Hs.38991	S100 calcium-binding protein A2	12.06	1.94
75	322810	AI962276	Hs.127444	ESTs	4.09	6.90
	322818	AW043782	Hs.293616	ESTs	1.20	1.63
	322820	AI377755	Hs.120695	ESTs	0.21	1.93
	322872	AA827228	Hs.126943	ESTs	2.04	1.63
	322882	AW248508	Hs.279727	Homo sapiens cDNA FLJ14035 fis, clone HE	5.26	1.22
80	322887	AI986306	Hs.86149	phosphoinositol 3-phosphate-binding prot	2.80	2.24
	322913	AI733737	Hs.68837	ESTs	2.38	6.61
	322926	AI825940	Hs.211192	ESTs	4.02	5.79
	322929	AI365585	Hs.146246	ESTs	0.30	1.14
	322968	AI905228	Hs.83484	SRY (sex determining region Y)-box 4	2.06	1.13
85	322971	C15953	Hs.212760	hypothetical protein FLJ13649	1.18	2.00
	322981	AA493252	Hs.159577	ESTs	2.28	2.61



	322988	C18727	Hs.171941	ESTs	0.39	2.00
	323003	AI733859	Hs.149089	ESTs	3.28	1.00
	323013	AA134042	Hs.191451	ESTs	3.38	5.68
5	323025	AL157565	Hs.315369	Homo sapiens cDNA: FLJ23075 fis, clone L	0.06	1.10
	323032	AW244073	Hs.145946	ESTs	10.18	21.27
	323052	R21124	Hs.85573	Homo sapiens DC29 mRNA, complete cds	1.46	1.90
	323064	AL119341	Hs.49359	Homo sapiens mRNA; cDNA DKFZp547E052 (fr	3.08	5.64
	323098	AI700025	Hs.270471	ESTs	2.31	4.49
10	323102	AL119913	Hs.163615	ESTs	5.38	11.64
	323155	AL135041		gb:DKFZp762K2310_r1 762 (synonym: hmel2)	2.38	5.56
	323176	AW071648	Hs.82101	pleckstrin homology-like domain, family	1.06	1.41
	323191	AA195600	Hs.301570	ESTs	0.73	1.24
	323225	AA205654	Hs.24790	KIAA1573 protein	5.25	11.95
15	323232	AA148722	Hs.224680	ESTs	0.45	1.35
	323266	AW003362	Hs.243886	nuclear autoantigenic sperm protein (his	1.71	1.83
	323281	AI697556	Hs.292659	ESTs	1.24	3.21
	323283	AA256014	Hs.86682	Homo sapiens cDNA: FLJ21578 fis, clone C	12.68	15.05
	323314	AA226310	Hs.191501	ESTs	4.42	9.61
20	323316	AL134620	Hs.280175	ESTs	2.98	5.93
	323334	AI336501	Hs.77273	ras homolog gene family, member A	1.98	3.30
	323338	R74219	Hs.23348	S-phase kinase-associated protein 2 (p45	1.62	1.00
	323348	AA233056	Hs.191518	ESTs	1.00	1.07
	323351	AA704103	Hs.24049	ESTs	1.43	1.68
25	323359	AA234172	Hs.137418	ESTs	0.34	1.18
	323360	AA716061	Hs.161719	ESTs	3.01	3.71
	323405	AW139550	Hs.115173	ESTs	1.90	8.81
	323420	AI672386	Hs.263780	ESTs	0.29	1.01
	323434	AW081455	Hs.120219	ESTs	2.27	1.92
30	323445	AA253103	Hs.135569	ESTs, Weakly similar to NEUROD [H.sapien	0.43	0.80
	323449	AA282865	Hs.284153	Fanconi anemia, complementation group A	3.19	3.85
	323492	H00978	Hs.20887	hypothetical protein FLJ10392	2.70	3.20
	323501	AA182461	Hs.84520	ESTs	2.04	3.31
	323505	AI652287		gb:EST382593 MAGE resequences, MAGK Homo2.21		3.08
35	323515	AA282274	Hs.256083	ESTs	2.69	3.40
	323541	AI185116	Hs.104613	RP42 homolog	1.20	1.09
	323545	AI814405	Hs.224569	ESTs	1.25	1.55
	323635	R63117	Hs.9691	Homo sapiens cDNA: FLJ23249 fis, clone C	0.27	0.72
40	323675	AA984759	Hs.272168	tumor differentially expressed 1	3.70	5.80
	323678	AL042121	Hs.20880	ESTs	3.33	5.10
	323691	AA317561	Hs.145599	ESTs	1.00	1.00
	323693	AW297758	Hs.249721	ESTs	2.01	1.54
	323746	AW298611	Hs.12808	MARK	4.11	5.53
	323774	AA329806	Hs.321056	Homo sapiens mRNA; cDNA DKFZp586F1322 (f	2.06	3.70
45	323856	AA355264	Hs.267604	hypothetical protein FLJ10450	3.42	8.13
	323857	T18988	Hs.293668	ESTs	5.97	12.51
	323870	AA341774	Hs.129212	ESTs	3.17	4.52
	323876	AL042492	Hs.147313	ESTs	0.36	1.00
	323885	AA344308	Hs.128427	Homo sapiens BAC clone RP11-335J18 from	2.31	3.33
50	323911	AL043212	Hs.92550	ESTs	4.38	5.41
	323919	AA862973	Hs.220704	ESTs	5.80	10.20
	323972	AI869964	Hs.182906	ESTs	3.10	5.14
	324005	AA610011	Hs.208021	ESTs	5.34	10.07
	324036	AI472078	Hs.303662	ESTs	1.00	5.03
55	324055	AA528794	Hs.128644	ESTs	0.86	1.00
	324063	AW292740	Hs.272813	dual oxidase 1	0.45	0.91
	324072	AA381829		gb:EST94855 Activated T-cells I Homo sap	2.82	5.12
	324092	AW269931	Hs.202473	Homo sapiens cDNA: FLJ22278 fis, clone H	2.40	2.52
	324095	AW377983	Hs.298140	Homo sapiens cDNA: FLJ22502 fis, clone H	1.32	4.30
60	324129	AI381918	Hs.285833	Homo sapiens cDNA: FLJ22135 fis, clone H	1.40	1.77
	324132	AW504860	Hs.288836	hypothetical protein FLJ12673	4.24	6.21
	324214	AA412395	Hs.225740	ESTs	6.96	10.69
	324227	AA295552	Hs.28631	Homo sapiens cDNA: FLJ22141 fis, clone H	0.81	0.53
	324266	AL047634	Hs.231913	ESTs	2.42	4.05
65	324275	AA429088	Hs.98523	ESTs	3.62	5.38
	324281	AL048026	Hs.124675	ESTs, Weakly similar to T14742 hypotheti	0.14	0.70
	324290	AA432032	Hs.304420	ESTs	3.71	4.34
	324303	AL118754		gb:DKFZp761P1910_r1 761 (synonym: hamy2)	0.95	0.91
70	324312	AI198841	Hs.128173	ESTs	4.06	5.91
	324325	AL138153	Hs.300410	ESTs	5.88	8.25
	324338	AL138357	Hs.145078	regulator of differentiation (in S. pombe	0.87	1.25
	324341	AW197734	Hs.99807	ESTs, Weakly similar to unnamed protein	1.28	1.00
	324343	AW452016	Hs.293232	ESTs	2.54	3.46
	324371	AA452305	Hs.270319	ESTs	5.85	8.36
75	324382	AW502749	Hs.24724	MFH-amplified sequences with leucine-ric	0.76	1.64
	324384	AA453396	Hs.127656	KIAA1349 protein	2.88	5.69
	324385	F28212	Hs.284247	KIAA1491 protein	1.81	1.99
	324388	AI924963	Hs.306206	hypothetical protein FLJ11215	1.00	1.00
	324432	AA464510	Hs.152812	ESTs	2.73	2.17
80	324497	AW152624	Hs.136340	ESTs, Weakly similar to unnamed protein	0.71	1.90
	324510	AI148353	Hs.287425	Homo sapiens cDNA FLJ11569 fis, clone HE	1.00	1.00
	324580	AA492588		gb:ng99c08.s1 NCL_CGAP_Thy1 Homo sapiens	2.18	3.50
	324582	AA506935	Hs.132036	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.96	11.36
	324633	AA572994	Hs.325489	ESTs	2.92	4.22
85	324640	AW295832	Hs.134798	ESTs, Moderately similar to TTL MOUSE TU	5.48	11.74
	324675	AW014734	Hs.157969	ESTs	0.39	0.73



	324699	AW504732	Hs.21275	hypothetical protein FLJ11011	0.93	0.93
	324747	AA603532	Hs.130807	ESTs	1.57	1.81
	324748	AA657457	Hs.292385	ESTs	1.55	1.34
5	324801	AI819924	Hs.14553	sterol O-acyltransferase (acyl-Coenzyme	1.00	6.56
	324804	AI692552		gb:wd73f12.x1 NCL_CGAP_Lu24 Homo sapiens	1.00	7.53
	324828	AA843926	Hs.124434	ESTs	2.00	3.25
	324855	AW152305	Hs.122364	ESTs	2.74	3.43
	324866	AI541214	Hs.46320	Small proline-rich protein SPRK (human,	1.07	0.95
10	324871	AW297755	Hs.271923	Homo sapiens cDNA: FLJ22785 fis, clone K	1.68	1.21
	324886	AA806794	Hs.131511	ESTs	2.56	5.61
	324889	D31010		gb:HUML12147 Human fetal lung Homo sapie	2.20	4.65
	324948	AW383618	Hs.265459	ESTs, Moderately similar to ALU2_HUMAN A	5.28	7.05
	324953	AI264628	Hs.125428	ESTs	3.37	5.51
15	324958	AA625076	Hs.132892	protocadherin 20	5.12	9.81
	324988	T06997	Hs.121028	hypothetical protein FLJ10549	2.52	1.08
	325024	F13254	Hs.78672	laminin, alpha 4	5.24	10.22
	325105	H97109	Hs.105421	ESTs	1.00	1.00
	325108	AA401863	Hs.22380	ESTs	1.99	2.14
20	325114	D83901	Hs.315562	ESTs	2.73	3.17
	325146	AI064690	Hs.171176	ESTs	1.86	3.41
	325149	D61117	Hs.187646	ESTs	0.42	0.93
	325187	AI653682	Hs.197812	ESTs	6.50	11.31
	325228				6.18	15.76
25	325235				2.64	4.12
	325328				2.87	4.42
	325340				0.29	0.33
	325367				16.56	24.29
	325373				0.63	1.22
30	325389				0.88	1.05
	325436				5.75	14.14
	325471				8.46	17.82
	325498				3.32	6.42
	325557				5.51	8.28
35	325559				7.48	21.40
	325560				4.08	6.25
	325569				4.20	5.24
	325585				1.10	1.13
	325587				1.00	1.00
40	325597				2.98	13.40
	325639				0.78	0.78
	325685				0.46	0.66
	325686				0.95	1.55
	325735				4.48	9.20
45	325739				0.59	0.88
	325740				2.42	6.61
	325792				7.88	9.83
	325819				4.74	7.18
	325883				2.02	2.64
50	325895				7.78	15.98
	325925				2.04	10.60
	325932				4.18	7.36
	325941				3.66	9.03
	325969				0.61	0.80
55	325971				4.88	7.42
	326025				0.55	1.07
	326046				7.21	14.72
	326099				3.60	5.98
	326108				1.27	1.06
60	326163				3.27	5.70
	326165				0.45	1.11
	326189				0.13	0.45
	326204				5.60	9.00
	326230				7.00	12.01
65	326274				1.00	8.09
	326360				9.86	15.35
	326393				0.52	0.77
	326505				1.00	1.42
	326515				1.24	5.84
70	326589				9.20	13.49
	326592				2.77	4.01
	326605				2.01	2.53
	326692				1.00	1.00
	326693				1.00	1.31
75	326720				0.19	0.65
	326742				2.34	7.20
	326770				0.25	0.83
	326818				3.09	4.56
	326936				2.08	3.45
80	326964				0.41	1.70
	326983				2.02	3.80
	326991				1.09	1.20
	327036				1.00	8.04
	327040				3.05	4.22
85	327053				3.55	6.31
	327075				1.59	1.40



	327085	2.50	12.57
	327130	5.38	8.04
	327156	3.74	6.58
5	327220	1.28	1.54
	327224	6.56	12.91
	327288	2.61	5.40
	327321	2.42	3.11
	327332	6.62	10.58
10	327361	2.69	4.41
	327377	2.04	6.72
	327396	2.61	4.50
	327414	1.00	8.01
	327442	5.91	9.65
15	327467	6.58	18.01
	327473	3.79	7.48
	327483	4.08	8.87
	327562	0.68	2.86
	327568	1.00	2.00
20	327606	2.06	3.61
	327611	5.90	14.26
	327642	4.06	8.74
	327654	1.05	2.08
	327734	1.00	1.00
25	327775	1.46	11.79
	327796	3.47	5.65
	327840	3.26	6.64
	327940	5.84	15.58
	327984	0.36	1.50
30	328004	1.87	1.42
	328021	0.42	0.59
	328068	2.83	4.68
	328100	3.04	5.39
	328101	3.54	5.20
35	328113	0.72	0.91
	328157	5.58	5.16
	328196	5.76	11.13
	328197	5.98	10.58
	328264	3.11	4.88
40	328299	2.20	3.06
	328342	1.49	1.94
	328365	1.00	1.00
	328369	4.40	7.36
	328381	1.86	4.93
45	328451	5.51	7.56
	328481	0.13	0.72
	328500	2.71	3.97
	328530	5.41	7.62
	328600	3.14	10.68
50	328608	4.56	8.17
	328616	2.24	11.91
	328623	3.04	5.46
	328632	0.70	1.19
	328664	3.48	6.80
55	328666	10.42	26.47
	328698	9.68	14.56
	328700	2.74	10.22
	328708	0.15	0.57
	328735	6.23	8.91
60	328743	3.62	6.54
	328806	0.22	0.78
	328861	3.68	10.54
	328908	5.42	16.36
	328933	2.02	5.29
65	328934	1.73	4.45
	328949	3.34	5.41
	329005	2.88	7.26
	329011	2.52	3.72
	329033	1.00	1.03
70	329037	5.07	8.16
	329067	1.98	2.41
	329134	2.24	3.25
	329157	2.30	11.04
	329178	2.64	5.02
75	329192	6.41	15.27
	329194	0.31	0.79
	329204	1.60	3.75
	329224	2.99	6.11
	329228	0.83	0.83
80	329288	0.63	1.01
	329337	1.00	1.00
	329541	0.76	1.68
	329560	1.34	2.02
	329588	1.68	2.22
85	329643	4.18	11.77
	329703	1.00	1.00



	329764			5.78	15.50	
	329816			2.09	5.44	
	329860			3.13	10.77	
5	329993			7.83	14.21	
	330020			5.58	13.12	
	330036			3.32	5.57	
	330052			4.31	7.97	
	330085			1.34	1.76	
10	330088			4.70	12.46	
	330093			0.44	1.06	
	330100			3.47	4.83	
	330106			2.14	3.61	
	330107			3.17	6.87	
	330120			5.61	11.89	
15	330123			4.50	12.74	
	330208			1.55	7.62	
	330263			13.10	23.38	
	330300			2.81	4.98	
20	330313			3.00	4.41	
	330366			0.67	0.76	
	330372			4.76	11.82	
	330385	AA449749	Hs.182971	karyopherin alpha 5 (importin alpha 6)	2.14	2.15
	330397	D14659	Hs.154387	KIAA0103 gene product	0.40	1.15
25	330468	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	1.11	0.94
	330472	L24203	Hs.82237	ataxia-telangiectasia group D-associated	1.67	1.17
	330478	L38486	Hs.296049	microfibrillar-associated protein 4	0.46	1.07
	330493	M27826	Hs.267319	endogenous retroviral protease	1.07	0.95
	330495	M31328	Hs.71642	guanine nucleotide binding protein (G pr	0.97	0.96
30	330506	M61906	Hs.6241	phosphoinositide-3-kinase, regulatory su	0.17	3.66
	330512	M80563	Hs.81256	S100 calcium-binding protein A4 (calcium	0.60	1.06
	330537	U19765	Hs.2110	zinc finger protein 9 (a cellular retrov	2.81	2.07
	330547	U32989	Hs.183671	tryptophan 2,3-dioxygenase	3.91	1.49
	330551	U39840	Hs.299867	hepatocyte nuclear factor 3, alpha	1.15	1.03
35	330568	U56244		(NONE)	2.83	4.79
	330599	U90437		gb:Human RP1 homolog mRNA, 3'UTR region	2.08	1.54
	330601	U90916	Hs.82845	Homo sapiens cDNA: FLJ21930 fis, clone H	0.89	1.35
	330605	X02419	Hs.77274	plasminogen activator, urokinase	1.87	1.55
	330609	X04741	Hs.76118	ubiquitin carboxyl-terminal esterase L1	1.83	1.30
40	330617	X53587	Hs.85266	integrin, beta 4	1.54	1.15
	330630	X78669	Hs.79088	reticulocalbin 2, EF-hand calcium bindin	1.39	1.19
	330644	Y07755	Hs.38991	S100 calcium-binding protein A2	3.83	1.13
	330650	Z68228	Hs.2340	junction plakoglobin	1.25	0.95
	330660	AA347868	Hs.139293	ESTs, Weakly similar to ALU7_HUMAN ALU S	15.50	29.07
45	330692	AA017045	Hs.6702	ESTs	1.00	1.00
	330707	AA133891	Hs.293690	ESTs	0.20	1.35
	330715	AA233707	Hs.11571	Homo sapiens cDNA FLJ11570 fis, clone HE	0.12	1.40
	330717	AA233926	Hs.52620	integrin, beta 8	6.62	5.42
	330722	AA243560	Hs.34382	ESTs	1.40	1.65
50	330740	AA297746	Hs.22654	Homo sapiens voltage-gated sodium channe	0.27	2.04
	330742	AA400979	Hs.25691	receptor (calcitonin) activity modifying	0.44	0.90
	330744	AA406142	Hs.12393	dTDP-D-glucose 4,6-dehydratase	0.71	3.23
	330751	AA428286	Hs.29643	Homo sapiens cDNA FLJ13103 fis, clone NT	1.66	1.52
	330760	AA448663	Hs.30469	ESTs	0.52	0.90
55	330763	AA450200	Hs.274337	hypothetical protein FLJ20666	0.37	0.97
	330786	D60374	Hs.49136	ESTs, Moderately similar to ALU7_HUMAN A	0.78	0.84
	330790	T48536	Hs.105807	ESTs	0.23	3.17
	330814	AA015730	Hs.265398	ESTs, Weakly similar to transformation-r	0.37	2.07
	330827	AA040332	Hs.12744	ESTs	1.60	1.00
60	330844	AA063037	Hs.66803	ESTs	0.93	1.16
	330901	AA157818	Hs.267319	endogenous retroviral protease	1.02	1.03
	330931	F01443	Hs.284256	hypothetical protein FLJ14033 similar to	0.24	0.88
	330952	H02855	Hs.29567	ESTs	0.08	1.31
	330961	H10998	Hs.7164	a disintegrin and metalloproteinase doma	1.29	1.26
65	330968	H16568	Hs.23748	ESTs	0.48	0.96
	331014	H98597	Hs.30340	hypothetical protein KIAA1165	0.29	0.74
	331046	N65563	Hs.191358	ESTs	0.99	8.56
	331060	N75081	Hs.157148	Homo sapiens cDNA FLJ11883 fis, clone HE	1.24	1.00
	331099	R36671	Hs.83937	hypothetical protein	0.75	1.03
70	331108	R41408	Hs.21983	ESTs	1.00	2.75
	331131	R54797		gb:y987b07.s1 Soares infant brain 1N1B H	6.04	10.68
	331135	R61398	Hs.4197	ESTs	0.80	0.96
	331170	T23461	Hs.159293	ESTs	2.63	4.29
	331180	T32446	Hs.6640	Human DNA sequence from PAC 75N13 on chr	1.78	2.71
75	331183	T40769	Hs.8469	ESTs	1.00	3.01
	331203	T82310		(NONE)	1.70	3.80
	331271	AA059347	Hs.82226	glycoprotein (transmembrane) nmb	1.20	3.19
	331306	AA252079	Hs.63931	dachshund (Drosophila) homolog	0.31	1.30
	331327	AA281076	Hs.109221	ESTs	2.09	2.41
80	331341	AA303125	Hs.23240	Homo sapiens cDNA FLJ13496 fis, clone PL	0.72	2.43
	331359	AA416979	Hs.46901	KIAA1462 protein	0.09	0.91
	331363	AA421562	Hs.91011	anterior gradient 2 (Xenopus laevis) hom	1.02	0.87
	331378	AA448881	Hs.49282	hypothetical protein FLJ11088	1.03	1.23
	331384	AA456001	Hs.93847	NADPH oxidase 4	1.40	1.00
85	331402	AA505135	Hs.44037	ESTs	1.80	3.93
	331422	F10802	Hs.163628	ESTs, Moderately similar to ALU7_HUMAN	1.65	1.89



	331490	N32912	Hs.26813	CDA14	2.48	1.73
	331531	N51343		gb:yz15g04.s1 Soares_multiple_sclerosis_	0.98	1.68
	331547	N54811		gb:od74f04.s1 NCI_CGAP_Ov2 Homo sapiens	3.80	5.75
5	331578	N67960	Hs.249989	ESTs	0.11	0.67
	331589	N71027	Hs.152618	ESTs	1.09	1.38
	331608	N89861	Hs.112110	PTD007 protein	0.93	0.76
	331614	N92293	Hs.240272	EST	0.17	1.34
	331668	W69707	Hs.58030	EST	2.24	3.82
10	331671	W72033	Hs.194695	ras homolog gene family, member I	1.00	1.24
	331676	W79834	Hs.58559	ESTs, Weakly similar to rhotekin [M.musc	0.08	1.07
	331681	W85712	Hs.119571	collagen, type III, alpha 1 (Ehlers-Danl	8.72	4.27
	331692	W93592	Hs.152213	wingless-type MMTV integration site fami	0.94	0.54
	331717	AA190888	Hs.153881	Homo sapiens NY-REN-62 antigen mRNA, par	1.57	1.34
	331718	AA191404	Hs.104072	ESTs	6.80	11.77
15	331811	AA404500	Hs.301570	ESTs	1.10	1.00
	331820	AA405970	Hs.97996	transcription termination factor, mitoc	0.73	0.59
	331831	AA412031	Hs.97901	EST	2.77	4.08
	331852	AA418988	Hs.98314	Homo sapiens mRNA; cDNA DKFZp586L0120 (f	0.23	0.93
20	331943	AA453418	Hs.21275	hypothetical protein FLJ11011	0.36	1.88
	331969	AA460702	Hs.82772	collagen, type XI, alpha 1	1.00	1.00
	331990	AA478102	Hs.139631	ESTs	3.04	3.87
	332002	AA482009	Hs.105104	ESTs	1.19	0.78
	332027	AA489671	Hs.65641	hypothetical protein FLJ20073	1.27	1.03
25	332029	AA489697	Hs.145053	ESTs	0.30	1.62
	332033	AA489840	Hs.251014	EST	2.30	3.70
	332048	AA498019	Hs.201591	ESTs	0.17	0.52
	332071	AA598594	Hs.205293	KIAA1211 protein	1.35	1.23
	332074	AA599012		gb:ae41e11.s1 Gessler Wilms tumor Homo s	0.19	2.00
30	332083	AA600200	Hs.155546	KIAA1080 protein; Golgi-associated, gamm	0.31	1.18
	332085	AA600353	Hs.173933	nuclear factor I/A	0.30	1.50
	332125	AA609861	Hs.312447	ESTs	0.22	0.62
	332177	F10812	Hs.101433	ESTs	8.21	18.03
	332180	H03348	Hs.7327	claudin 1	2.27	1.57
35	332185	H10356	Hs.101689	ESTs	0.09	1.18
	332203	H49388	Hs.317769	EST	8.05	5.02
	332232	N48891	Hs.101915	Stargardt disease 3 (autosomal dominant)	0.78	0.85
	332240	N54803	Hs.324267	ESTs, Weakly similar to putative p150 [	0.96	1.23
	332261	N70294	Hs.269137	ESTs	2.40	3.74
40	332275	R08838	Hs.26530	serum deprivation response (phosphatidyl	0.27	0.75
	332280	R38100	Hs.146381	RNA binding motif protein, X chromosome	0.39	1.88
	332299	R69250	Hs.21201	neclin 3; DKFZP566B0846 protein	5.24	12.76
	332304	R74041	Hs.101539	ESTs	1.44	3.18
	332314	T25862	Hs.101774	hypothetical protein FLJ23045	0.68	1.32
45	332384	M11433	Hs.101850	retinol-binding protein 1, cellular	1.71	0.88
	332434	N75542	Hs.289068	Homo sapiens cDNA FLJ11918 fis, clone HE	0.43	0.86
	332445	T63781	Hs.11112	ESTs	0.68	1.00
	332453	L00205	Hs.111758	keratin 6A	31.54	1.00
	332458	M33493	Hs.250700	trypsin beta 1	0.51	1.00
50	332504	AA053917	Hs.15106	chromosome 14 open reading frame 1	0.79	1.24
	332525	M17252	Hs.278430	cytochrome P450, subfamily XXIA (steroid	0.98	1.70
	332530	M31682	Hs.1735	inhibin, beta B (activin AB beta polypep	0.88	0.66
	332535	N20284	Hs.19280	cysteine-rich motor neuron 1	0.22	1.46
	332539	AA412528	Hs.20183	ESTs, Weakly similar to AF164793 1 prote	0.93	1.49
55	332559	M13955	Hs.166189	cytokeratin 2	0.35	1.13
	332563	N92924	Hs.274407	protease, serine, 16 (thymus)	1.00	1.00
	332565	AA234896	Hs.25272	E1A binding protein p300	0.36	1.05
	332594	AA279313	Hs.3239	methyl CpG binding protein 2 (Rett syndr	0.53	0.59
	332634	S38953	Hs.283750	tenascin XA	0.38	1.16
60	332638	AA283034	Hs.50640	JAK binding protein	1.00	1.70
	332640	AA417152	Hs.5101	protein regulator of cytokinesis 1	6.15	1.16
	332654	AA001296	Hs.288217	hypothetical protein MGC2941	1.50	2.73
	332665	AA223335	Hs.63788	propionyl Coenzyme A carboxylase, beta p	1.20	0.91
	332692	AA496035	Hs.247926	gap junction protein, alpha 5, 40kD (con	0.17	1.12
65	332716	L00058	Hs.79070	v-myc avian myelocytomatosis viral oncog	1.00	1.44
	332736	L13773	Hs.114765	myeloid/lymphoid or mixed-lineage leukem	1.00	1.81
	332758	X93921	Hs.296938	dual specificity phosphatase 7	0.53	0.78
	332781	AA233258	Hs.247112	hypothetical protein FLJ10902	1.44	1.56
	332792				1.70	1.19
70	332816				1.85	2.47
	332858				1.04	1.57
	332906				3.48	8.04
	332911				1.00	1.00
	332912				1.06	4.40
75	332922				1.00	1.00
	332956				0.42	0.88
	332959				1.96	6.34
	332982				0.66	0.99
	332984				0.30	0.78
80	332998				1.47	2.01
	333058				0.47	1.38
	333097				2.14	3.19
	333121				2.76	3.70
	333122				1.92	1.21
85	333123				1.85	1.39
	333138				0.47	0.52



	333139	1.88	0.84
	333140	0.21	0.64
	333221	1.51	1.11
5	333260	0.75	1.01
	333380	6.68	15.75
	333387	4.56	12.61
	333512	5.05	8.01
	333524	2.28	3.98
10	333585	2.31	1.53
	333603	2.23	1.17
	333604	2.51	1.58
	333618	0.52	0.98
	333627	1.44	1.36
15	333628	1.90	1.90
	333650	1.85	2.10
	333678	1.85	2.35
	333750	2.18	5.67
	333763	1.99	2.60
20	333767	1.02	0.96
	333768	1.78	1.65
	333769	2.15	2.13
	333772	1.46	2.53
	333777	1.00	1.42
25	333846	2.99	4.50
	333884	0.47	0.94
	333887	0.50	1.00
	333891	0.43	0.89
	333892	0.51	0.91
30	333904	0.26	1.13
	333906	0.55	0.98
	333948	1.70	2.15
	333954	0.37	1.09
	333966	8.10	14.30
35	333968	0.63	1.38
	334061	4.24	12.30
	334094	1.30	12.03
	334113	4.55	8.63
	334161	0.82	1.59
40	334183	0.47	0.76
	334187	1.36	3.70
	334219	0.69	1.04
	334222	1.88	1.70
	334223	4.72	3.14
45	334239	0.79	0.62
	334255	0.45	1.10
	334333	1.00	3.56
	334378	3.98	5.76
	334382	1.50	1.31
50	334492	3.59	4.75
	334562	5.94	15.40
	334588	8.14	19.53
	334616	1.55	1.56
	334633	5.16	8.07
55	334648	0.59	2.13
	334787	3.70	7.15
	334866	8.13	10.60
	334891	0.32	1.14
	334933	1.00	3.84
60	334934	4.01	7.43
	334945	1.04	2.96
	334967	0.29	1.14
	334990	1.50	1.39
	335015	5.88	18.65
65	335093	0.55	1.75
	335120	4.31	8.01
	335125	0.38	1.97
	335179	1.24	1.98
	335188	0.46	1.47
70	335211	1.61	1.42
	335288	0.73	0.97
	335289	0.20	0.26
	335361	2.18	1.58
	335379	0.50	0.71
75	335414	3.64	14.94
	335416	2.93	3.98
	335496	0.96	0.91
	335497	1.71	1.92
	335548	1.15	2.40
80	335551	3.22	10.54
	335558	3.42	4.89
	335586	5.50	12.75
	335619	2.99	3.07
	335620	3.80	8.29
85	335621	0.28	0.57
	335682	0.46	1.17



	335686	2.55	3.81
	335755	2.24	1.07
	335784	0.20	0.97
5	335814	1.13	1.48
	335815	2.45	3.51
	335823	1.00	4.16
	335835	0.49	1.70
	335851	1.66	1.39
10	335868	2.98	6.43
	335896	0.98	0.99
	335936	12.10	21.93
	335948	1.00	1.64
	335983	1.00	4.21
	335995	0.37	1.17
15	336021	1.04	0.84
	336034	11.40	23.54
	336038	1.19	1.21
	336066	0.54	1.63
20	336107	0.95	0.70
	336205	3.13	6.29
	336275	3.20	10.10
	336292	2.34	3.09
	336331	1.00	1.00
25	336419	0.65	0.79
	336632	2.33	2.16
	336633	2.55	2.23
	336634	2.19	2.03
	336635	2.69	2.48
30	336636	2.13	1.83
	336637	2.43	2.24
	336638	2.31	2.03
	336659	0.60	1.31
	336675	0.31	1.18
35	336684	1.50	1.14
	336694	4.74	7.10
	336716	4.43	6.37
	336721	2.20	0.74
	336798	1.64	2.14
40	336900	6.14	12.73
	336948	1.00	1.00
	337028	1.30	2.09
	337043	4.01	11.53
	337046	1.67	1.84
45	337054	2.78	7.35
	337128	7.20	16.14
	337162	3.45	5.34
	337183	5.72	11.41
	337184	3.72	5.90
50	337192	1.27	1.06
	337194	1.88	1.68
	337229	0.22	1.03
	337268	1.00	3.31
	337299	3.23	5.14
55	337325	2.76	3.72
	337389	5.80	10.42
	337493	2.06	6.30
	337497	7.88	20.29
	337500	3.80	4.48
60	337549	1.66	2.31
	337603	1.27	8.54
	337605	5.76	7.16
	337671	0.73	0.97
	337755	1.54	0.92
65	337786	5.07	9.73
	337809	6.18	12.87
	337862	3.78	12.97
	337871	2.66	8.16
	337958	0.26	1.34
70	338008	1.48	1.12
	338033	2.38	14.59
	338083	0.65	2.16
	338110	1.00	1.61
	338112	5.86	8.25
75	338145	1.70	1.97
	338148	8.07	18.19
	338158	1.30	4.55
	338161	2.58	3.57
	338179	1.00	1.00
80	338182	3.32	4.63
	338189	1.00	3.34
	338197	0.99	1.69
	338199	4.58	7.62
	338215	6.01	15.85
85	338279	0.53	0.95
	338316	20.58	38.66



	338322	3.23	7.39
	338357	4.10	11.39
	338359	10.12	21.59
5	338366	0.69	1.02
	338374	0.40	1.18
	338414	0.47	1.06
	338418	6.12	13.86
	338469	3.09	5.11
10	338501	6.28	10.32
	338506	6.97	12.41
	338523	3.10	5.84
	338549	1.70	2.70
	338561	0.79	0.81
15	338662	1.72	1.46
	338671	0.17	0.91
	338676	2.10	15.86
	338726	1.20	1.09
	338779	0.12	0.57
20	338804	0.99	1.67
	338836	1.00	1.00
	338871	4.30	9.81
	338872	5.02	12.81
	338879	0.23	1.12
25	338937	6.55	12.26
	338966	1.76	5.42
	338993	1.00	2.40
	339047	5.26	10.81
	339100	5.10	6.88
30	339114	1.00	1.70
	339121	1.00	3.75
	339170	10.36	19.67
	339229	4.08	13.48
	339264	2.64	3.83
35	339293	1.73	1.94

TABLE 8B shows the accession numbers for those Pkeys in Table 8A lacking unigenelD's. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number  
CAT number: Gene cluster number  
Accession: Genbank accession numbers

Pkey	CAT number	Accessions
322044	187363_1	AW340926 AA249063 N86075
322060	44320_1	AI341937 AW003063 U34725 AA904742
321430	42705_1	X57414 X57415
321467	43034_1	X13075 X13076
322125	46779_1	R93901 AF075073 R93902
322166	46861_1	H69434 AF085958 H69846
322173	46873_1	H52567 H52557 AF085970 H52164
322178	46882_1	H56535 AF085980 H56712
322179	46885_1	H92891 AF085982 H92777
321577	1615102_1	H84849 H84252 H84260 H86664 H85320
321587	1615333_1	H95531 H95521 H84529
313723	111953_1	AA070412 AA102346 AA081885
320997	627492_1	H22544 H46842 AI204929
322278	47271_1	W69304 AF086283 W69200
321687	218439_1	AA625149 AA313030 AA313052 H97463
313883	129439_1	AA665089 AA135130 AA484059 AA102419 AW877765
322320	47422_1	W79150 AF086419
322339	814584_1	AI668646 AI734214 W17348
314648	293660_1	AW979268 AA878419 AA431342 AA431628
300201	682222_1	AI308300 AI308296
306897	25196_2	AI093967
323155	979809_1	AL120701 AL135041 AL121524
322527	38927_1	AF147359 T58511 T58560
322585	473768_2	W88919 W89125
300362	1574395_1	Z42308 H23514
322635	82296_1	AA005129 AA679084 AA694399
322664	85042_1	AA011522 AA702841 AA011691 AA330797
315454	380580_1	AI239464 AI239473 AA625812 AI208703
322687	37372_1	AF074666 AI110759 AF090902
314852	327472_1	AI903735 AA491283 AI694953 AW976903 AA761362
307783	697809_1	AI347274 AW844024
324072	269032_1	AA381722 AA381829 AW963906 AW963902 AA381242
300627	221345_1	AA488472 W27363 AA317053 BE082689 AW967036 BE079872
323505	196389_1	AW970512 AA280251 AI652287 BE466438 AI650725 AA551854 AA281574 AW571481
315791	403558_1	AA678177 AA677034
324303	233842_1	AL118754 AA333202 H38001
316519	442885_1	AA847835 AA768376
300926	333127_1	AA504860 AA504911



	324580	328264_1	AA492588 AA492498 AA492571
	301882	275087_1	T78054 T79888 AA398185
	324804	398093_1	AI692552 AI393343 AI800510 AI377711 F24263 AA661876
5	324889	1515978_1	D31010 D30991 D31168 D31166 D31465
	302697	43219_1	AJ001409 AJ001410
	302711	45419_1	L08442 D51348
	302742	458_39	L12061
	318499	364430_1	T25451 AA585296 AA585305
10	310624	34624_4	U88896 U88898 AA916056 T03285 AI341594 AI359534 AI634031 U88897
	302847	458_105	X98941 X98942 X98943 X98953 X98949
	304122	77271_5	H28966
	303598	270283_1	AA382814 AA402411 AA412355
	311409	837264_1	AI698839 AI909260 AI909259
15	312094	797889_1	Z78390 T97427
	319312	1540116_1	Z45481 F12393 T74437
	319407	1688823_1	R05329 R01555 R08276
	319425	1689571_1	T82930 R02424 T85145
	320007	229683_1	AA336314 T82938 AA327744 AW967388 AA639967 T10753
20	320018	1815987_1	T83263 T85731 T85730
	319484	1691553_1	T91772 R07257 R07098
	318865	1535937_1	H10818 F07831 Z43072
	312220	1671607_1	N74613 T98756 T98589
	319546	243305_1	R09692 R09414 AA346353
25	312389	902067_1	AI863140 W80703 R43474
	319611	1566863_1	H14957 R56522 R11908
	312437	291472_1	BE080180 AW827313 AW231970 AA995028 AA428584 AW872716 AW892508 AW854593 AA578441 AW975234 AA664937 AA984131
			AA528743 AA552874 AA564758 AW063245 AI267534 AW070190 AW893483 AA770330 AA906928 AA906582 AA758746 AA551717
			AW063311 AA429538
30	311896	579192_1	AW206447 AI248530 AI084433 AI400976 R16553
	319834	112523_1	AA071267 T65940 T64515 AA071334
	321102	80531_1	AA018306 H38925 AA001221
	321158	410938_1	H79670 H47798 AA700289
	321199	212379_1	N34524 AA305071 AW954803 AA502335 AI433430 AI203597 AW026670 AW265323 AW850787 AA317554 AW993643 AW835572
			AW385512 AI334966 W32951 H62656 H53902 R88904 AW835732
35	305528	28832_3	AA769156
	321270	1662057_1	N59537 N78278 R83560
	314126	177666_1	AA226431 AA226569 AA488748
	320714	743644_1	R91883 AI445591
40	306442	AA976899	
	306446	AA977348	
	306458	AA978186	
	306510	AA988546	
	306557	AA994530	
45	306572	AA995686	
	306582	AA996248	
	306656	AI004024	
	306686	AI015615	
	306751	AI032589	
50	308011	AI439473	
	306892	AI092465	
	308106	AI476803	
	308154	AI500600	
	306956	AI125111	
55	306958	AI125152	
	308213	AI557041	
	308216	AI557135	
	308219	AI557246	
	308588	AI718299	
60	308599	AI719893	
	308643	AI745040	
	308673	AI760864	
	308697	AI767143	
	308778	AI811109	
65	308808	AI818289	
	308875	AI832332	
	308886	AI833240	
	308898	AI858845	
	308966	AI870704	
70	308979	AI873111	
	303011	41689_1	AF090405 AF090407 AF090406
	303077	44060_1	AF163305 AF163307 AF163303
	305016	AA626876	
	305034	AA630128	
75	305072	AA641012	
	305148	AA654070	
	305190	AA665955	
	303978	AW513315	
	303990	AW515465	
80	303998	AW516449	
	303999	AW516611	
	305235	AA670480	
	305312	AA700201	
	305413	AA724659	
85	305447	AA737856	
	321244	29327_1	AF068654 AF068656 AF068655



	305614	AA782866	
	305637	AA806124	
	305639	AA806138	
5	305650	AA807709	
	305690	AA813477	
	305728	AA828209	
	305759	AA835353	
	305792	AA845256	
10	307041	AI144243	
	307091	AI167439	
	307181	AI189251	
	305901	AA872968	
	305910	AA875981	
15	307415	AI242118	
	307426	AI243364	
	307517	AI275055	
	307551	AI281556	
	307561	AI282207	
20	307608	AI290295	
	307691	AI318285	
	307730	AI336092	
	307760	AI342387	
	307764	AI342731	
25	307796	AI350556	
	309045	AI910902	
	309051	AI911975	
	307807	AI351799	
	307808	AI351826	
30	307820	AI355761	
	307852	AI365541	
	309122	AI928178	
	309164	AI937761	
	309177	AI951118	
35	307902	AI380462	
	309299	AW003478	
	309303	AW004823	
	309476	AW129368	
	309532	AW151119	
40	309747	AW264889	
	309769	AW272346	
	309799	AW276964	
	309866	AW299916	
45	302679	311853_1	H65022 AA186889
	309923	AW340684	
	309928	AW341418	
	309931	AW341683	
	309933	AW341936	
50	302705	31765_1	U09060 U09061
	302789	34161_1	AJ245067 AJ245070
	304006	AW517947	
	304024	T03036	
	304026	T03160	
	304028	T03266	
55	304046	T54803	
	304061	T61521	
	304063	T62536	
	302802	34487_1	Y08250 Y08245
	304114	R78946	
60	304155	H68696	
	304203	N56929	
	304234	W81608	
	304348	AA179868	
	304430	AA347682	
65	304456	AA411240	
	304521	AA464716	
	304526	AA476427	
	304607	AA513322	
	304735	AA576453	
70	304760	AA580401	
	306015	AA897116	
	306063	AA906316	
	306065	AA906725	
	306104	AA910956	
75	306109	AA911861	
	306242	AA932805	
	306288	AA936900	
	306396	AA970223	
80	330568	NOT_FOUND_entrez	U56244
	330599	15323_-12	U90437
	331131	genbank_R54797	R54797
	331203	NOT_FOUND_entrez	T82310
	331531	genbank_N51343	N51343
	331547	467396_1	AA828597 N54811
85	332074	genbank_AA599012	AA599012



TABLE 8C shows the genomic position for those Pkeys in Table 8A lacking unigene ID's and accession numbers. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

5	Pkey:	Unique number corresponding to an Eos probeset		
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.		
	Strand:	Indicates DNA strand from which exons were predicted.		
10	Nt_position:	Indicates nucleotide positions of predicted exons.		
	Pkey	Ref	Strand	Nt_position
	332792	Dunham, I. et.al.	Plus	73381-73768
	332816	Dunham, I. et.al.	Plus	359844-360030
15	332906	Dunham, I. et.al.	Plus	1923101-1923205
	332911	Dunham, I. et.al.	Plus	1961767-1961858
	332912	Dunham, I. et.al.	Plus	1962120-1962246
	332922	Dunham, I. et.al.	Plus	2009620-2009738
20	332956	Dunham, I. et.al.	Plus	2510528-2510658
	332959	Dunham, I. et.al.	Plus	2518145-2518213
	333138	Dunham, I. et.al.	Plus	3369205-3369323
	333139	Dunham, I. et.al.	Plus	3369495-3369571
	333221	Dunham, I. et.al.	Plus	3978070-3978187
25	333380	Dunham, I. et.al.	Plus	4904775-4904846
	333387	Dunham, I. et.al.	Plus	4910935-4910997
	333512	Dunham, I. et.al.	Plus	5560510-5560564
	333524	Dunham, I. et.al.	Plus	5612620-5612780
	333585	Dunham, I. et.al.	Plus	6234778-6234894
30	333618	Dunham, I. et.al.	Plus	6562391-6562566
	333627	Dunham, I. et.al.	Plus	6620584-6620903
	333628	Dunham, I. et.al.	Plus	6629004-6629233
	333650	Dunham, I. et.al.	Plus	6796852-6797128
	333678	Dunham, I. et.al.	Plus	7068223-7068288
35	333750	Dunham, I. et.al.	Plus	7608165-7608234
	333763	Dunham, I. et.al.	Plus	7692491-7692630
	333767	Dunham, I. et.al.	Plus	7694407-7694623
	333768	Dunham, I. et.al.	Plus	7695440-7695697
	333769	Dunham, I. et.al.	Plus	7696625-7696707
40	333772	Dunham, I. et.al.	Plus	7706773-7706902
	333777	Dunham, I. et.al.	Plus	7746805-7746916
	333846	Dunham, I. et.al.	Plus	8008623-8008757
	333884	Dunham, I. et.al.	Plus	8153960-8154161
	333887	Dunham, I. et.al.	Plus	8154882-8155025
45	333891	Dunham, I. et.al.	Plus	8156437-8156709
	333892	Dunham, I. et.al.	Plus	8156825-8157001
	333948	Dunham, I. et.al.	Plus	8583497-8583627
	333954	Dunham, I. et.al.	Plus	8563186-8563335
	333966	Dunham, I. et.al.	Plus	8655643-8655826
50	333968	Dunham, I. et.al.	Plus	8681004-8681241
	334061	Dunham, I. et.al.	Plus	9686941-9687077
	334094	Dunham, I. et.al.	Plus	9889953-9890105
	334113	Dunham, I. et.al.	Plus	10282459-10282597
	334161	Dunham, I. et.al.	Plus	10599033-10599180
55	334219	Dunham, I. et.al.	Plus	12716160-12716384
	334239	Dunham, I. et.al.	Plus	13056569-13056693
	334333	Dunham, I. et.al.	Plus	13603544-13603657
	334378	Dunham, I. et.al.	Plus	13907239-13907370
	334382	Dunham, I. et.al.	Plus	13915866-13916036
60	334562	Dunham, I. et.al.	Plus	14987847-14987940
	334588	Dunham, I. et.al.	Plus	15032740-15032817
	334616	Dunham, I. et.al.	Plus	15176123-15176470
	334633	Dunham, I. et.al.	Plus	15333206-15333305
	334866	Dunham, I. et.al.	Plus	18872214-18872317
	334891	Dunham, I. et.al.	Plus	19299770-19299944
65	334934	Dunham, I. et.al.	Plus	20103970-20104058
	335015	Dunham, I. et.al.	Plus	20682792-20682945
	335120	Dunham, I. et.al.	Plus	21436286-21436384
	335125	Dunham, I. et.al.	Plus	21441390-21441471
70	335179	Dunham, I. et.al.	Plus	21634405-21634526
	335188	Dunham, I. et.al.	Plus	21669118-21669328
	335211	Dunham, I. et.al.	Plus	21774611-21774680
	335361	Dunham, I. et.al.	Plus	22807292-22807445
	335379	Dunham, I. et.al.	Plus	22899306-22899420
75	335414	Dunham, I. et.al.	Plus	23235546-23235684
	335416	Dunham, I. et.al.	Plus	23237354-23237465
	335496	Dunham, I. et.al.	Plus	24164386-24164545
	335497	Dunham, I. et.al.	Plus	24167666-24167869
	335558	Dunham, I. et.al.	Plus	24740167-24740347
80	335586	Dunham, I. et.al.	Plus	24990333-24990497
	335686	Dunham, I. et.al.	Plus	25439839-25439920
	335784	Dunham, I. et.al.	Plus	25942710-25942792
	335823	Dunham, I. et.al.	Plus	26365925-26366004
	335983	Dunham, I. et.al.	Plus	27938968-27939070
85	335995	Dunham, I. et.al.	Plus	28009044-28009184
	336021	Dunham, I. et.al.	Plus	28686482-28686559



	336034	Dunham, I. et.al.	Plus	29014404-29014590
	336038	Dunham, I. et.al.	Plus	29022963-29023165
	336107	Dunham, I. et.al.	Plus	29987731-29987869
5	336632	Dunham, I. et.al.	Plus	983890-985529
	336633	Dunham, I. et.al.	Plus	985591-986221
	336634	Dunham, I. et.al.	Plus	986296-986670
	336635	Dunham, I. et.al.	Plus	987908-988364
	336636	Dunham, I. et.al.	Plus	988418-989185
10	336637	Dunham, I. et.al.	Plus	989276-990813
	336638	Dunham, I. et.al.	Plus	991906-993240
	336659	Dunham, I. et.al.	Plus	1896402-1896478
	336694	Dunham, I. et.al.	Plus	2420546-2420616
	336721	Dunham, I. et.al.	Plus	3371522-3371586
15	336900	Dunham, I. et.al.	Plus	10236423-10236523
	336948	Dunham, I. et.al.	Plus	12692290-12692381
	337028	Dunham, I. et.al.	Plus	16644817-16644942
	337054	Dunham, I. et.al.	Plus	17821742-17821922
	337162	Dunham, I. et.al.	Plus	23478943-23479145
20	337183	Dunham, I. et.al.	Plus	23943606-23943696
	337184	Dunham, I. et.al.	Plus	23973949-23974016
	337268	Dunham, I. et.al.	Plus	28011979-28012034
	337299	Dunham, I. et.al.	Plus	29022656-29022775
	337389	Dunham, I. et.al.	Plus	31401509-31401579
25	337493	Dunham, I. et.al.	Plus	33330760-33330981
	337549	Dunham, I. et.al.	Plus	34474472-34474531
	337755	Dunham, I. et.al.	Plus	3971764-3971900
	337809	Dunham, I. et.al.	Plus	4449069-4449193
	337871	Dunham, I. et.al.	Plus	5443027-5443101
30	337958	Dunham, I. et.al.	Plus	6969162-6969270
	338008	Dunham, I. et.al.	Plus	7697068-7697236
	338033	Dunham, I. et.al.	Plus	8092128-8092271
	338110	Dunham, I. et.al.	Plus	10384481-10384621
	338112	Dunham, I. et.al.	Plus	10391398-10391600
35	338145	Dunham, I. et.al.	Plus	11386629-11386692
	338148	Dunham, I. et.al.	Plus	11448985-11449085
	338179	Dunham, I. et.al.	Plus	12808775-12808833
	338197	Dunham, I. et.al.	Plus	13638107-13638181
	338279	Dunham, I. et.al.	Plus	16168944-16169091
40	338316	Dunham, I. et.al.	Plus	17089711-17089988
	338322	Dunham, I. et.al.	Plus	17132477-17132547
	338357	Dunham, I. et.al.	Plus	18062184-18062402
	338359	Dunham, I. et.al.	Plus	18074402-18074501
	338366	Dunham, I. et.al.	Plus	18252026-18252189
45	338374	Dunham, I. et.al.	Plus	18371200-18371282
	338414	Dunham, I. et.al.	Plus	19345573-19345660
	338418	Dunham, I. et.al.	Plus	19435506-19435596
	338501	Dunham, I. et.al.	Plus	21244713-21244828
	338506	Dunham, I. et.al.	Plus	21221871-21221953
50	338523	Dunham, I. et.al.	Plus	21509763-21509864
	338662	Dunham, I. et.al.	Plus	24404720-24404899
	338804	Dunham, I. et.al.	Plus	27236005-27236108
	338836	Dunham, I. et.al.	Plus	27792166-27792272
	338879	Dunham, I. et.al.	Plus	28410653-28410734
55	338937	Dunham, I. et.al.	Plus	29160655-29160725
	338993	Dunham, I. et.al.	Plus	30077787-30078184
	339047	Dunham, I. et.al.	Plus	30760793-30760968
	339100	Dunham, I. et.al.	Plus	31141580-31141765
	339114	Dunham, I. et.al.	Plus	31456454-31456519
60	339121	Dunham, I. et.al.	Plus	31583467-31583536
	339170	Dunham, I. et.al.	Plus	32216399-32216527
	339293	Dunham, I. et.al.	Plus	33223671-33223819
	332858	Dunham, I. et.al.	Minus	1339607-1339397
	332982	Dunham, I. et.al.	Minus	2628296-2628109
65	332984	Dunham, I. et.al.	Minus	2632606-2632457
	332998	Dunham, I. et.al.	Minus	2711704-2711565
	333058	Dunham, I. et.al.	Minus	3028925-3028811
	333097	Dunham, I. et.al.	Minus	3204124-3204036
	333121	Dunham, I. et.al.	Minus	3308446-3308358
70	333122	Dunham, I. et.al.	Minus	3309596-3309531
	333123	Dunham, I. et.al.	Minus	3310817-3310749
	333140	Dunham, I. et.al.	Minus	3377220-3376309
	333260	Dunham, I. et.al.	Minus	4308400-4308304
	333603	Dunham, I. et.al.	Minus	6466335-6465727
75	333604	Dunham, I. et.al.	Minus	6467090-6466768
	333904	Dunham, I. et.al.	Minus	8217374-8217261
	333906	Dunham, I. et.al.	Minus	8218238-8218063
	334183	Dunham, I. et.al.	Minus	11832582-11832508
	334187	Dunham, I. et.al.	Minus	11921456-11921205
80	334222	Dunham, I. et.al.	Minus	12732417-12732289
	334223	Dunham, I. et.al.	Minus	12734365-12734269
	334255	Dunham, I. et.al.	Minus	13200776-13200692
	334492	Dunham, I. et.al.	Minus	14478333-14478172
	334648	Dunham, I. et.al.	Minus	15363301-15363222
85	334787	Dunham, I. et.al.	Minus	16299093-16298937
	334933	Dunham, I. et.al.	Minus	20078117-20077991



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	334945	Dunham, I. et.al.	Minus	20138885-20138637
	334967	Dunham, I. et.al.	Minus	20173311-20173218
	334990	Dunham, I. et.al.	Minus	20341159-20341087
5	335093	Dunham, I. et.al.	Minus	21297367-21297214
	335288	Dunham, I. et.al.	Minus	22304275-22303770
	335289	Dunham, I. et.al.	Minus	22305950-22305708
	335548	Dunham, I. et.al.	Minus	24662773-24662673
	335551	Dunham, I. et.al.	Minus	24679828-24678961
10	335619	Dunham, I. et.al.	Minus	25082677-25082498
	335620	Dunham, I. et.al.	Minus	25092561-25092434
	335621	Dunham, I. et.al.	Minus	25098878-25098767
	335682	Dunham, I. et.al.	Minus	25421215-25421093
	335755	Dunham, I. et.al.	Minus	25763806-25763747
15	335814	Dunham, I. et.al.	Minus	26320043-26319845
	335815	Dunham, I. et.al.	Minus	26320518-26320421
	335835	Dunham, I. et.al.	Minus	26393311-26393245
	335851	Dunham, I. et.al.	Minus	26604863-26604742
	335868	Dunham, I. et.al.	Minus	26711437-26711300
	335896	Dunham, I. et.al.	Minus	26977639-26977558
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	335948	Dunham, I. et.al.	Minus	27555924-27555788
	336066	Dunham, I. et.al.	Minus	29241080-29240842
	336205	Dunham, I. et.al.	Minus	30477456-30477311
25	336275	Dunham, I. et.al.	Minus	32086675-32086536
	336292	Dunham, I. et.al.	Minus	32818035-32817927
	336331	Dunham, I. et.al.	Minus	33594527-33594371
	336419	Dunham, I. et.al.	Minus	34052568-34052445
	336675	Dunham, I. et.al.	Minus	2020758-2020664
30	336684	Dunham, I. et.al.	Minus	2158060-2157993
	336716	Dunham, I. et.al.	Minus	3259952-3259862
	336798	Dunham, I. et.al.	Minus	5888954-5888757
	337043	Dunham, I. et.al.	Minus	17407330-17407251
	337046	Dunham, I. et.al.	Minus	17610892-17610821
35	337128	Dunham, I. et.al.	Minus	22215251-22215034
	337192	Dunham, I. et.al.	Minus	24591853-24591771
	337194	Dunham, I. et.al.	Minus	24610510-24610359
	337229	Dunham, I. et.al.	Minus	26716579-26716481
	337325	Dunham, I. et.al.	Minus	30015948-30015800
40	337497	Dunham, I. et.al.	Minus	33371317-33371258
	337500	Dunham, I. et.al.	Minus	33376212-33376158
	337603	Dunham, I. et.al.	Minus	1299296-1299194
	337605	Dunham, I. et.al.	Minus	1346555-1346397
	337671	Dunham, I. et.al.	Minus	3260634-3260547
45	337786	Dunham, I. et.al.	Minus	4133203-4133081
	337862	Dunham, I. et.al.	Minus	5347658-5347650
	338083	Dunham, I. et.al.	Minus	9318438-9318301
	338158	Dunham, I. et.al.	Minus	11794465-11794343
	338161	Dunham, I. et.al.	Minus	12124716-12124658
50	338182	Dunham, I. et.al.	Minus	12824919-12824827
	338189	Dunham, I. et.al.	Minus	12878594-12878478
	338199	Dunham, I. et.al.	Minus	13760865-13760780
	338215	Dunham, I. et.al.	Minus	14055447-14055355
	338469	Dunham, I. et.al.	Minus	20520387-20520242
55	338549	Dunham, I. et.al.	Minus	22049171-22049081
	338561	Dunham, I. et.al.	Minus	22311966-22311856
	338671	Dunham, I. et.al.	Minus	24508421-24508346
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	338726	Dunham, I. et.al.	Minus	25926206-25925618
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	338871	Dunham, I. et.al.	Minus	28301708-28301611
	338872	Dunham, I. et.al.	Minus	28300921-28300790
	338966	Dunham, I. et.al.	Minus	29614876-29614749
	339229	Dunham, I. et.al.	Minus	32722330-32722199
55	339264	Dunham, I. et.al.	Minus	32975145-32975053
	325228	6381940	Plus	2630-2694
	325235	6381943	Minus	162154-162264
	329588	3962484	Plus	1169-1619
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	325328	5866875	Plus	86780-86854
	325340	6017033	Minus	166656-166819
	325373	5866920	Minus	1136686-1136777
	325367	5866920	Minus	922881-922958
75	325389	5866921	Plus	239672-239759
	325436	5866939	Minus	29778-29907
	325498	5866967	Plus	173372-173930
	325471	6017034	Minus	289268-289342
	325557	6056302	Plus	50921-51050
30	325559	6249595	Minus	118590-119172
	325560	6249595	Minus	133794-133981
	325569	6249599	Plus	79927-80217
	325587	6682462	Plus	126724-126967
	325585	6682462	Plus	73476-73574
35	325597	5866992	Plus	1065020-1065089
	325639	5867002	Plus	253525-253608



	325739	5867038	Minus	205138-205269
	325740	5867038	Minus	207533-207690
	325792	6469828	Minus	1018-1176
5	325735	6552447	Minus	269122-269190
	325685	6682468	Plus	117397-117483
	325686	6682468	Plus	118337-118439
	325819	6682490	Minus	130314-130370
	329764	6048195	Minus	109733-109968
10	329703	6065793	Minus	139994-140138
	329643	6448539	Plus	53403-53537
	329816	6624888	Minus	70296-70423
	329860	6687260	Minus	163474-163605
	325883	5867087	Plus	22498-22663
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	325925	5867124	Plus	115749-115962
	325932	5867127	Plus	7369-7441
	325941	5867133	Minus	64228-64402
	325969	5867153	Plus	101911-102081
20	325971	5867153	Plus	105841-106035
	329993	4567166	Minus	101307-101434
	330020	6671887	Plus	172397-172491
	326163	5867168	Minus	7831-8035
	326274	5867171	Minus	410289-410404
25	326025	5867176	Plus	70854-70915
	326046	5867182	Minus	62668-62825
	326099	5867186	Minus	661381-661510
	326108	5867187	Minus	23784-23903
	326165	5867208	Minus	62787-62929
30	326189	5867212	Plus	69288-69413
	326204	5867218	Minus	148088-148200
	326230	5867230	Minus	301868-301972
	330052	4567182	Plus	352560-352963
	330036	6042048	Plus	117120-117216
35	326360	5867293	Plus	13627-13844
	326589	5867320	Plus	22760-22919
	326393	5867341	Plus	41702-41841
	326505	5867435	Minus	8818-8949
	326515	5867439	Plus	36683-36809
40	326592	6138928	Plus	23689-23828
	330107	6015249	Minus	100091-100282
	330106	6015249	Minus	99443-99778
	330100	6015253	Plus	21166-21301
	330093	6015278	Plus	1043-1199
45	330088	6015293	Plus	37517-37638
	330085	6015302	Minus	59613-59770
	330120	6671864	Minus	127553-127656
	330123	6671869	Minus	35311-35406
	326742	5867611	Minus	95187-95248
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	326818	6117831	Minus	15199-15309
	326720	6552456	Plus	84525-84677
	326770	6598307	Minus	513603-513668
	326692	6682502	Plus	117697-117899
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	326983	5867657	Minus	16023-16581
	326991	5867660	Plus	18147-18339
	326936	6004446	Minus	10217-10357
	326964	6469836	Plus	75340-75456
60	327040	6531965	Plus	783670-783817
	327053	6531965	Plus	2247267-2247437
	327075	6531965	Plus	4041318-4041431
	327085	6531965	Plus	4734947-4735069
	327036	6531965	Plus	319951-320040
65	327130	6531976	Plus	20247-22343
	327156	5866841	Minus	2462-2620
	327288	5867481	Plus	48583-48773
	327332	5867516	Minus	56361-56532
	327220	5867525	Minus	65701-65781
70	327224	5867534	Plus	188468-188544
	327321	6249562	Minus	99745-99836
	327361	6552412	Minus	61013-62130
	327396	5867743	Plus	8702-8820
	327414	5867750	Plus	102461-102586
75	327442	5867759	Plus	111483-111618
	327467	5867772	Plus	88030-88151
	327473	5867775	Plus	75101-75181
	327483	5867783	Plus	181573-181662
	327377	5867793	Minus	37610-37676
80	327562	5867804	Minus	343989-344474
	327568	5867811	Minus	46152-46287
	327606	6004463	Plus	200262-200495
	327611	5867868	Minus	175063-175392
	327642	5867891	Minus	2513-2743
85	327654	5867910	Minus	97564-97710
	327734	5867940	Minus	31003-31583



	327775	5867964	Minus	130791-130871
	327796	5867982	Plus	85267-85405
	327840	6249578	Minus	73065-73206
5	330208	6013599	Plus	66517-66931
	330263	6671884	Minus	101503-101634
	328004	5867993	Minus	157407-157887
	328101	5868020	Plus	289920-290014
	328100	5868020	Minus	263545-263635
10	328113	5868024	Minus	80378-80491
	328157	5868064	Plus	73326-73615
	328196	5868080	Minus	16551-16729
	328197	5868081	Minus	42133-42438
	327940	5868197	Minus	95240-95428
	327984	5868216	Plus	66611-66677
15	328021	5902482	Plus	713478-714590
	328068	6117819	Plus	253903-254022
	328264	6381912	Plus	55086-55404
	330300	2905862	Minus	3246-3302
20	328608	5868222	Minus	87770-87953
	328600	5868229	Minus	38889-40010
	328616	5868239	Plus	293920-294224
	328623	5868246	Minus	120020-120126
	328632	5868247	Plus	76734-76853
25	328666	5868254	Minus	778-901
	328698	5868264	Minus	625555-625633
	328700	5868264	Plus	764089-764203
	328708	5868271	Minus	68114-68854
	328735	5868289	Plus	89389-89455
30	328743	5868289	Plus	274638-274726
	328806	5868324	Plus	29408-29684
	328299	5868366	Minus	149708-149889
	328342	5868383	Plus	59955-60094
	328365	5868387	Minus	270724-270798
35	328369	5868388	Plus	75371-75583
	328381	5868392	Plus	662758-662848
	328451	5868425	Minus	217275-217336
	328481	5868449	Minus	8987-9180
	328500	5868464	Plus	59098-59481
40	328530	5868482	Plus	334973-335406
	328664	6004473	Plus	1193739-1193866
	328861	6381928	Minus	108317-108403
	328908	5868493	Plus	117002-117059
	328933	5868500	Plus	771755-771889
45	328934	5868500	Plus	846342-846448
	328949	6456765	Minus	43552-43619
	330313	6042030	Minus	33642-33775
	329005	5868542	Plus	85470-85673
	330366	2944106	Plus	151837-151914
50	330372	6580495	Minus	317461-317688
	329033	5868561	Minus	5390-5479
	329037	5868562	Minus	32466-32562
	329067	5868591	Minus	146417-147652
	329134	5868679	Plus	29959-30018
55	329157	5868687	Minus	145940-146155
	329178	5868704	Plus	179177-179463
	329192	5868716	Plus	166936-167020
	329194	5868716	Minus	304450-304559
	329204	5868720	Minus	3050-3190
60	329224	5868728	Plus	27422-27664
	329228	5868728	Minus	50118-50287
	329288	5868771	Plus	25554-26299
	329337	5868806	Minus	467155-467222
	329011	6682532	Plus	48658-48741



TABLE 9A: Potential Therapeutic, Diagnostic and Prognostic targets for Therapy of Lung Cancer

Table 9A shows about 1312 genes up-regulated in lung tumors (including squamous cell carcinomas, adenocarcinomas, small cell carcinomas, granulomatous and carcinoid tumors) relative to normal body tissues. These genes were selected from about 59680 probesets on the Eos/Affymetrix Hu03 Genechip array.

Table 9B show the accession numbers for those Pkey's lacking UnigenelD's for table 9A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Table 9C show the genomic positioning for those Pkey's lacking UnigenelD's and accession numbers in table 9A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Pkey: Unique Eos probeset identifier number  
 ExAccn: Exemplar Accession number, Genbank accession number  
 UnigenelD: Unigene number  
 Unigene Title: Unigene gene title  
 R1: Average of lung tumors (including squamous cell carcinomas, adenocarcinomas, small cell carcinomas, granulomatous and carcinoid tumors) divided by the average of normal lung samples  
 R2: Average of non-malignant lung disease samples (including bronchitis, emphysema, fibrosis, atelectasis, asthma) divided by the average of normal lung samples

Pkey	ExAccn	UnigenelD	Unigene Title	R1	R2
400195			NM_007057*:Homo sapiens ZW10 interactor	1.00	1.00
400205			NM_006265*:Homo sapiens RAD21 (S. pombe)	15.80	396.00
400220			Eos Control	2.28	2.84
400277			Eos Control	7.68	9.72
400285			Eos Control	1.00	1.00
400288	X06256	Hs.149609	integrin, alpha 5 (fibronectin receptor,	1.04	2.24
400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	132.45	4.00
400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	43.86	74.00
400301	X03635	Hs.1657	estrogen receptor 1	1.00	1.00
400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	1.75	1.65
400328	X87344	Hs.180062	transporter 2, ATP-binding cassette, sub	0.87	1.80
400419	AF084545		Target	156.55	253.00
400512			NM_030878*:Homo sapiens cytochrome P450,	1.00	2.00
400517	AF242388		lengsin	3.67	87.00
400560			NM_030878*:Homo sapiens cytochrome P450,	1.00	1.00
400664			NM_002425:Homo sapiens matrix metallopro	20.26	45.00
400665			NM_002425:Homo sapiens matrix metallopro	1.36	1.07
400666			NM_002425:Homo sapiens matrix metallopro	3.26	3.22
400749			NM_003105*:Homo sapiens sortilin-related	1.00	91.00
400763			Target Exon	7.63	24.00
401027			Target Exon	1.00	1.00
401093			C12000586*:gij6330167[dbj]BA86477.1 (A	1.00	155.00
401203			Target Exon	1.00	86.00
401212			C12000457*:gij7512178[pir]T30337 polypr	1.00	400.00
401411			ENSP00000247172*:HYPOTHETICAL 126.2 kDa	1.00	72.00
401435			C14000397*:gij7499898[pir]T33295 hypoth	1.00	64.00
401464	AF039241		histone deacetylase 5	3.82	49.00
401714			ENSP00000241802*:CDNA FLJ11007 FIS, CLON	2.02	40.00
401747			Homo sapiens keratin 17 (KRT17)	128.43	68.00
401760			Target Exon	1.74	35.00
401780			NM_005557*:Homo sapiens keratin 16 (foca	26.47	10.50
401781			Target Exon	10.33	4.61
401785			NM_002275*:Homo sapiens keratin 15 (KRT1	4.13	2.70
401797			Target Exon	1.44	2.10
401961			NM_021626:Homo sapiens serine carboxypep	1.41	1.86
401985	AF053004		class I cytokine receptor	1.00	177.00
401994			Target Exon	61.84	47.00
402075			ENSP00000251056*:Plasma membrane calcium	1.00	1.00
402260			NM_001436*:Homo sapiens fibrillarlin (FBL	1.58	1.39
402265			Target Exon	2.09	35.00
402297			Target Exon	1.00	92.00
402408			NM_030920*:Homo sapiens hypothetical pro	28.87	13.00
402420			C1000823*:gij10432400[emb]CAC10290.1 (A	1.00	1.44
402674			Target Exon	7.44	243.00
402802			NM_001397:Homo sapiens endothelin conver	1.00	70.00
402994			NM_002463*:Homo sapiens myxovirus (influ	1.37	1.43
403137			NM_005381*:Homo sapiens nucleolin (NCL),	1.00	19.00
403306	NM_006825		transmembrane protein (63kD), endoplasmic	1.00	43.00
403329			Target Exon	1.00	61.00
403381			ENSP00000231844*:Ecotropic virus integra	1.00	119.00
403478			NM_022342:Homo sapiens kinesin protein 9	28.13	136.00
403485			C3001813*:gij12737279[ref]XP_012163.1 (k	20.23	76.00
403627			Target Exon	6.30	29.33
403715			Target Exon	1.30	35.00
404044			ENSP00000237855*:DJ398G3.2 (NOVEL PROTEI	1.00	54.00
404076			NM_016020*:Homo sapiens CGI-75 protein (	14.29	91.00
404101			C8000950:gij423560[pir]A47318 RNA-bindin	1.00	1.00
404140			NM_006510:Homo sapiens ret finger protei	1.42	1.44
404165			ENSP00000244562:NRH dehydrogenase [quino	1.00	54.00
404185			Target Exon	1.00	117.00
404210			NM_005936:Homo sapiens myeloid/lymphoid	5.93	13.77
404253			NM_021058*:Homo sapiens H2B histone fami	1.00	1.00



	404287		C6001909:gi 704441 dbj BAA18909.1  (D298	29.71	42.00
	404298		C6001238*:gi 121715 sp P26697 GTA3_CHICK	1.30	1.00
	404347		Target Exon	1.00	1.00
5	404440		NM_021048:Homo sapiens melanoma antigen,	1.00	15.00
	404721		NM_005596*:Homo sapiens nuclear factor I	1.00	60.00
	404794	NM_000078	cholesterol ester transfer protein, plas	1.07	1.38
	404854		Target Exon	1.61	2.01
	404877		NM_005365:Homo sapiens melanoma antigen,	1.00	1.00
10	404927		Target Exon	1.00	1.00
	404996		Target Exon	1.00	1.00
	405449		CY000047*:gi 11427234 ref XP_009399.1  z	1.00	1.00
	405568		NM_031413*:Homo sapiens cat eye syndrome	1.00	78.00
	405572		Target Exon	0.76	1.14
15	405646		C12000200:gi 4557225 ref NP_000005.1  al	1.01	1.28
	405676	BE336714	cytochrome c-1	1.13	2.89
	405770		NM_002362:Homo sapiens melanoma antigen,	45.52	37.00
	405932		C15000305:gi 3806122 gb AAC69198.1  (AF0	1.99	1.99
	406137		NM_000179*:Homo sapiens mutS (E. coli) h	2.77	2.38
	406360		Target Exon	1.00	35.00
20	406399		NM_003122*:Homo sapiens serine protease	1.00	39.00
	406467		Target Exon	1.00	1.00
	406621	X57809 Hs.181125	immunoglobulin lambda locus	1.41	1.74
	406642	AJ245210	gb:Homo sapiens mRNA for immunoglobulin	2.16	3.91
25	406663	U24683 Hs.293441	immunoglobulin heavy constant mu	2.07	2.93
	406671	AA129547 Hs.285754	met proto-oncogene (hepatocyte growth fa	15.00	51.00
	406673	M34996 Hs.198253	major histocompatibility complex, class	0.98	3.09
	406676	X58399 Hs.81221	Human L2-9 transcript of unrearranged im,	1.30	1.53
	406678	U77534	gb:Human clone 1A11 immunoglobulin varia	1.33	1.45
30	406685	M18728	gb:Human nonspecific crossreacting antig	1.46	2.85
	406687	M31126 Hs.272822	pregnancy specific beta-1-glycoprotein 9	8.61	8.50
	406690	M29540 Hs.220529	carcinoembryonic antigen-related cell ad	226.37	350.00
	406698	X03068 Hs.73931	major histocompatibility complex, class	1.01	2.52
	406815	AA833930 Hs.288036	tRNA isopentenylpyrophosphate transferas	20.25	32.00
35	406861	AA609784	major histocompatibility complex, class	0.75	1.91
	406964	M21305	gb:Human alpha satellite and satellite 3	38.15	1114.00
	406967	M24349	gb:Human parathyroid hormone-like protei	1.00	1.00
	406974	M57293	gb:Human parathyroid hormone-related pep	1.00	1.00
	407103	AA424881 Hs.256301	hypothetical protein MGC13170	1.77	1.10
40	407128	R83312 Hs.237260	EST	1.00	1.00
	407137	T97307	gb:ye53h05.s1 Soares fetal liver spleen	142.70	135.00
	407168	R45175 Hs.117183	ESTs	2.16	18.00
	407239	AA076350 Hs.67846	leukocyte immunoglobulin-like receptor,	1.10	1.57
	407242	M18728	gb:Human nonspecific crossreacting antig	1.12	2.85
45	407244	M10014 Hs.75431	fibrinogen, gamma polypeptide	3.24	15.38
	407289	AA135159 Hs.203349	Homo sapiens cDNA FLJ12149 fis, clone MA	3.53	3.68
	407300	AA102616 Hs.120769	gb:zn43e07.s1 Stratagene HeLa cell s3 93	19.74	73.00
	407366	AF026942 Hs.271530	gb:Homo sapiens cig33 mRNA, partial sequ	0.06	8.25
	407378	AA299264 Hs.57776	ESTs, Moderately similar to I38022 hypot	1.00	26.00
50	407430	AF169351	gb:Homo sapiens protein tyrosine phospho	1.00	25.00
	407453	AJ132087	gb:Homo sapiens mRNA for axonemal dynein	1.00	75.00
	407577	AW131324 Hs.246759	hypothetical protein MGC12538	1.00	1.00
	407634	AW016569 Hs.136414	UDP-GlcNAc:betaGal beta-1,3-N-acetylgluc	111.20	228.00
	407710	AW022727 Hs.23616	ESTs	1.00	28.00
55	407720	AB037776 Hs.38002	KIAA1355 protein	1.89	1.31
	407746	AK001962	hypothetical protein FLJ11100	1.00	1.00
	407756	AA116021 Hs.38260	ubiquitin specific protease 18	4.51	5.00
	407758	D50915 Hs.38365	KIAA0125 gene product	1.00	28.00
	407782	AA608956 Hs.112619	ESTs, Moderately similar to PURKINJE CEL	0.97	1.14
60	407788	BE514982 Hs.38991	S100 calcium-binding protein A2	7.88	3.83
	407790	AI027274 Hs.288941	Homo sapiens cDNA FLJ14866 fis, clone PL	3.63	42.00
	407811	AW190902 Hs.40098	cysteine knot superfamily 1, BMP antagon	89.96	109.00
	407839	AA045144 Hs.161566	ESTs	173.91	108.00
	407944	R34008 Hs.239727	desmocollin 2	111.30	70.00
65	408000	L11690 Hs.620	bullous pemphigoid antigen 1 (230/240kD)	151.17	8.00
	408031	AA081395 Hs.42173	Homo sapiens cDNA FLJ10366 fis, clone NT	9.91	93.00
	408063	BE086548 Hs.42346	calcineurin-binding protein calsarcin-1	195.78	231.00
	408070	AW148852	gb:xf05d05.x1 NCI_CGAP_Bm35 Homo sapien	1.00	1.00
70	408101	AW968504 Hs.123073	CDC2-related protein kinase 7	37.84	61.00
	408122	AI432652 Hs.42824	hypothetical protein FLJ10718	0.85	1.71
	408212	AA297567 Hs.43728	hypothetical protein	5.88	7.91
	408243	Y00787 Hs.624	interleukin 8	4.27	9.98
	408349	BE546947 Hs.44276	homeo box C10	3.79	3.46
	408353	BE439838 Hs.44298	mitochondrial ribosomal protein S17	1.88	1.65
75	408354	AI382803 Hs.159235	ESTs	1.00	73.00
	408369	R38438 Hs.182575	solute carrier family 15 (H??? transport	1.41	16.50
	408380	AF123050 Hs.44532	diubiquitin	15.19	37.22
	408482	NM_000676 Hs.45743	adenosine A2b receptor	1.65	1.19
	408522	AI541214 Hs.46320	Small proline-rich protein SPRK [human,	1.98	1.24
80	408536	AW381532 Hs.135188	ESTs	1.55	1.50
	408545	AW235405 Hs.253690	ESTs	1.00	1.00
	408572	AA055611 Hs.226568	ESTs, Moderately similar to ALU4_HUMAN A	1.00	44.00
	408633	AW963372 Hs.46677	PRO2000 protein	107.16	56.00
	408660	AA525775	ESTs, Moderately similar to PC4259 ferri	1.00	1.00
85	408761	AA057264 Hs.238936	ESTs, Weakly similar to (define not ava	52.24	141.00
	408771	AW732573 Hs.47584	potassium voltage-gated channel, delayed	3.05	109.00



	408783	AF192522	Hs.47701	NPC1 (Niemann-Pick disease, type C1, gen	1.02	1.07
	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,	41.19	61.00
	408805	H69912	Hs.48269	vaccinia related kinase 1	24.67	45.00
5	408841	AW438865	Hs.256862	ESTs	1.00	58.00
	408873	AL046017	Hs.182278	calmodulin 2 (phosphorylase kinase, delt	1.00	89.00
	408908	BE296227	Hs.250822	serine/threonine kinase 15	7.76	1.00
	408992	AA059325	Hs.71642	guanine nucleotide binding protein (G pr	1.00	1.00
	408996	AI979168	Hs.344096	glycoprotein (transmembrane) nmb	3.71	5.50
10	409015	BE389387	Hs.49767	NM_004553:Homo sapiens NADH dehydrogenas	1.44	1.24
	409038	T97490	Hs.50002	small inducible cytokine subfamily A (Cy	4.28	5.32
	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	112.42	195.00
	409077	AA401369	Hs.190721	ESTs	1.00	17.00
	409093	BE243834	Hs.50441	CGI-04 protein	2.02	1.93
15	409103	AF251237	Hs.112208	XAGE-1 protein	80.44	40.00
	409142	AL136877	Hs.50758	SMC4 (structural maintenance of chromoso	14.87	6.00
	409187	AF154830	Hs.50966	carbamoyl-phosphate synthetase 1, mitoch	1.00	1.00
	409228	AI654298	Hs.271695	ESTs, Weakly similar to 2109260A B cell	1.22	1.00
	409234	AI879419	Hs.27206	ESTs	1.00	1.00
20	409268	AA625304	Hs.187579	ESTs	11.90	23.00
	409269	AA576953	Hs.22972	hypothetical protein FLJ13352	1.00	1.00
	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	168.91	35.00
	409404	BE220053	Hs.129056	ESTs	1.00	1.00
	409420	Z15008	Hs.54451	laminin, gamma 2 (nicein (100kD), kalini	79.74	96.00
25	409430	R21945	Hs.346735	splicing factor, arginine/serine-rich 5	1.45	2.10
	409446	AI561173	Hs.67688	ESTs	1.00	4.00
	409506	NM_006153	Hs.54589	NCK adaptor protein 1	3.97	28.00
	409522	AA075382		gb:zm87b03.s1 Stratagene ovarian cancer	15.98	141.00
	409582	AA401369	Hs.190721	ESTs	1.00	17.00
30	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibito	292.12	79.00
	409705	M37762	Hs.56023	brain-derived neurotrophic factor	1.00	82.00
	409719	AI769160	Hs.108681	Homo sapiens brain tumor associated prot	1.00	1.00
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	0.12	18.12
	409744	AW676258	Hs.56265	Homo sapiens mRNA; cDNA DKFpZ586P2321 (f	20.75	51.00
35	409757	NM_001898	Hs.123114	cystatin SN	22.46	15.80
	409866	AW502152		gb:UI-HF-BR0p-ajr-f-11-0-UI.r1 NIH_MGC_5	1.00	1.00
	409893	AW247090	Hs.57101	minichromosome maintenance deficient (S.	1.50	1.09
	409902	AI337658	Hs.156351	ESTs	25.92	50.00
	409935	AW511413	Hs.278025	ESTs	2.63	2.11
40	409956	AW103364	Hs.727	inhibin, beta A (activin A, activin AB a	2.17	4.01
	409958	NM_001523	Hs.57697	hyaluronan synthase 1	0.91	2.07
	410001	AB041036	Hs.57771	kallikrein 11	1.04	2.28
	410032	BE065985		gb:RC3-BT0319-120200-014-a09 BT0319 Homo	1.00	58.00
	410037	AB020725	Hs.58009	KIAA0918 protein	1.00	34.00
45	410044	BE566742	Hs.58169	highly expressed in cancer, rich in leuc	1.00	1.00
	410048	W76467	Hs.58218	proline oxidase homolog	1.03	1.44
	410076	T05387	Hs.7991	ESTs	1.12	1.50
	410102	AW248508	Hs.279727	Homo sapiens cDNA FLJ14035 fis, clone HE	9.89	1.00
	410153	BE311926	Hs.15830	hypothetical protein FLJ12691	1.00	1.00
50	410166	AK001376	Hs.59346	hypothetical protein FLJ10514	1.00	1.00
	410193	AJ132592	Hs.59757	zinc finger protein 281	42.01	51.00
	410274	AA381807	Hs.61762	hypoxia-inducible protein 2	1.72	1.32
	410309	BE043077	Hs.278153	ESTs	1.00	2.00
	410340	AW182833	Hs.112188	hypothetical protein FLJ13149	32.08	75.00
55	410348	AW182663	Hs.95469	ESTs	1.00	1.00
	410407	X66839	Hs.63287	carbonic anhydrase IX	1.40	1.11
	410418	D31382	Hs.63325	transmembrane protease, serine 4	4.30	2.03
	410438	AB037756	Hs.45207	hypothetical protein KIAA1335	1.00	18.00
	410553	AW016824	Hs.255527	hypothetical protein MGC14128	1.34	1.04
60	410555	W27235	Hs.64311	a disintegrin and metalloproteinase doma	23.99	1.41
	410561	BE540255	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone H	10.04	1.00
	410681	AW246890	Hs.65425	calbindin 1, (28kD)	10.88	18.92
	410781	AI375672	Hs.165028	ESTs	1.00	57.00
	411027	AF072099	Hs.67846	leukocyte immunoglobulin-like receptor,	1.62	3.78
65	411074	X60435	Hs.68137	adenylate cyclase activating polypeptide	1.00	1.15
	411089	AA456454		cell division cycle 2-like 1 (PITSLRE pr	1.56	1.58
	411152	BE069199		gb:QV3-BT0379-010300-105-g03 BT0379 Homo	1.00	84.00
	411248	AA551538	Hs.334605	Homo sapiens cDNA FLJ14408 fis, clone HE	1.82	1.45
70	411252	AB018549	Hs.69328	MD-2 protein	7.32	12.74
	411263	BE297802	Hs.69360	kinesin-like 6 (mitotic centromere-assoc	3.44	2.55
	411365	M76477	Hs.289082	GM2 ganglioside activator protein	1.35	2.02
	411402	BE297855	Hs.69855	NRAS-related gene	1.00	46.00
	411573	AB029000	Hs.70823	KIAA1077 protein	11.40	11.35
75	411579	AC005258	Hs.70830	U6 snRNA-associated Sm-like protein LSm7	1.08	1.90
	411617	AA247994	Hs.90063	neurocalcin delta	1.74	2.57
	411732	AA059325	Hs.71642	guanine nucleotide binding protein (G pr	1.02	1.00
	411773	NM_006799	Hs.72026	protease, serine, 21 (testisin)	1.34	2.19
	411789	AF245505	Hs.72157	Adican	2.19	2.79
	411800	N39342	Hs.103042	microtubule-associated protein 1B	23.34	34.00
80	411945	AL033527	Hs.92137	v-myc avian myelocytomatosis viral oncog	1.00	8.00
	412115	AK001763	Hs.73239	hypothetical protein FLJ10901	2.07	1.64
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	118.48	92.00
	412276	BE262621	Hs.73798	macrophage migration inhibitory factor (	1.98	1.49
	412464	T78141	Hs.22826	ESTs, Weakly similar to I55214 salivary	1.16	1.34
85	412530	AA766268	Hs.266273	hypothetical protein FLJ13346	41.52	84.00
	412537	AL031778		nuclear transcription factor Y, alpha	17.90	55.00



	412659	AW753865	Hs.74376	olfactomedin related ER localized protei	14.65	47.00
	412719	AW016610	Hs.816	ESTs	382.46	128.00
	412723	AA648459	Hs.335951	hypothetical protein AF301222	54.90	1.00
5	412811	H06382		ESTs	1.00	11.00
	412817	AL037159	Hs.74619	proteasome (prosome, macropain) 26S subu	1.63	1.42
	412863	AA121673	Hs.59757	zinc finger protein 281	17.63	56.00
	412924	BE018422	Hs.75258	H2A histone family, member Y	1.00	22.00
	413004	T35901	Hs.75117	interleukin enhancer binding factor 2, 4	2.19	2.05
10	413011	AW068115	Hs.821	biglycan	1.22	1.88
	413048	M93221	Hs.75182	mannose receptor, C type 1	0.30	6.23
	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	3.43	8.71
	413129	AF292100	Hs.104613	RP42 homolog	4.67	4.77
	413142	M81740	Hs.75212	ornithine decarboxylase 1	1.92	2.59
15	413223	AI732182	Hs.191866	ESTs	5.73	27.00
	413248	T64858	Hs.21433	hypothetical protein DKFZp547J036	0.99	1.06
	413273	U75679	Hs.75257	stem-loop (histone) binding protein	1.00	18.00
	413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	1.10	1.09
	413281	AA861271	Hs.222024	transcription factor BMAL2	95.94	69.00
20	413364	BE536218	Hs.137516	fidgetin-like 1	1.00	1.00
	413385	M34455	Hs.840	indoleamine-pyrrole 2,3 dioxygenase	0.95	2.09
	413409	AI638418	Hs.1440	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	1.00	1.00
	413453	AA129640	Hs.128065	ESTs	1.00	31.00
	413527	BE250788	Hs.179882	hypothetical protein FLJ12443	1.08	1.46
25	413554	AA319146	Hs.75426	secretogranin II (chromogranin C)	79.15	114.00
	413573	AI733859	Hs.149089	ESTs	1.00	1.00
	413582	AW295647	Hs.71331	hypothetical protein MGC5350	8.80	10.00
	413597	AW302885	Hs.117183	ESTs	1.00	1.00
30	413690	BE157489		gb:RC1-HT0375-120200-011-e06 HT0375 Homo	1.00	1.00
	413691	AB023173	Hs.75478	ATPase, Class VI, type 11B	3.16	2.32
	413719	BE439580	Hs.75498	small inducible cytokine subfamily A (Cy	2.88	9.52
	413753	U17760	Hs.75517	laminin, beta 3 (nicein (125kD), kalinin	144.10	108.00
	413801	M62246	Hs.35406	ESTs, Highly similar to unnamed protein	1.00	17.00
	413833	Z15005	Hs.75573	centromere protein E (312kD)	1.00	1.00
35	413882	AA132973	Hs.184492	ESTs	64.24	148.00
	413926	AA133338	Hs.54310	ESTs	1.00	67.00
	413943	AW294416	Hs.144687	Homo sapiens cDNA FLJ12981 fis, clone NT	43.42	42.00
	413995	BE048146	Hs.75671	syntaxin 1A (brain)	1.23	1.11
40	414035	Y00630	Hs.75716	serine (or cysteine) proteinase inhibito	2.02	2.51
	414142	AW368397	Hs.334485	Homo sapiens cDNA FLJ14438 fis, clone HE	1.00	102.00
	414180	AI863304	Hs.120905	Homo sapiens cDNA FLJ11448 fis, clone HE	6.92	77.00
	414245	BE148072	Hs.75850	WAS protein family, member 1	1.00	1.00
	414275	AW970254	Hs.889	Charot-Leyden crystal protein	1.00	59.00
45	414317	BE263280	Hs.75888	phosphogluconate dehydrogenase	1.52	1.73
	414334	AA824298	Hs.21331	hypothetical protein FLJ10036	1.78	1.72
	414341	D80004	Hs.75909	KIAA0182 protein	33.90	151.00
	414368	W70171	Hs.75939	uridine monophosphate kinase	171.60	97.00
	414416	AW409985	Hs.76084	hypothetical protein MGC2721	2.32	1.85
	414430	AI346201	Hs.76118	ubiquitin carboxyl-terminal esterase L1	226.15	66.00
50	414570	Y00285	Hs.76473	insulin-like growth factor 2 receptor	1.64	1.98
	414618	AI204600	Hs.96978	hypothetical protein MGC10764	1.87	72.00
	414675	R79015	Hs.296281	interleukin enhancer binding factor 1	1.51	1.39
	414683	S78296	Hs.76888	hypothetical protein MGC12702	43.61	64.00
	414696	AF002020	Hs.76918	Niemann-Pick disease, type C1	28.63	71.00
55	414711	AI310440	Hs.288735	Homo sapiens cDNA FLJ13522 fis, clone PL	14.86	42.00
	414718	H95348	Hs.107987	ESTs	1.00	5.00
	414732	AW410976	Hs.77152	minichromosome maintenance deficient (S.	1.64	1.44
	414747	U30872	Hs.77204	centromere protein F (350/400kD, mitotin	65.01	74.00
	414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	130.35	121.00
60	414774	X02419	Hs.77274	plasminogen activator, urokinase	2.24	2.19
	414806	D14694	Hs.77329	phosphatidylserine synthase 1	1.63	1.53
	414809	AI434699	Hs.77356	transferrin receptor (p90, CD71)	1.97	2.60
	414812	X72755	Hs.77367	monokine induced by gamma interferon	3.48	10.60
	414825	X06370	Hs.77432	epidermal growth factor receptor (avian	103.22	143.00
65	414839	X63692	Hs.77462	DNA (cytosine-5)-methyltransferase 1	1.80	1.69
	414883	AA926960		CDC28 protein kinase 1	14.29	10.06
	414907	X90725	Hs.77597	polo (Drosophila)-like kinase	1.95	2.20
	414914	U49844	Hs.77613	ataxia telangiectasia and Rad3 related	3.00	2.90
70	414945	BE076358	Hs.77667	lymphocyte antigen 6 complex, locus E	1.02	1.21
	414972	BE263782	Hs.77695	KIAA0008 gene product	1.00	1.00
	415014	AW954064	Hs.24951	ESTs	1.42	2.84
	415091	AL044872	Hs.77910	3-hydroxy-3-methylglutaryl-Coenzyme A sy	1.00	30.00
	415138	C18356	Hs.295944	tissue factor pathway inhibitor 2	34.72	107.00
75	415227	AW821113	Hs.72402	ESTs	1.87	49.00
	415238	R37780	Hs.21422	ESTs	1.00	1.00
	415263	AA948033	Hs.130853	ESTs	1.00	1.00
	415295	R41450	Hs.6546	ESTs	1.00	1.00
80	415339	NM_015156	Hs.78398	KIAA0071 protein	51.18	166.00
	415669	NM_005025	Hs.78589	serine (or cysteine) proteinase inhibito	30.84	63.00
	415674	BE394784	Hs.78596	proteasome (prosome, macropain) subunit,	1.48	1.39
	415709	AA649850	Hs.278558	ESTs	1.00	1.00
	415735	AA704162	Hs.120811	ESTs, Weakly similar to I38022 hypotheti	1.00	72.00
	415799	AA653718	Hs.225841	DKFZP434D193 protein	6.23	31.00
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	24.30	1.00
85	415857	AA866115	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	32.51	35.00
	415989	AI267700		ESTs	78.89	1.00



	416018	AW138239	Hs.78977	proprotein convertase subtilisin/kexin t	1.00	1.00
	416065	BE267931	Hs.78996	proliferating cell nuclear antigen	3.35	2.32
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (	39.03	3.00
5	416177	AA174069	Hs.187607	ESTs	1.00	9.00
	416178	AI808527	Hs.192822	serologically defined breast cancer anti	3.83	3.76
	416208	AW291168	Hs.41295	ESTs, Weakly similar to MUC2_HUMAN MUCIN	3.67	1.00
	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h	9.70	1.00
	416239	AL038450	Hs.48948	ESTs	83.87	129.00
10	416250	AA581386	Hs.73452	hypothetical protein MGC10791	1.96	2.12
	416322	BE019494	Hs.79217	pyrroline-5-carboxylate reductase 1	2.08	1.73
	416423	H54375	Hs.268921	ESTs	1.00	89.00
	416448	L13210	Hs.79339	lectin, galactoside-binding, soluble, 3	1.28	1.54
	416498	U33632	Hs.79351	potassium channel, subfamily K, member 1	27.29	67.00
	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	53.29	51.00
15	416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	9.96	5.00
	416722	AA354604	Hs.122546	hypothetical protein FLJ23017	3.68	33.00
	416819	U77735	Hs.80205	pim-2 oncogene	1.59	1.84
	416936	N21352	Hs.42987	ESTs, Weakly similar to S21348 probable	1.00	1.00
20	417034	NM_006183	Hs.80962	neurotensin	1.00	1.00
	417061	AI675944	Hs.188691	Homo sapiens cDNA FLJ12033 fis, clone HE	32.95	156.00
	417079	U65590	Hs.81134	interleukin 1 receptor antagonist	3.91	4.93
	417218	AA129547	Hs.285754	met proto-oncogene (hepatocyte growth fa	1.00	51.00
	417233	W25005	Hs.24395	small inducible cytokine subfamily B (Cy	3.38	2.05
25	417308	H60720	Hs.81892	KIAA0101 gene product	82.94	25.36
	417315	AI080042	Hs.180450	ribosomal protein S24	106.61	121.00
	417324	AW265494		ESTs	1.20	1.28
	417366	BE185289	Hs.1076	small proline-rich protein 1B (cornifin)	8.97	3.27
	417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor	2.59	1.82
30	417428	N87579	Hs.278871	gb:LL2030F Human fetal heart, Lambda ZAP	1.00	52.00
	417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	304.75	173.00
	417466	AI681547	Hs.59457	hypothetical protein FLJ22127	1.24	1.34
	417512	AI979168	Hs.344096	glycoprotein (transmembrane) nmb	2.14	5.50
	417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated	2.66	1.68
35	417542	J04129	Hs.82269	progesterone-associated endometrial prote	1.28	1.35
	417576	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	42.76	51.00
	417715	AW969587	Hs.86366	ESTs	6.35	2.75
	417720	AA205625	Hs.208067	ESTs	113.31	56.00
	417791	AW965339	Hs.111471	ESTs	39.98	16.00
40	417830	AW504786	Hs.122579	hypothetical protein FLJ10461	2.61	31.00
	417866	AW067903	Hs.82772	collagen, type XI, alpha 1	2.35	2.44
	417900	BE250127	Hs.82906	CDC20 (cell division cycle 20, S. cerevi	1.52	1.11
	417933	X02308	Hs.82962	thymidylate synthetase	4.74	2.55
	417944	AU077196	Hs.82985	collagen, type V, alpha 2	3.61	5.21
45	417975	AA641836	Hs.30085	hypothetical protein FLJ23186	12.49	38.00
	417991	AA731452	Hs.190008	ESTs	1.00	26.00
	418004	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	3.02	2.12
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	187.59	1.00
	418054	NM_002318	Hs.83354	lysyl oxidase-like 2	2.85	2.63
50	418057	NM_012151	Hs.83363	coagulation factor VIII-associated (intr	1.54	1.69
	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	6.82	5.22
	418140	BE613836	Hs.83551	microfibrillar-associated protein 2	1.26	1.46
	418203	X54942	Hs.83758	CDC28 protein kinase 2	134.19	144.00
	418207	C14685	Hs.34772	ESTs	1.00	1.00
55	418216	AA662240	Hs.283099	AF15q14 protein	64.66	61.00
	418236	AW994005	Hs.337534	ESTs	18.53	147.00
	418249	H89226	Hs.34892	KIAA1323 protein	30.53	106.00
	418281	U09550	Hs.1154	oviductal glycoprotein 1, 120kD (mucin 9	1.00	3.00
	418283	S79895	Hs.83942	calhepsin K (pseudosynostosis)	3.96	5.16
60	418300	AI433074	Hs.86682	Homo sapiens cDNA: FLJ21578 fis, clone C	3.18	2.91
	418322	AA284166	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK	11.96	6.68
	418327	U70370	Hs.84136	paired-like homeodomain transcription fa	9.23	2.22
	418345	AJ001696	Hs.241407	serine (or cysteine) proteinase inhibito	1.00	1.00
	418379	AA218940	Hs.137516	fidgetin-like 1	21.68	44.00
65	418397	NM_001269	Hs.84746	chromosome condensation 1	1.00	8.00
	418403	D86978	Hs.84790	KIAA0225 protein	16.91	18.98
	418462	BE001596	Hs.85266	integrin, beta 4	1.56	1.16
	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	3.22	2.38
	418506	AA084248	Hs.85339	G protein-coupled receptor 39	2.66	2.22
70	418526	BE019020	Hs.85838	solute carrier family 16 (monocarboxylic	2.04	2.21
	418538	BE244323	Hs.85951	exportin, tRNA (nuclear export receptor	1.33	37.00
	418543	NM_005329	Hs.85962	hyaluronan synthase 3	1.04	1.23
	418574	N28754		M-phase phosphoprotein 9	48.60	85.00
	418592	X99226	Hs.284153	Fanconi anemia, complementation group A	18.24	26.00
75	418641	BE243136	Hs.86947	a disintegrin and metalloproteinase doma	1.19	1.41
	418661	NM_001949	Hs.1189	E2F transcription factor 3	29.05	43.00
	418663	AK001100	Hs.41690	desmocollin 3	112.17	19.00
	418678	NM_001327	Hs.87225	cancer/testis antigen	1.18	1.10
	418686	Z36830	Hs.87268	annexin A8	1.54	1.98
	418689	AI360883	Hs.274448	hypothetical protein FLJ11029	1.19	1.04
80	418712	Z42183		gb:HSC0BF041 normalized infant brain cDN	1.00	12.00
	418727	AA227609	Hs.94834	ESTs	1.00	49.00
	418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino	49.85	1.00
	418819	AA228776	Hs.191721	ESTs	1.00	140.00
	418830	BE513731	Hs.88959	hypothetical protein MGC4816	20.97	23.00
85	418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C (CFTR	57.09	35.00



	418971	AA360392	Hs.87113	ESTs	1.00	12.00
	418973	AA233056	Hs.191518	ESTs	4.89	28.00
	419078	M93119	Hs.89584	insulinoma-associated 1	1.00	10.00
5	419079	AW014836	Hs.18844	ESTs	1.09	1.98
	419080	AW150835	Hs.18878	hypothetical protein FLJ21620	2.06	1.68
	419088	AI538323	Hs.52620	integrin, beta 8	15.60	51.00
	419092	J05581	Hs.89503	mucin 1, transmembrane	1.11	1.83
	419121	AA374372	Hs.89626	parathyroid hormone-like hormone	1.00	1.00
10	419171	NM_002846	Hs.89655	protein tyrosine phosphatase, receptor t	1.10	1.14
	419183	U60669	Hs.89663	cytochrome P450, subfamily XXIV (vitamin	1.00	1.00
	419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy	3.18	2.43
	419288	AA256106	Hs.87507	ESTs	1.00	34.00
	419335	AW960146	Hs.284137	hypothetical protein FLJ12888	1.00	8.00
	419354	M62839	Hs.1252	apolipoprotein H (beta-2-glycoprotein I)	22.63	54.00
15	419359	AL043202	Hs.90073	chromosome segregation 1 (yeast homolog)	2.50	1.98
	419423	D26488	Hs.90315	KIAA0007 protein	1.00	7.00
	419443	D62703		gb:HUM316G10B Clontech human aorta polyA	1.00	12.00
	419452	U36335	Hs.90572	PTK7 protein tyrosine kinase 7	1.64	1.84
	419474	AW968619	Hs.155849	ESTs	13.63	62.00
20	419485	AA489023	Hs.99807	ESTs, Weakly similar to unnamed protein	4.27	2.26
	419488	AA316241	Hs.90691	nucleophosmin/nucleoplasmin 3	3.66	3.63
	419502	AU076704	Hs.93002	fibrinogen, A alpha polypeptide	13.05	115.00
	419539	AF070590	Hs.90869	Homo sapiens clones 24622 and 24623 mRNA	74.60	117.00
25	419556	U29615	Hs.91093	chitinase 1 (chitotriosidase)	1.47	4.98
	419569	AI971651	Hs.91143	jagged 1 (Alagille syndrome)	1.00	4.00
	419594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	94.30	94.00
	419703	AI793257	Hs.128151	ESTs	15.26	50.00
	419721	NM_001650	Hs.286650	aquaporin 4	1.00	191.00
30	419729	AA586442	Hs.21411	gb:no53a03.s1 NCI_CGAP_SS1 Homo sapiens	1.00	59.00
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	2.02	1.08
	419745	AF042001	Hs.93005	slug (chicken homolog), zinc finger prot	1.00	1.00
	419752	AA249573	Hs.152618	ESTs, Moderately similar to ZN91_HUMAN Z	29.87	77.00
	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	50.99	214.00
35	419936	AI792788		gb:ol91d05.y5 NCI_CGAP_Kid5 Homo sapiens	1.00	1.00
	419937	AB040959	Hs.93836	DKFZP434N014 protein	1.64	2.47
	419983	W55956	Hs.94030	Homo sapiens mRNA; cDNA DKFZp586E1624 (f	15.72	94.00
	420005	AW271106	Hs.133294	ESTs	3.15	1.43
	420047	AI478658	Hs.94631	brefeldin A-inhibited guanine nucleotide	12.45	39.00
40	420058	AK001423	Hs.94694	Homo sapiens cDNA FLJ10561 fis, clone NT	1.00	117.00
	420162	BE378432	Hs.95577	cyclin-dependent kinase 4	1.43	1.21
	420251	AW374968	Hs.348112	Human DNA sequence from clone RP5-1103G7	2.35	3.23
	420259	AF004884	Hs.96253	calcium channel, voltage-dependent, P/Q	0.77	1.15
	420281	AI623693	Hs.323494	ESTs	45.04	54.00
45	420309	AW043637	Hs.21766	ESTs, Weakly similar to ALU5_HUMAN ALU S	49.22	31.00
	420332	NM_001756	Hs.1305	serine (or cysteine) proteinase inhibito	0.05	2.82
	420380	AA640891	Hs.102406	ESTs	0.99	2.74
	420462	AF050147	Hs.97932	chondromodulin 1 precursor	1.00	1.00
	420520	AK001978	Hs.98510	similar to rab11-binding protein	49.74	133.00
50	420552	AK000492	Hs.98806	hypothetical protein	94.65	88.00
	420560	AW207748	Hs.59115	ESTs	1.00	17.00
	420610	AI683183	Hs.99348	distal-less homeo box 5	1.00	13.00
	420689	H79979	Hs.88678	ESTs	50.09	95.00
	420721	AA927802	Hs.159471	ZAP3 protein	1.00	31.00
55	420759	T11832	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	1.00	48.00
	420783	AI659838	Hs.99923	lectin, galactoside-binding, soluble, 7	3.04	1.25
	420900	AL045633	Hs.44269	ESTs	2.24	7.00
	420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	1.00	8.00
	421002	AF116030	Hs.100932	transcription factor 17	1.00	27.00
60	421027	AA761198	Hs.55254	ESTs	2.87	38.00
	421037	AI684808	Hs.197653	ESTs	1.00	46.00
	421041	N36914	Hs.14691	ESTs, Moderately similar to I38022 hypot	1.00	98.00
	421073	NM_004689	Hs.101448	metastasis associated 1	1.34	1.46
	421110	AJ250717	Hs.1355	cathepsin E	119.47	427.00
65	421133	AA401369	Hs.190721	ESTs	1.10	17.00
	421150	AI913562	Hs.189902	ESTs	1.45	1.63
	421155	H87879	Hs.102267	lysyl oxidase	1.00	15.00
	421307	BE539976	Hs.103305	Homo sapiens mRNA; cDNA DKFZp434B0425 (f	1.37	1.10
	421316	AA287203	Hs.324728	SMA5	1.00	21.00
70	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	1.92	3.94
	421451	AA291377	Hs.50831	ESTs	5.89	14.00
	421474	U76362	Hs.104637	solute carrier family 1 (glutamate trans	1.46	1.76
	421506	BE302796	Hs.105097	thymidine kinase 1, soluble	1.56	1.08
	421508	NM_004833	Hs.105115	absent in melanoma 2	5.11	5.23
75	421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialyltransferase I, I	1.00	3.00
	421524	AA312082	Hs.105445	GDNF family receptor alpha 1	2.63	10.58
	421526	AL080121	Hs.105460	DKFZP564O0823 protein	1.46	1.88
	421552	AF026692	Hs.105700	secreted frizzled-related protein 4	30.21	50.32
	421574	AJ000152	Hs.105924	defensin, beta 2	1.67	1.74
80	421582	AI910275		trefoil factor 1 (breast cancer, estroge	1.23	1.00
	421633	AF121860	Hs.106260	sorting nexin 10	1.00	116.00
	421659	NM_014459	Hs.106511	protocadherin 17	0.05	6.33
	421677	H64092	Hs.38282	ESTs	1.31	1.42
	421753	BE314828	Hs.107911	ATP-binding cassette, sub-family B (MDR/	1.41	1.20
85	421773	W69233	Hs.112457	ESTs	1.12	1.14
	421777	BE562088	Hs.108196	HSPC037 protein	1.97	1.29



	421800	AA298151	Hs.222969	ESTs	1.03	1.30
	421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR	1.88	1.59
	421896	N62293	Hs.45107	ESTs	11.84	22.80
5	421928	AF013758	Hs.109643	polyadenylate binding protein-interactin	45.89	90.00
	421931	NM_000814	Hs.1440	gamma-aminobutyric acid (GABA) A recepto	1.13	1.49
	421948	L42583	Hs.334309	keratin 6A	51.83	20.25
	421975	AW961017	Hs.6459	hypothetical protein FLJ11856	1.17	1.15
	422026	U80736	Hs.110826	trinucleotide repeat containing 9	1.00	52.00
10	422094	AF129535	Hs.272027	F-box only protein 5	67.61	62.00
	422095	AI868872	Hs.282804	hypothetical protein FLJ22704	4.37	2.34
	422109	S73265	Hs.1473	gastrin-releasing peptide	4.18	95.50
	422128	AW881145		gb:QV0-OT0033-010400-182-a07 OT0033 Homo	40.89	71.00
	422129	AU076635	Hs.1478	serine (or cysteine) proteinase inhibito	1.13	1.38
	422134	AW179019	Hs.112110	mitochondrial ribosomal protein L42	41.59	96.00
15	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	2.37	1.10
	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias	3.29	1.68
	422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	4.93	5.73
	422282	AF019225	Hs.114309	apolipoprotein L	1.49	1.71
20	422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis	25.99	10.91
	422310	AA316622	Hs.98370	cytochrome P450, subfamily IIS, polypept	1.54	1.41
	422311	AF073515	Hs.114948	cytokine receptor-like factor 1	1.15	1.78
	422330	D30783	Hs.115263	epiregulin	1.00	112.00
	422364	AF067800	Hs.115515	C-type (calcium dependent, carbohydrate-	9.39	60.00
25	422406	AF025441	Hs.116206	Opa-interacting protein 5	18.33	53.00
	422424	AI186431	Hs.296638	prostate differentiation factor	1.71	3.21
	422440	NM_004812	Hs.116724	aldo-keto reductase family 1, member B10	47.53	32.00
	422487	AJ010901	Hs.198267	mucin 4, tracheobronchial	73.68	35.54
	422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	173.97	26.00
30	422515	AW500470	Hs.117950	multifunctional polypeptide similar to S	4.68	2.92
	422656	AI870435	Hs.1569	LIM homeobox protein 2	1.00	1.00
	422737	M26939	Hs.119571	collagen, type III, alpha 1 (Ehlers-Danl	3.89	4.55
	422756	AA441787	Hs.119689	glycoprotein hormones, alpha polypeptide	1.05	1.46
	422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	3.88	1.53
35	422809	AK001379	Hs.121028	hypothetical protein FLJ10549	99.56	53.00
	422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	1.69	3.17
	422938	NM_001809	Hs.1594	centromere protein A (17kD)	70.46	61.00
	422956	BE545072	Hs.122579	ECT2 protein (Epithelial cell transformi	77.74	3.00
	422960	AW890487	Hs.63984	cadherin 13, H-cadherin (heart)	5.88	8.55
40	422963	AA401369	Hs.190721	ESTs	171.41	17.00
	422976	AU076657	Hs.1600	chaperonin containing TCP1, subunit 5 (e	2.12	1.62
	422981	AF026445	Hs.122752	TATA box binding protein (TBP)-associate	10.49	35.00
	422986	AA319777	Hs.221974	ESTs	12.40	32.47
	423034	AL119930		gb:DKFZp761A092_r1 761 (synonym: hamy2)	16.41	60.00
45	423049	X59373	Hs.188023	ESTs, Moderately similar to HXDA_HUMAN H	1.00	1.00
	423081	AF262992	Hs.123159	sperm associated antigen 4	1.82	2.96
	423184	NM_004428	Hs.1624	ephrin-A1	1.14	1.53
	423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys	2.14	1.69
	423248	AA380177	Hs.125845	ribulose-5-phosphate-3-epimerase	7.18	14.00
50	423309	BE006775	Hs.126782	sushi-repeat protein	21.90	64.00
	423361	AW170055	Hs.47628	ESTs	1.00	1.00
	423453	AW450737	Hs.128791	CGI-09 protein	55.52	66.00
	423511	AF036329	Hs.129715	gonadotropin-releasing hormone 2	0.88	1.17
	423516	AB007933	Hs.129729	ligand of neuronal nitric oxide synthase	1.76	5.40
55	423551	AA327598	Hs.233785	ESTs	3.54	4.33
	423554	M90516	Hs.1674	glutamine-fructose-6-phosphate transamin	1.00	50.00
	423575	C18863	Hs.163443	Homo sapiens cDNA FLJ11576 fis, clone HE	38.88	70.00
	423624	AI807408	Hs.166368	ESTs	1.00	67.00
	423634	AW959908	Hs.1690	heparin-binding growth factor binding pr	76.02	1.00
60	423642	AW452650	Hs.157148	hypothetical protein MGC13204	19.14	58.00
	423662	AA642452	Hs.130881	B-cell CLL/lymphoma 11A (zinc finger pro	3.61	13.57
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	240.73	40.00
	423698	AA329796	Hs.1098	DKFZp434J1813 protein	1.00	59.00
	423725	AJ403108	Hs.132127	hypothetical protein LOC57822	4.20	1.00
65	423761	NM_006194	Hs.132576	paired box gene 9	1.00	1.00
	423787	AJ295745	Hs.236204	nuclear pore complex protein	7.18	6.64
	423816	AF151064		hypothetical protein	1.00	44.00
	423826	U20325	Hs.1707	cocaine- and amphetamine-regulated trans	1.00	1.00
70	423849	AL157425	Hs.133315	Homo sapiens mRNA; cDNA DKFZp761J1324 (f	1.00	1.00
	423887	AL080207	Hs.134585	DKFZP434G232 protein	1.00	1.00
	423934	U89995	Hs.159234	forkhead box E1 (thyroid transcription f	31.33	31.00
	423954	AW753164	Hs.288604	KIAA1632 protein	5.81	10.87
	423961	D13666	Hs.136348	osteoblast specific factor 2 (fascilin	3.55	3.30
	424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	233.42	68.00
75	424016	AW163729	Hs.6140	hypothetical protein MGC15730	0.93	1.01
	424028	AF055084	Hs.153692	Homo sapiens cDNA FLJ14354 fis, clone Y7	21.30	52.00
	424046	AF027866	Hs.138202	serine (or cysteine) proteinase inhibito	1.00	1.00
	424086	AI351010	Hs.102267	lysyl oxidase	21.91	70.00
	424098	AF077374	Hs.139322	small proline-rich protein 3	137.82	54.00
80	424120	T80579	Hs.290270	ESTs	1.00	1.00
	424165	AW582904	Hs.142255	islet amyloid polypeptide	1.00	34.00
	424200	AA337221		gb:EST41944 Endometrial tumor Homo sapie	13.06	48.00
	424279	L29306	Hs.171814	tryptophan hydroxylase (tryptophan 5-mon	1.00	1.00
	424308	AW975531	Hs.154443	minichromosome maintenance deficient (S.	164.58	87.00
	424326	NM_014479	Hs.145296	disintegrin protease	53.72	302.00
85	424340	AA339036	Hs.7033	ESTs	0.88	1.15



	424351	BE622117	Hs.145567	hypothetical protein	0.93	1.03
	424364	AW383226	Hs.201189	ESTs, Weakly similar to G01763 atrophin-	7.02	3.24
	424381	AA285249	Hs.146329	protein kinase Chk2	95.55	92.00
5	424411	NM_005209	Hs.146549	crystallin, beta A2	1.63	3.25
	424420	BE614743	Hs.146688	prostaglandin E synthase	1.63	1.33
	424441	X14850	Hs.147097	H2A histone family, member X	1.82	1.29
	424502	AF242388	Hs.149585	lengsin	1.00	1.00
	424503	X06256	Hs.149609	Integrin, alpha 5 (fibronectin receptor,	1.02	2.24
10	424513	BE385864	Hs.149894	mitochondrial translational initiation f	1.00	17.00
	424539	L02911	Hs.150402	Activin A receptor, type I (ACVR1) (ALK	32.46	108.00
	424568	AF005418	Hs.150595	cytochrome P450, subfamily XXVIA, polype	3.40	2.58
	424602	AK002055	Hs.151046	hypothetical protein FLJ11193	31.87	25.00
	424629	M90656	Hs.151393	glutamate-cysteine ligase, catalytic sub	3.58	2.37
15	424645	NM_014682	Hs.151449	KIAA0535 gene product	1.00	1.00
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	2.12	2.23
	424717	AW992292	Hs.152213	wingless-type MMTV integration site fami	1.00	1.00
	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT	56.19	12.00
	424840	D79987	Hs.153479	extra spindle poles, S. cerevisiae, homo	2.65	1.30
20	424867	AI024860	Hs.153591	Not56 (D. melanogaster)-like protein	1.23	1.05
	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	21.35	1.00
	424979	D87989	Hs.154073	UDP-galactose transporter related	1.36	1.35
	424999	AW953120		gb:EST365190 MAGE resequences, MAGB Homo	1.24	1.41
	425048	H05468	Hs.164502	ESTs	1.00	11.00
25	425057	AA826434	Hs.1619	achaete-scute complex (Drosophila) homol	7.46	87.00
	425081	X74794	Hs.154443	minichromosome maintenance deficient (S.	2.52	3.82
	425118	AI0076611	Hs.154672	methylene tetrahydrofolate dehydrogenase	4.84	4.03
	425169	NM_004341	Hs.154868	carbamoyl-phosphate synthetase 2, aspart	3.62	2.73
	425202	AW962282	Hs.152049	ESTs, Weakly similar to I38022 hypotheti	1.00	53.00
30	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypotheti	100.77	44.00
	425236	AW067800	Hs.155223	stanniocalcin 2	3.30	2.90
	425245	AI751768	Hs.155314	KIAA0095 gene product	1.91	2.32
	425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin	1.41	1.49
	425266	J00077	Hs.155421	alpha-fetoprotein	1.00	68.00
35	425274	BE281191	Hs.155462	minichromosome maintenance deficient (mi	1.97	1.63
	425322	U63630	Hs.155637	protein kinase, DNA-activated, catalytic	141.49	123.00
	425349	AA425234	Hs.79886	ribose 5-phosphate isomerase A (ribose 5	1.00	84.00
	425371	D49441	Hs.155981	mesothelin	0.87	1.59
	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	14.90	5.76
40	425420	BE536911	Hs.234545	hypothetical protein NUF2R	1.00	1.00
	425424	NM_004954	Hs.157199	ELKL motif kinase	10.58	9.74
	425483	AF231022	Hs.158159	FAT tumor suppressor (Drosophila) homolo	1.74	1.40
	425566	AW162943	Hs.250618	UL16 binding protein 2	1.49	1.14
	425580	L11144	Hs.1907	galanin	53.29	233.00
45	425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen	33.45	1.00
	425692	D90041	Hs.155956	N-acetyltransferase 1 (arylamine N-acety	1.00	55.00
	425695	NM_005401	Hs.159238	protein tyrosine phosphatase, non-recept	1.00	10.00
	425734	AF056209	Hs.159396	peptidylglycine alpha-amidating monooxyg	1.00	41.00
	425776	U25128	Hs.159499	parathyroid hormone receptor 2	1.00	48.00
50	425810	AI923627	Hs.31903	ESTs	27.39	98.00
	425811	AL039104	Hs.159557	karyopherin alpha 2 (RAG cohort 1, Impor	1.99	1.58
	425849	AI077288	Hs.296323	serum/glucocorticoid regulated kinase	71.16	3.42
	425852	AK001504	Hs.159651	death receptor 6, TNF superfamily member	1.35	1.34
	426067	AA401369	Hs.190721	ESTs	1.01	17.00
55	426088	AF038007	Hs.166196	ATPase, Class I, type 8B, member 1	26.26	47.00
	426215	AW067800	Hs.155223	stanniocalcin 2	1.91	2.90
	426227	U67058	Hs.154299	Human proteinase activated receptor-2 mR	22.40	25.00
	426269	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp566A1046 (f	1.00	1.00
	426283	NM_003937	Hs.169139	kynureninase (L-kynurenine hydrolase)	91.39	229.00
60	426329	AL389951	Hs.271623	nucleoporin 50kD	4.34	4.08
	426427	M86699	Hs.169840	TTK protein kinase	7.02	1.00
	426432	AF001601	Hs.169857	paraoxonase 2	1.16	1.68
	426440	BE382756	Hs.169902	solute carrier family 2 (facilitated glu	2.59	1.71
	426459	AF151812	Hs.169992	hypothetical 43.2 Kd protein	1.56	1.66
65	426471	M22440	Hs.170009	transforming growth factor, alpha	20.60	26.00
	426496	D31765	Hs.170114	KIAA0061 protein	9.81	22.00
	426501	AA401369	Hs.190721	ESTs	19.23	17.00
	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic	103.74	41.00
	426536	AI949749	Hs.44441	ESTs	4.65	23.00
70	426572	AB037783	Hs.170623	hypothetical protein FLJ11183	1.00	43.00
	426682	AV660038	Hs.2056	UDP glycosyltransferase 1 family, polype	160.06	8.00
	426691	NM_006201	Hs.171834	PCTAIRE protein kinase 1	1.51	1.35
	426746	J03626	Hs.2057	uridine monophosphate synthetase (orolat	2.13	1.68
	426752	X69490	Hs.172004	titin	0.02	5.14
75	426784	U03749	Hs.172216	chromogranin A (parathyroid secretory pr	1.72	1.71
	426807	AA385315	Hs.156682	ESTs	1.30	1.64
	426812	AF105365	Hs.172613	solute carrier family 12 (potassium/chlo	1.47	1.53
	426814	AF036943	Hs.172619	myelin transcription factor 1-like	1.00	1.00
	426831	BE296216	Hs.172673	S-adenosylhomocysteine hydrolase	1.51	1.25
80	426897	AA401369	Hs.190721	ESTs	141.56	17.00
	426925	NM_001196	Hs.315689	Homo sapiens cDNA: FLJ22373 fis, clone H	32.61	38.00
	426935	NM_000088	Hs.172928	collagen, type I, alpha 1	2.65	3.16
	426964	AA393739	Hs.287416	Homo sapiens cDNA FLJ11439 fis, clone HE	1.97	3.49
	426966	AI493134		sclerostin	1.00	1.00
85	426991	AK001536		Homo sapiens cDNA FLJ10674 fis, clone NT	3.39	2.28
	427099	AB032953	Hs.173560	odd Oz/ten-m homolog 2 (Drosophila, mous	4.24	17.00



	427239	BE270447	Hs.174070	ubiquitin carrier protein	1.58	1.05
	427260	AA663848		gb:ae70b06.s1 Stratagene schizo brain S1	1.34	1.60
	427281	AA906147	Hs.102869	ESTs	1.00	66.00
	427335	AA448542	Hs.251677	G antigen 7B	51.83	4.00
5	427354	T57896	Hs.191095	ESTs	1.17	1.95
	427356	AW023482	Hs.97849	ESTs	7.31	41.00
	427376	AA401533	Hs.19440	ESTs	1.00	57.00
	427383	NM_005411	Hs.177582	surfactant, pulmonary-associated protein	0.42	1.32
10	427427	AF077345	Hs.177936	lectin, superfamily member 1 (cartilage-	1.00	20.00
	427441	AA412605	Hs.343879	SPANX family, member C	1.00	1.00
	427445	X80818	Hs.178078	glutamate receptor, metabotropic 4	0.97	1.03
	427505	AA361562	Hs.178761	26S proteasome-associated pad1 homolog	4.60	4.04
	427510	Z47542	Hs.179312	small nuclear RNA activating complex, po	22.00	45.00
15	427528	AU077143	Hs.179565	minichromosome maintenance deficient (S.	97.45	92.00
	427546	AA188763	Hs.36793	hypothetical protein FLJ23188	1.50	3.24
	427562	R56424	Hs.26534	ESTs	6.81	40.00
	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	69.91	62.00
	427600	AI741320	Hs.114121	Homo sapiens cDNA: FLJ23228 fis, clone C	2.70	49.00
20	427666	AI791495	Hs.180142	calmodulin-like skin protein	1.37	1.88
	427668	AA298760	Hs.180191	hypothetical protein FLJ14904	29.55	67.00
	427677	NM_007045	Hs.180296	FGFR1 oncogene partner	3.62	2.63
	427701	AA411101	Hs.243886	nuclear autoantigenic sperm protein (his	7.41	34.00
	427711	M31659	Hs.180408	solute carrier family 25 (mitochondrial	15.84	70.00
25	427719	AI393122	Hs.134726	ESTs	7.03	4.52
	427722	AK000123	Hs.180479	hypothetical protein FLJ20116	2.92	1.74
	427747	AW411425	Hs.180655	serine/threonine kinase 12	1.76	1.26
	427912	AI022310	Hs.181097	tumor necrosis factor (ligand) superfam	9.63	59.00
	427961	AW293165	Hs.143134	ESTs	41.97	118.00
30	428004	AA449563	Hs.151393	glutamate-cysteine ligase, catalytic sub	23.82	1.00
	428023	AL038843		Homo sapiens cDNA: FLJ23602 fis, clone L	1.40	1.33
	428046	AW812795	Hs.337534	ESTs, Moderately similar to I38022 hypot	96.28	167.00
	428093	AW594506	Hs.104830	ESTs	1.25	1.29
	428098	AU077258	Hs.182429	protein disulfide isomerase-related prot	1.86	1.60
35	428129	AI244311	Hs.26912	ESTs	1.00	42.00
	428169	AI928984	Hs.182793	golgi phosphoprotein 2	2.76	2.11
	428182	BE386042	Hs.293317	ESTs, Weakly similar to GGC1_HUMAN G ANT	1.00	1.00
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	85.59	181.00
	428242	H55709	Hs.2250	leukemia inhibitory factor (cholinergic	8.57	21.64
40	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	7.77	15.90
	428434	AI909935	Hs.65551	Homo sapiens, Similar to DNA segment, Ch	0.58	1.43
	428450	NM_014791	Hs.184339	KIAA0175 gene product	237.53	204.00
	428471	X57348	Hs.184510	stratifin	6.00	4.60
	428479	Y00272	Hs.334562	cell division cycle 2, G1 to S and G2 to	56.54	16.00
45	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino	3.53	2.15
	428505	AL035461	Hs.2281	chromogranin B (secretogranin 1)	1.00	1.00
	428532	AF157326	Hs.184786	TBP-interacting protein	1.00	58.00
	428645	AA431400	Hs.98729	ESTs, Weakly similar to 2017205A dihydro	1.00	16.00
	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	1.00	1.00
50	428698	AA852773	Hs.334838	KIAA1866 protein	187.37	255.00
	428728	NM_016625	Hs.191381	hypothetical protein	47.24	80.00
	428748	AW593206	Hs.98785	Ksp37 protein	1.00	87.00
	428758	AA433988	Hs.98502	hypothetical protein FLJ14303	1.06	1.13
	428771	AB028992	Hs.193143	KIAA1069 protein	1.98	92.00
55	428801	AW277121	Hs.254881	ESTs	1.67	6.15
	428810	AF068236	Hs.193788	nitric oxide synthase 2A (inducible, hep	1.03	1.27
	428839	AI767756	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	124.17	43.00
	428845	AL157579	Hs.153610	KIAA0751 gene product	1.00	1.00
	428959	AF100779	Hs.194680	WNT1 inducible signaling pathway protein	15.16	27.00
60	428969	AF120274	Hs.194689	artemin	1.36	1.24
	429038	AL023513	Hs.194766	seizure related gene 6 (mouse)-like	0.97	3.31
	429065	AI753247	Hs.29643	Homo sapiens cDNA FLJ13103 fis, clone NT	6.82	16.47
	429164	AI688663	Hs.116586	ESTs	19.08	67.00
	429170	NM_001394	Hs.2359	dual specificity phosphatase 4	16.18	105.00
65	429183	AB014604	Hs.197955	KIAA0704 protein	79.72	104.00
	429201	X03178	Hs.198246	group-specific component (vitamin D bind	1.00	1.00
	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3	1.33	1.09
	429220	AW207206		ESTs	1.00	7.00
	429228	AI553633	Hs.326447	ESTs	39.47	29.25
70	429259	AA420450	Hs.292911	ESTs, Highly similar to S60712 band-6-pr	2.01	1.18
	429263	AA019004	Hs.198396	ATP-binding cassette, sub-family A (ABC1	1.07	1.00
	429276	AF056085	Hs.198612	G protein-coupled receptor 51	3.70	142.00
	429359	W00482	Hs.2399	matrix metalloproteinase 14 (membrane-in	1.30	1.94
	429412	NM_006235	Hs.2407	POU domain, class 2, associating factor	94.09	86.00
75	429413	NM_014058	Hs.201877	DESC1 protein	41.91	10.00
	429486	AF155827	Hs.203963	hypothetical protein FLJ10339	12.19	1.00
	429504	X99133	Hs.204238	lipocalin 2 (oncogene 24p3)	1.61	1.08
	429538	BE182592	Hs.11261	small proline-rich protein 2A	4.43	2.90
	429547	AA401369	Hs.190721	ESTs	1.06	17.00
80	429551	AW450624	Hs.220931	ESTs	2.89	65.00
	429563	BE619413	Hs.2437	eukaryotic translation initiation factor	1.49	1.37
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	61.86	100.00
	429610	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas	1.59	1.69
	429612	AF062649	Hs.252587	pituitary tumor-transforming 1	2.78	1.74
	429616	AI982722	Hs.120845	ESTs	1.00	1.00
85	429656	X05608	Hs.211584	neurofilament, light polypeptide (68kD)	1.00	4.00



	429663	M68874	Hs.211587	phospholipase A2, group IVA (cytosolic,	69.95	104.00
	429736	AF125304	Hs.212680	tumor necrosis factor receptor superfam	1.25	1.21
	429782	NM_005754	Hs.220689	Ras-GTPase-activating protein SH3-domain	1.00	7.00
	429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	11.80	1.00
5	429918	AW873986	Hs.119383	ESTs	1.00	78.00
	429978	AA249027		ribosomal protein S6	1.98	3.09
	429986	AF092047	Hs.227277	sine oculis homeobox ( <i>Drosophila</i> ) homolo	1.00	48.00
	430044	AA464510	Hs.152812	ESTs	69.27	59.00
	430114	AA847744	Hs.99640	ESTs	1.00	1.00
10	430134	BE380149	Hs.105223	ESTs, Weakly similar to T33188 hypotheti	1.00	51.00
	430147	R60704	Hs.234434	hairly/enhancer-of-split related with YRP	1.10	2.22
	430287	AW182459	Hs.125759	ESTs, Weakly similar to LEU5_HUMAN LEUKE	1.00	127.00
	430294	AI538226	Hs.32976	guanine nucleotide binding protein 4	3.80	1.47
15	430300	U60805	Hs.238648	oncocalin M receptor	1.00	35.00
	430315	NM_004293	Hs.239147	guanine deaminase	92.31	28.00
	430337	M36707	Hs.239600	calmodulin-like 3	1.18	1.08
	430378	Z29572	Hs.2556	tumor necrosis factor receptor superfam	5.28	66.00
	430388	AA356923	Hs.240770	nuclear cap binding protein subunit 2, 2	16.76	38.00
	430393	BE185030	Hs.241305	estrogen-responsive B box protein	1.63	1.50
20	430439	AL133561		DKFZP434B061 protein	1.00	1.00
	430451	AA836472	Hs.297939	cathepsin B	1.64	2.12
	430454	AW469011	Hs.105635	ESTs	63.35	44.00
	430466	AF052573	Hs.241517	polymerase (DNA directed), theta	2.47	1.91
25	430481	AA479678	Hs.203269	ESTs, Moderately similar to ALU8_HUMAN A	1.00	31.00
	430486	BE062109	Hs.241551	chloride channel, calcium activated, fam	12.28	41.00
	430508	AI015435	Hs.104637	ESTs	4.75	7.27
	430533	AA480895	Hs.57749	ESTs, Weakly similar to T17288 hypotheti	1.00	1.00
	430563	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR	1.00	1.59
30	430677	Z26317	Hs.94560	desmoglein 2	1.72	1.30
	430678	AA401369	Hs.190721	ESTs	0.90	17.00
	430686	NM_001942	Hs.2633	desmoglein 1	1.00	1.00
	430788	AI742925	Hs.7179	ESTs, Weakly similar to 2004399A chromos	1.62	1.84
	430890	X54232	Hs.2699	glypican 1	1.58	1.40
35	430935	AW072916		zinc finger protein 131 (clone pHZ-10)	90.28	132.00
	430985	AA490232	Hs.27323	ESTs, Weakly similar to I78885 serine/th	0.94	1.28
	431009	BE149762	Hs.48956	gap junction protein, beta 6 (connexin 3	60.25	28.00
	431089	BE041395		ESTs, Weakly similar to unknown protein	23.32	941.00
	431092	AI332764	Hs.125757	ESTs	13.46	63.00
40	431124	AF284221	Hs.59506	doublesex and mab-3 related transcriptio	49.43	62.00
	431164	AA493650	Hs.94367	Homo sapiens cDNA: FLJ23494 fis, clone L	0.44	2.20
	431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	182.26	101.00
	431221	AW207837	Hs.286145	SRB7 (suppressor of RNA polymerase B, ye	4.15	13.97
	431277	AA501806	Hs.345824	ESTs	1.00	86.00
45	431322	AW970622		gb:EST382704 MAGE resequences, MAGK Homo	40.55	200.00
	431342	AW971018	Hs.21659	ESTs	1.00	53.00
	431384	BE158000	Hs.285026	gb:MR2-HT0377-150200-202-e03 HT0377 Homo	0.94	1.14
	431462	AW583672	Hs.256311	granin-like neuroendocrine peptide precu	1.30	1.25
	431494	AA991355	Hs.298312	hypothetical protein DKFZp434A1315	3.90	26.00
50	431515	NM_012152	Hs.258583	endothelial differentiation, lysophospha	1.41	1.87
	431548	AI834273	Hs.9711	novel protein	5.66	15.00
	431630	NM_002204	Hs.265829	integrin, alpha 3 (antigen CD49C, alpha	0.99	1.44
	431745	AW972448	Hs.163425	ESTs	0.99	3.51
	431770	BE221880	Hs.268555	5'-3' exoribonuclease 2	67.12	91.00
55	431830	Y16645	Hs.271387	small inducible cytokine subfamily A (Cy	3.36	4.71
	431846	BE019924	Hs.271580	uroplakin 1B	4.49	2.51
	431890	X17033	Hs.271986	integrin, alpha 2 (CD49B, alpha 2 subuni	2.20	3.32
	431934	AB031481	Hs.272214	STG protein	1.01	1.04
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	51.17	46.35
60	432006	AL137382	Hs.272320	Homo sapiens mRNA; cDNA DKFZp434L1226 (f	0.94	1.65
	432023	R43020	Hs.236223	EST	0.94	47.00
	432201	AI538613	Hs.298241	Transmembrane protease, serine 3	1.10	2.24
	432210	AI567421	Hs.273330	Homo sapiens, clone IMAGE:3544662, mRNA,	1.42	1.45
	432226	AW182766	Hs.273558	phosphate cytidylyltransferase 1, cholin	1.00	1.00
65	432239	X81334	Hs.2936	matrix metalloproteinase 13 (collagenase	18.67	1.00
	432265	BE382679	Hs.285753	SCG10-like-protein	1.09	1.21
	432281	AK001239	Hs.274263	hypothetical protein FLJ10377	40.98	58.00
	432365	AK001106	Hs.274419	hypothetical protein FLJ10244	1.00	214.00
	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	157.34	37.00
70	432375	BE536069	Hs.2962	S100 calcium-binding protein P	1.65	1.06
	432407	AA221036		gb:zr03f12.r1 Stratagene NT2 neuronal pr	73.71	75.00
	432441	AW292425	Hs.163484	ESTs	56.35	72.00
	432489	AI804855	Hs.207530	ESTs	1.00	24.00
	432543	AA552690	Hs.152423	Homo sapiens cDNA: FLJ21274 fis, clone C	137.72	98.00
75	432552	AI537170	Hs.173725	ESTs, Weakly similar to ALU8_HUMAN ALU S	1.00	31.00
	432583	AW023624	Hs.162282	potassium channel TASK-4; potassium chan	0.27	35.18
	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	2.87	6.22
	432625	AI243596	Hs.94830	ESTs, Moderately similar to T03094 A-kin	26.63	56.00
	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci	1.92	5.29
80	432677	NM_004482	Hs.278611	UDP-N-acetyl-alpha-D-galactosamine:polyp	1.00	48.00
	432715	AA247152	Hs.200483	ESTs, Weakly similar to KIAA1074 protein	45.13	31.00
	432753	NM_014075	Hs.336938	Homo sapiens PRO0593 mRNA, complete cds	1.00	68.00
	432788	AA521091	Hs.178499	Homo sapiens cDNA: FLJ23117 fis, clone L	2.69	3.67
	432842	AW674093	Hs.334822	hypothetical protein MGC4485	1.22	1.34
85	432867	AW016936	Hs.233364	ESTs	1.00	1.00
	432917	NM_014125	Hs.241517	PRO0327 protein	10.25	6.62



	432920	U37689	Hs.3128	polymerase (RNA) II (DNA directed) polyp	1.44	1.30
	433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	154.79	85.64
	433023	AW864793	Hs.87409	thrombospondin 1	20.96	100.00
5	433042	AW193534	Hs.281895	Homo sapiens cDNA FLJ11660 fis, clone HE	1.00	10.00
	433091	Y12642	Hs.3185	lymphocyte antigen 6 complex, locus D	1.20	1.09
	433159	AB035898	Hs.150587	kinesin-like protein 2	13.82	39.00
	433183	AF231338	Hs.222024	transcription factor BMAL2	1.00	69.00
	433258	AA622788	Hs.203613	ESTs, Weakly similar to ALUB_HUMAN !!!!	1.00	1.25
10	433409	AI278802	Hs.25661	ESTs	44.81	117.00
	433437	U20536	Hs.3280	caspase 6, apoptosis-related cysteine pr	70.39	105.00
	433485	AI493076	Hs.201967	aldo-keto reductase family 1, member C2	11.55	2.00
	433537	AI733692	Hs.112488	ESTs	8.66	55.00
	433547	W04978	Hs.303023	beta tubulin 1, class VI	25.16	83.00
15	433556	W56321	Hs.111460	calcium/calmodulin-dependent protein kin	1.00	19.00
	433647	AA603367	Hs.222294	ESTs	20.30	49.00
	433658	L03678	Hs.156110	immunoglobulin kappa constant	5.92	10.03
	433800	AI094221	Hs.135150	lung type-I cell membrane-associated gly	2.29	2.22
	433819	AW511097	Hs.112765	ESTs	3.71	8.00
20	433862	D86960	Hs.3610	KIAA0205 gene product	62.08	104.00
	433980	AA137152	Hs.286049	phosphoserine aminotransferase	108.91	47.00
	434088	AF116677	Hs.249270	hypothetical protein PRO1966	1.00	1.00
	434094	AA305599	Hs.238205	hypothetical protein PRO2013	121.27	87.00
	434105	AW952124	Hs.13094	presenilins associated rhomboid-like pro	1.22	1.23
25	434217	AW014795	Hs.23349	ESTs	14.11	57.00
	434340	AI193043	Hs.128685	ESTs, Weakly similar to T17226 hypotheti	2.10	2.56
	434360	AA401369	Hs.190721	ESTs	40.98	17.00
	434414	AI798376		gb:tr34b07.x1 NCL_CGAP_Ov23 Homo sapiens	1.48	1.56
	434424	AI811202	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L	1.00	64.00
30	434467	BE552368	Hs.231853	Homo sapiens cDNA FLJ13445 fis, clone PL	54.91	85.00
	434551	BE387162	Hs.280858	ESTs, Highly similar to A35661 DNA excis	2.46	2.00
	434627	AI221894	Hs.39311	ESTs	1.00	1.00
	434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HE	1.00	23.00
	434769	AA648884	Hs.134278	Homo sapiens cDNA FLJ12676 fis, clone NT	7.08	56.00
35	434792	AA649253	Hs.132458	ESTs	8.52	44.00
	434808	AF155108	Hs.256150	Homo sapiens, Similar to RIKEN cDNA 2810	11.33	1.00
	434828	D90070	Hs.96	phorbol-12-myristate-13-acetate-induced	1.00	1.00
	434876	AF160477	Hs.61460	Ig superfamily receptor LNIR	1.25	1.29
	434891	AA814309	Hs.123583	ESTs	1.00	6.00
40	434928	AW015595	Hs.4267	Homo sapiens clones 24714 and 24715 mRNA	1.00	1.00
	435013	H91923	Hs.110024	Target CAT	1.26	1.10
	435066	BE261750	Hs.4747	dyskeratosis congenita 1, dyskerin	1.69	1.37
	435087	AW975241	Hs.23567	ESTs	1.00	1.00
	435099	AC004770	Hs.4756	flap structure-specific endonuclease 1	2.90	1.93
45	435159	AA668879	Hs.116649	ESTs	1.00	1.00
	435205	X54136	Hs.181125	immunoglobulin lambda locus	1.02	1.46
	435232	NM_001262	Hs.4854	cyclin-dependent kinase inhibitor 2C (p1	2.04	2.70
	435304	H10709	Hs.269524	ESTs	27.58	139.00
	435313	AI769400	Hs.189729	ESTs	1.00	14.00
50	435505	AF200492	Hs.211238	interleukin-1 homolog 1	1.00	38.00
	435509	AI458679	Hs.181915	ESTs	1.00	1.00
	435525	AI831297	Hs.123310	ESTs	1.00	56.00
	435532	AW291488	Hs.117305	Homo sapiens, clone IMAGE:3682908, mRNA	1.00	2.00
	435550	AI224456	Hs.324507	H.sapiens polyA site DNA	3.42	3.92
55	435602	AF217515	Hs.283532	uncharacterized bone marrow protein BM03	3.95	1.80
	435766	R11673	Hs.186498	ESTs	1.00	28.00
	435793	AB037734	Hs.4993	KIAA1313 protein	23.68	42.00
	436069	AI056879	Hs.263209	ESTs	1.00	58.00
	436170	AW450381	Hs.14529	ESTs	1.00	18.00
60	436211	AK001581	Hs.334828	hypothetical protein FLJ10719; KIAA1794	5.84	22.00
	436213	AA325512	Hs.71472	hypothetical protein FLJ10774; KIAA1709	1.42	1.27
	436217	T53925	Hs.107	fibrinogen-like 1	57.97	31.00
	436238	AK002163	Hs.301724	hypothetical protein FLJ11301	2.51	1.71
	436251	BE515065	Hs.296585	nucleolar protein (KKE/O repeat)	2.33	1.64
65	436291	BE568452	Hs.344037	protein regulator of cytokinesis 1	108.99	52.00
	436302	AL355841	Hs.99330	hypothetical protein FLJ23588	0.75	2.81
	436396	AW992292	Hs.152213	wingless-type MMTV integration site fami	60.01	1.00
	436414	BE264633	Hs.143638	WD repeat domain 4	2.50	2.19
	436419	AI948626	Hs.171356	ESTs	0.95	1.33
70	436443	AW138211	Hs.128746	ESTs	1.12	9.26
	436474	AJ270693	Hs.199887	ESTs	1.00	1.00
	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	3.28	1.56
	436486	AA742221	Hs.120633	ESTs	1.00	19.00
	436511	AA721252	Hs.291502	ESTs	16.76	14.00
75	436553	X57809	Hs.181125	immunoglobulin lambda locus	1.08	1.74
	436557	W15573	Hs.5027	ESTs, Weakly similar to A47582 B-cell gr	19.20	9.75
	436608	AA628980		down syndrome critical region protein DS	33.92	25.00
	436667	AW025183	Hs.127680	ESTs	0.89	1.19
	436771	AW975687	Hs.292979	ESTs	1.00	10.00
80	436839	AA401369	Hs.190721	ESTs	1.00	17.00
	436887	AW953157	Hs.193235	hypothetical protein DKFZp547D155	1.06	1.15
	436944	AW268614	Hs.5840	ESTs	1.00	1.00
	436961	AW375974	Hs.156704	ESTs	25.13	25.00
	436972	AA284679	Hs.25640	claudin 3	1.59	1.46
	437016	AU076916	Hs.5398	guanine monophosphate synthetase	2.35	1.78
85	437044	AL035864	Hs.69517	cDNA for differentially expressed CO16 g	1.34	1.13



	437181	AI306615	Hs.125343	ESTs, Weakly similar to KIAA0758 protein	1.00	17.00
	437204	AL110216	Hs.22826	ESTs, Weakly similar to I55214 salivary	40.55	82.00
	437205	AL110232	Hs.279243	Homo sapiens mRNA; cDNA DKFZp564D2071 (f	1.00	112.00
	437259	AI377755	Hs.120695	ESTs	1.00	205.00
5	437270	R18087	Hs.323769	cisplatin resistance related protein CRR	1.56	1.54
	437271	AL137445	Hs.28846	Homo sapiens mRNA; cDNA DKFZp566O134 (fr	113.25	125.00
	437370	AL359567	Hs.161962	Homo sapiens mRNA; cDNA DKFZp547D023 (fr	1.82	4.57
	437390	AI125859	Hs.112607	ESTs	1.35	1.75
10	437412	BE069288	Hs.34744	Homo sapiens mRNA; cDNA DKFZp547C136 (fr	3.58	3.20
	437435	AI306152	Hs.27027	hypothetical protein DKFZp762H1311	3.03	1.08
	437444	H46008	Hs.31518	ESTs	1.00	39.00
	437568	AI954795	Hs.156135	ESTs	1.00	19.00
	437623	D63880	Hs.5719	chromosome condensation-related SMC-asso	1.95	1.57
	437789	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheti	1.00	3.00
15	437814	AI088192	Hs.135474	ESTs, Weakly similar to DDX9_HUMAN ATP-D	1.00	45.00
	437840	AA884836	Hs.292014	ESTs	1.07	1.78
	437852	BE001836	Hs.256897	ESTs, Weakly similar to dJ365O12.1 [H.sa	1.68	3.26
	437879	BE262082	Hs.5894	hypothetical protein FLJ10305	1.87	2.52
	437915	AI637993	Hs.202312	Homo sapiens clone N11 Ntera2D1 teratoca	74.05	35.00
20	437916	BE566249	Hs.20999	hypothetical protein FLJ23142	23.15	89.00
	437937	AI917222	Hs.121655	ESTs	1.00	1.00
	437942	AI888256	Hs.307526	ESTs	12.28	31.00
	438091	AW373062		nuclear receptor subfamily 1, group I, m	1.53	10.85
	438113	AI467908	Hs.8882	ESTs	1.80	2.39
25	438119	AW963217	Hs.203961	ESTs, Moderately similar to AF116721 89	22.67	36.90
	438274	AI918906	Hs.55080	ESTs	1.00	1.00
	438378	AW970529	Hs.86434	hypothetical protein FLJ21816	38.92	38.00
	438403	AA806607	Hs.292206	ESTs	1.00	1.00
	438494	AA908678	Hs.130183	ESTs	2.05	80.00
30	438546	AW297204	Hs.125811	ESTs	1.00	131.00
	438552	AJ245820	Hs.6314	type I transmembrane receptor (seizure-r	1.43	1.45
	438702	AI879064	Hs.54618	ESTs	1.00	34.00
	438724	AW612553	Hs.114670	Human DNA sequence from clone RP11-16L21	1.33	1.10
	438746	AI885815	Hs.184727	Human melanoma-associated antigen p97 (m	2.42	1.59
35	438779	NM_003787	Hs.6414	nucleolar protein 4	1.00	18.00
	438821	AA826425	Hs.192375	ESTs	2.03	2.57
	438885	AI886558	Hs.184987	ESTs	6.42	88.00
	438898	AA401369	Hs.190721	ESTs	22.41	17.00
40	438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regi	1.00	1.00
	438956	W00847	Hs.135056	Human DNA sequence from clone RP5-850E9	2.20	1.88
	439000	AW979121		gb:EST391231 MAGE resequences, MAGP Homo	2.78	4.81
	439023	AA745978	Hs.28273	ESTs	1.17	1.31
	439024	R96696	Hs.35598	ESTs	1.00	28.00
45	439128	AI949371	Hs.153089	ESTs	1.00	67.00
	439146	AW138909	Hs.156110	immunoglobulin kappa constant	1.38	1.41
	439223	AW238299	Hs.250618	UL16 binding protein 2	1.93	1.64
	439285	AL133916		hypothetical protein FLJ20093	46.23	139.00
	439318	AW837046	Hs.6527	G protein-coupled receptor 56	2.00	2.20
50	439343	AF086161	Hs.114611	hypothetical protein FLJ11808	6.10	7.37
	439394	AA401369	Hs.190721	ESTs	3.39	17.00
	439410	AA632012	Hs.188746	ESTs	1.83	3.07
	439451	AF086270	Hs.278554	heterochromatin-like protein 1	23.28	52.00
	439452	AA918317	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	18.76	122.00
55	439453	BE264974	Hs.6566	thyroid hormone receptor interactor 13	2.78	1.58
	439477	W69813	Hs.58042	ESTs, Moderately similar to GFR3_HUMAN G	1.22	1.44
	439492	AF086310	Hs.103159	ESTs	7.46	39.00
	439523	W72348	Hs.185029	ESTs	1.00	1.19
	439592	AF086413	Hs.58399	ESTs	1.00	1.00
60	439606	W79123	Hs.58561	G protein-coupled receptor 87	33.61	1.00
	439670	AF088076	Hs.59507	ESTs, Weakly similar to AC004858 3 U1 sm	1.00	1.00
	439702	AW085525	Hs.134182	ESTs	4.30	10.00
	439706	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	86.55	11.00
	439738	BE245502	Hs.9598	sema domain, immunoglobulin domain (Ig),	2.36	1.88
65	439750	AL359053	Hs.57664	Homo sapiens mRNA full length insert cDN	2.02	6.08
	439759	AL359055	Hs.67709	Homo sapiens mRNA full length insert cDN	1.00	21.00
	439780	AL109588		gb:Homo sapiens mRNA full length insert	7.27	25.00
	439840	AW449211	Hs.105445	GDNF family receptor alpha 1	1.00	1.00
	439926	AW014875	Hs.137007	ESTs	32.58	71.00
70	439963	AW247529	Hs.6793	platelet-activating factor acetylhydrola	21.28	9.55
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	68.83	61.00
	440006	AK000517	Hs.6844	hypothetical protein FLJ20510	1.83	4.02
	440028	AW473675	Hs.125843	ESTs, Weakly similar to T17227 hypotheti	1.42	2.54
	440106	AA864968	Hs.127699	KIAA1603 protein	1.00	54.00
75	440138	AB033023	Hs.318127	hypothetical protein FLJ10201	24.18	52.00
	440273	AI805392	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L	3.21	4.72
	440289	AW450991	Hs.192071	ESTs	38.63	113.00
	440325	NM_003812	Hs.7164	a disintegrin and metalloproteinase doma	62.88	147.00
	440492	R39127	Hs.21433	hypothetical protein DKFZp547J036	2.35	3.62
80	440527	AV657117	Hs.184164	ESTs, Moderately similar to S65657 alpha	10.84	57.00
	440659	AF134160	Hs.7327	claudin 1	3.18	2.37
	440704	M69241	Hs.162	insulin-like growth factor binding prote	2.89	2.09
	440943	AW082298	Hs.146161	hypothetical protein MGC2408	2.02	1.41
	440984	AI160011	Hs.272068	ESTs	1.29	1.14
85	441020	AA401369	Hs.190721	ESTs	142.99	17.00
	441031	AI110684	Hs.7645	fibrinogen, B beta polypeptide	1.41	99.00



	441128	AA570256		ESTs, Weakly similar to T23273 hypotheti	4.13	3.50
	441290	W27501	Hs.89605	cholinergic receptor, nicotinic, alpha p	1.00	1.00
	441362	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coll Re	130.23	43.00
	441377	BE218239	Hs.202656	ESTs	22.03	1.00
5	441390	AI692560	Hs.131175	ESTs	3.65	7.70
	441497	R51064	Hs.23172	ESTs	1.00	1.00
	441525	AW241867	Hs.127728	ESTs	1.53	1.42
	441553	AA281219	Hs.121296	ESTs	1.89	1.57
10	441607	NM_005010	Hs.7912	neuronal cell adhesion molecule	1.47	2.11
	441633	AW958544	Hs.112242	normal mucosa of esophagus specific 1	216.22	363.00
	441636	AA081846	Hs.7921	Homo sapiens mRNA; cDNA DKFZp566E183 (fr	2.31	2.05
	441737	X79449	Hs.7957	adenosine deaminase, RNA-specific	1.30	1.49
	441790	AA401369	Hs.190721	ESTs	44.15	17.00
15	441801	AW242799	Hs.86366	ESTs	1.00	1.00
	441919	AI553802	Hs.128121	ESTs	1.00	122.00
	441937	R41782	Hs.22279	ESTs	0.86	1.37
	441954	AI744935	Hs.8047	Fanconi anemia, complementation group G	1.48	1.39
	442025	AW887434	Hs.11810	CDA11 protein	1.00	46.00
20	442029	AW956698	Hs.14456	neural precursor cell expressed, develop	9.92	45.00
	442072	AI740832	Hs.12311	Homo sapiens clone 23570 mRNA sequence	25.05	77.00
	442108	AW452649	Hs.166314	ESTs	3.61	3.14
	442117	AW664964	Hs.128899	ESTs	3.00	5.49
25	442137	AA977235	Hs.128830	ESTs, Weakly similar to Z192_HUMAN ZINC	1.00	1.00
	442159	AW163390	Hs.278554	heterochromatin-like protein 1	1.92	1.66
	442179	AA983842	Hs.333555	chromosome 2 open reading frame 2	27.22	50.00
	442328	AI952430	Hs.150614	ESTs, Weakly similar to ALU4_HUMAN ALU S	5.00	3.42
	442432	BE093589	Hs.38178	hypothetical protein FLJ23468	181.59	76.00
	442530	AI580830	Hs.176508	Homo sapiens cDNA FLJ14712 fis, clone NT	10.59	144.00
30	442547	AA306997	Hs.217484	ESTs, Weakly similar to ALU1_HUMAN ALU S	109.23	98.00
	442556	AL137761	Hs.8379	Homo sapiens mRNA; cDNA DKFZp586L2424 (f	1.00	53.00
	442619	AA447492	Hs.20183	ESTs, Weakly similar to AF164793 1 prote	29.02	50.00
	442710	AI015631	Hs.23210	ESTs	1.00	19.00
	442717	R88362	Hs.180591	ESTs, Weakly similar to T23976 hypotheti	1.00	5.00
35	442875	BE623003	Hs.23625	Homo sapiens clone TCCCTA00142 mRNA sequ	22.85	50.00
	442914	AW188551	Hs.99519	hypothetical protein FLJ14007	25.33	82.00
	442932	AA457211	Hs.8858	bromodomain adjacent to zinc finger doma	3.18	4.41
	442942	AW167087	Hs.131562	ESTs	8.45	64.00
	443068	AI188710		ESTs	1.00	27.00
40	443204	AW205878	Hs.29643	Homo sapiens cDNA FLJ13103 fis, clone NT	1.00	24.00
	443211	AI128388	Hs.143655	ESTs	12.42	2.00
	443247	BE614387	Hs.333893	c-Myc target JPO1	128.84	96.00
	443324	R44013	Hs.164225	ESTs	0.02	4.59
	443383	AI792453	Hs.166507	ESTs	1.00	47.00
45	443400	R28424	Hs.250648	ESTs	18.52	61.00
	443426	AF098158	Hs.9329	chromosome 20 open reading frame 1	4.02	1.75
	443572	AA025610	Hs.9605	cleavage and polyadenylation specific fa	2.98	2.57
	443575	AI078022	Hs.269636	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.00	29.00
	443614	AV655386	Hs.7645	fibrinogen, B beta polypeptide	1.00	16.00
50	443633	AL031290	Hs.9654	similar to pregnancy-associated plasma p	1.00	39.00
	443648	AI085377	Hs.143610	ESTs	39.81	70.00
	443715	AI583187	Hs.9700	cyclin E1	48.74	7.00
	443723	AI144442	Hs.157144	syntaxin 6	1.29	1.30
	443802	AW504924	Hs.9805	KIAA1291 protein	1.75	1.61
55	443859	NM_013409	Hs.9914	folistatin	1.35	1.13
	443892	AA401369	Hs.190721	ESTs	1.00	17.00
	443947	W24187		gb:zb47f09.r1 Soares_fetal_lung_NbHL19W	1.33	1.64
	443991	NM_002250	Hs.10082	potassium intermediate/small conductance	5.71	6.87
	444006	BE395085	Hs.10086	type I transmembrane protein Fn14	1.47	1.92
60	444009	AI380792	Hs.135104	ESTs	1.00	77.00
	444017	U04840	Hs.214	neuro-oncological ventral antigen 1	1.00	1.00
	444127	N63620	Hs.13281	ESTs	1.00	29.00
	444129	AW294292	Hs.256212	ESTs	1.00	1.00
	444279	U62432	Hs.89605	cholinergic receptor, nicotinic, alpha p	0.60	7.80
65	444371	BE540274	Hs.239	forkhead box M1	2.91	1.14
	444378	R41339	Hs.12569	ESTs	1.00	1.00
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	469.00	556.00
	444461	R53734	Hs.25978	ESTs, Weakly similar to 2109260A B cell	12.88	105.00
	444471	AB020684	Hs.11217	KIAA0877 protein	24.91	90.00
70	444489	AI151010	Hs.157774	ESTs	1.00	111.00
	444619	BE538082	Hs.8172	ESTs, Moderately similar to A46010 X-link	1.00	70.00
	444665	BE613126	Hs.47783	B aggressive lymphoma gene	30.56	139.00
	444707	AI188613	Hs.41690	desmocollin 3	1.00	1.00
	444735	BE019923	Hs.243122	hypothetical protein FLJ13057 similar to	77.02	90.00
75	444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote	1.57	1.31
	444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	77.55	2.00
	445236	AK001676	Hs.12457	hypothetical protein FLJ10814	1.00	27.00
	445258	AI635931	Hs.147613	ESTs	1.00	73.00
	445413	AA151342	Hs.12677	CGI-147 protein	28.14	50.00
80	445417	AK001058	Hs.12680	Homo sapiens cDNA FLJ10196 fis, clone HE	1.81	2.62
	445443	AV653838	Hs.322971	ESTs	1.00	1.00
	445462	AA378776	Hs.288649	hypothetical protein MGC3077	2.09	1.70
	445517	AF208855	Hs.12830	hypothetical protein	1.87	70.00
	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	1.71	2.72
85	445580	AF167572	Hs.12912	skb1 (S. pombe) homolog	1.52	1.34
	445654	X91247	Hs.13046	thioredoxin reductase 1	1.51	1.52



	445669	AI570830	Hs.174870	ESTs	10.95	11.45
	445818	BE045321	Hs.136017	ESTs	1.00	1.00
	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-l	49.42	54.00
	445885	AI734009	Hs.127699	KIAA1603 protein	1.00	132.00
5	445888	AF070623	Hs.13423	Homo sapiens clone 24468 mRNA sequence	1.00	1.00
	445903	AI347487	Hs.132781	class I cytokine receptor	1.00	36.00
	445932	BE046441	Hs.333555	Homo sapiens clone 24859 mRNA sequence	2.41	2.88
	445982	BE410233	Hs.13501	pescadillo (zebrafish) homolog 1, contai	1.60	1.35
10	446078	AI339982	Hs.156061	ESTs	1.00	42.00
	446102	AW168067	Hs.317694	ESTs	1.00	1.00
	446157	BE270828	Hs.131740	Homo sapiens cDNA: FLJ22562 fis, clone H	1.70	1.53
	446269	AW263155	Hs.14559	hypothetical protein FLJ10540	73.01	48.00
	446292	AF081497	Hs.279682	Rh type C glycoprotein	1.55	1.26
15	446293	AI420213	Hs.149722	ESTs	1.00	2.00
	446423	AW139655	Hs.150120	ESTs	1.10	4.19
	446428	AW082270	Hs.12496	ESTs, Weakly similar to ALU4_HUMAN ALU S	0.53	3.26
	446432	AI377320	Hs.150059	ESTs	1.00	5.00
	446528	AU076640	Hs.15243	nucleolar protein 1 (120kD)	1.36	1.31
20	446574	AI310135	Hs.335933	ESTs	3.89	72.00
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	32.03	20.23
	446636	AC002563	Hs.15767	citron (rho-interacting, serine/threonin	4.19	5.07
	446783	AW138343	Hs.141867	ESTs	2.82	9.47
	446839	BE091926	Hs.16244	mitotic spindle coiled-coil related prot	110.28	28.00
25	446849	AU076617	Hs.16251	cleavage and polyadenylation specific fa	3.26	2.94
	446856	AI814373	Hs.164175	ESTs	6.38	11.30
	446872	X97058	Hs.16362	pyrimidinergic receptor P2Y, G-protein c	1.98	2.03
	446880	AI811807	Hs.108646	Homo sapiens cDNA FLJ14934 fis, clone PL	94.90	113.00
	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	1.67	3.90
30	446989	AK001898	Hs.16740	hypothetical protein FLJ11036	2.82	3.12
	447022	AW291223	Hs.157573	ESTs	1.00	170.00
	447033	AI357412	Hs.157601	ESTs	7.15	107.00
	447078	AW885727	Hs.9914	ESTs	47.24	24.00
35	447081	Y13896	Hs.17287	potassium inwardly-rectifying channel, s	0.12	17.88
	447131	NM_004585	Hs.17466	retinoic acid receptor responder (tazaro	0.97	1.48
	447149	BE299857	Hs.326	TAR (HIV) RNA-binding protein 2	1.24	1.26
	447153	AA805202	Hs.315562	ESTs	1.00	54.00
	447164	AF026941	Hs.17518	Homo sapiens cig5 mRNA, partial sequence	1.00	67.00
40	447178	AW594641	Hs.192417	ESTs	3.42	50.00
	447250	AI878909	Hs.17883	protein phosphatase 1G (formerly 2C), ma	1.60	1.52
	447289	AW247017	Hs.36978	melanoma antigen, family A, 3	1.00	1.00
	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	28.63	1.00
	447343	AA256641	Hs.236894	ESTs, Highly similar to S02392 alpha-2-m	146.62	51.00
	447350	AI375572	Hs.172634	ESTs	1.00	12.00
45	447377	N27687	Hs.334334	transcription factor AP-2 alpha (activat	2.55	63.00
	447415	AW937335	Hs.28149	ESTs, Weakly similar to KF3B_HUMAN KINES	0.91	1.13
	447425	AI963747	Hs.18573	acylphosphatase 1, erythrocyte (common)	1.00	35.00
	447519	U46258	Hs.339665	ESTs	59.89	49.00
	447532	AK000614	Hs.18791	hypothetical protein FLJ20607	1.23	1.63
50	447534	AA401369	Hs.190721	ESTs	1.00	17.00
	447636	Y10043		high-mobility group (nonhistone chromoso	1.41	1.11
	447688	N87079	Hs.19236	Target CAT	1.00	39.00
	447733	AF157482	Hs.19400	MAD2 (mitotic arrest deficient, yeast, h	1.17	1.12
	447769	AW873704	Hs.320831	Homo sapiens cDNA FLJ14597 fis, clone NT	6.47	5.95
55	447802	AW593432	Hs.161455	ESTs	0.73	2.34
	447850	AB018298	Hs.19822	SEC24 (S. cerevisiae) related gene famil	86.45	116.00
	447924	AI817226	Hs.313413	ESTs, Weakly similar to T23110 hypotheti	1.00	1.00
	447973	AB011169	Hs.20141	similar to S. cerevisiae SSM4	3.50	4.27
	448030	N30714	Hs.325960	membrane-spanning 4-domains, subfamily A	4.13	142.00
60	448105	AI538613	Hs.298241	Transmembrane protease, serine 3	1.15	2.24
	448243	AW369771	Hs.52620	integrin, beta 8	15.84	1.00
	448278	W07369	Hs.11782	ESTs	0.97	1.90
	448290	AK002107	Hs.20843	Homo sapiens cDNA FLJ11245 fis, clone PL	1.00	1.00
	448296	BE622756	Hs.10949	Homo sapiens cDNA FLJ14162 fis, clone NT	2.42	2.17
65	448357	BE274396	Hs.108923	RAB38, member RAS oncogene family	1.44	1.08
	448390	AL035414	Hs.21068	hypothetical protein	1.00	43.00
	448469	AW504732	Hs.21275	hypothetical protein FLJ11011	2.63	2.49
	448569	BE382657	Hs.21486	signal transducer and activator of trans	1.84	2.53
	448663	BE614599	Hs.106823	hypothetical protein MGC14797	3.29	46.00
70	448672	AI955511	Hs.225106	ESTs	1.00	21.00
	448733	NM_005629	Hs.187958	solute carrier family 6 (neurotransmitte	1.82	1.08
	448741	BE614567	Hs.19574	hypothetical protein MGC5469	2.48	1.92
	448757	AI366784	Hs.48820	TATA box binding protein (TBP)-associate	23.53	20.00
	448775	AB025237	Hs.388	nudix (nucleoside diphosphate linked moi	2.34	1.97
75	448826	AI580252	Hs.293246	ESTs, Weakly similar to putative p150 [H	74.07	62.67
	448830	AL031658	Hs.22181	hypothetical protein dJ310013.3	1.37	1.31
	448844	AI581519	Hs.177164	ESTs	1.00	31.00
	448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	1.84	1.95
	448993	AI471630		KIAA0144 gene product	1.63	1.49
80	449003	X76342	Hs.389	alcohol dehydrogenase 7 (class IV), mu o	1.00	1.00
	449029	N28989	Hs.22891	solute carrier family 7 (cationic amino	1.97	2.26
	449040	AF040704	Hs.149443	putative tumor suppressor	0.97	1.56
	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	27.13	90.00
	449053	AI625777	Hs.344766	ESTs	8.33	44.00
85	449054	AF148848	Hs.22934	myoneurin	73.85	104.00
	449101	AA205847	Hs.23016	G protein-coupled receptor	2.58	27.00



	449167	T05095	Hs.19597	KIAA1694 protein	1.61	2.36
	449207	AL044222	Hs.23255	nucleoporin 155kD	2.36	1.56
	449228	AJ403107	Hs.148590	protein related with psoriasis	1.15	1.15
5	449230	BE613348	Hs.211579	melanoma cell adhesion molecule	206.65	151.00
	449305	AI638293		gb:tt09b07.x1 NCL_CGAP_GC6 Homo sapiens	17.28	45.00
	449318	AW236021	Hs.78531	Homo sapiens, Similar to RIKEN cDNA 5730	26.39	35.00
	449448	D60730	Hs.57471	ESTs	1.00	1.00
	449467	AW205006	Hs.197042	ESTs	1.00	1.00
10	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	56.80	216.86
	449722	BE280074	Hs.23960	cyclin B1	150.03	1.00
	449976	H06350	Hs.135056	Human DNA sequence from clone RP5-850E9	2.16	2.85
	450001	NM_001044	Hs.406	solute carrier family 6 (neurotransmitter)	1.17	1.45
	450098	W27249	Hs.8109	hypothetical protein FLJ21080	1.79	2.38
15	450101	AV649989	Hs.24385	Human hbc647 mRNA sequence	1.00	69.00
	450149	AW969781	Hs.132863	Zic family member 2 (odd-paired Drosophila)	1.00	1.00
	450193	AI916071	Hs.15607	Homo sapiens Fanconi anemia complemental	29.85	34.00
	450221	AA328102	Hs.24641	cytoskeleton associated protein 2	1.00	1.00
	450372	BE218107	Hs.202436	ESTs	1.00	1.00
20	450375	AA009647	Hs.8850	a disintegrin and metalloproteinase domain	51.26	93.00
	450447	AF212223	Hs.25010	hypothetical protein P15-2	123.20	181.00
	450588	AL050078	Hs.25159	Homo sapiens cDNA FLJ10784 fis, clone NT	1.00	19.00
	450589	AI701505	Hs.202526	ESTs	1.00	23.00
	450684	AA872605	Hs.25333	interleukin 1 receptor, type II	1.00	100.00
25	450701	H39960	Hs.288467	Homo sapiens cDNA FLJ12280 fis, clone MA	1.89	1.55
	450705	U90304	Hs.25351	iroquois homeobox protein 2A (IRX-2A) (	1.00	45.00
	450832	AA401369	Hs.190721	ESTs	25.17	17.00
	450937	R49131	Hs.26267	ATP-dependant interferon response protein	90.92	90.00
	450983	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	3.33	1.70
30	451105	AI761324		gb:wi60b11.x1 NCL_CGAP_Co16 Homo sapiens	15.02	124.00
	451110	AI955040	Hs.265398	ESTs, Weakly similar to transformation-r	1.00	143.00
	451253	H48299	Hs.26126	claudin 10	3.02	2.29
	451291	R39288	Hs.6702	ESTs	1.00	1.00
	451320	AW498974		diacylglycerol kinase, zeta (104kD)	2.92	18.00
35	451380	H09280	Hs.13234	ESTs	6.90	6.67
	451386	AB029006	Hs.26334	spastic paraplegia 4 (autosomal dominant)	35.75	72.00
	451437	H24143	Hs.31945	hypothetical protein FLJ11071	1.00	69.00
	451462	AK000367	Hs.26434	hypothetical protein FLJ20360	1.83	2.10
	451524	AK001466	Hs.26516	hypothetical protein FLJ10604	1.13	1.07
40	451541	BE279383	Hs.26557	plakophilin 3	1.88	1.33
	451592	AI805416	Hs.213897	ESTs	1.00	1.00
	451635	AA018899	Hs.127179	cryptic gene	1.52	1.92
	451743	AA401369	Hs.190721	ESTs	4.95	17.00
	451806	NM_003729	Hs.27076	RNA 3'-terminal phosphate cyclase	13.55	31.00
45	451807	W52854		hypothetical protein FLJ23293 similar to	1.55	35.00
	451871	AI821005	Hs.118599	ESTs	1.81	2.53
	451952	AL120173	Hs.301663	ESTs	1.00	22.00
	452012	AA307703	Hs.279766	kinesin family member 4A	3.43	2.26
	452046	AB018345	Hs.27657	KIAA0802 protein	56.59	19.00
50	452194	AI894413	Hs.332649	olfactory receptor, family 2, subfamily	1.67	4.09
	452206	AW340281	Hs.33074	Homo sapiens, clone IMAGE:3606519, mRNA,	9.31	53.00
	452240	AA401369	Hs.190721	ESTs	13.42	17.00
	452256	AK000933	Hs.28661	Homo sapiens cDNA FLJ10071 fis, clone HE	39.03	94.00
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	153.01	340.00
55	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisiae)	1.95	23.00
	452295	BE379936	Hs.28866	programmed cell death 10	42.33	61.00
	452304	AA025386	Hs.61311	ESTs, Weakly similar to S10590 cysteine	1.17	2.14
	452340	NM_002202	Hs.605	ISL1 transcription factor, LIM/homeodomain	1.00	13.00
	452349	AB028944	Hs.29189	ATPase, Class VI, type 11A	1.09	1.42
60	452367	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	54.49	53.00
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced protein	1.00	32.00
	452410	AL133619		Homo sapiens mRNA; cDNA DKFZp434E2321 (f	1.26	1.99
	452461	N78223	Hs.108106	transcription factor	24.47	35.00
	452571	W31518	Hs.34665	ESTs	54.61	102.00
65	452613	AA461599	Hs.23459	ESTs	1.39	1.32
	452699	AW295390	Hs.213062	ESTs	1.00	26.00
	452705	H49805	Hs.246005	ESTs	1.00	1.00
	452747	AF160477	Hs.61460	Ig superfamily receptor LNIR	112.87	1.29
70	452787	AW294022	Hs.222707	KIAA1718 protein	1.00	1.00
	452795	AW392555	Hs.18878	hypothetical protein FLJ21620	1.00	1.00
	452823	AB012124	Hs.30696	transcription factor-like 5 (basic helix	7.91	75.00
	452833	BE559681	Hs.30736	KIAA0124 protein	3.16	1.92
	452838	U65011	Hs.30743	preferentially expressed antigen in melanoma	174.35	1.00
	452862	AA401369	Hs.190721	ESTs	98.26	17.00
75	452865	AW173720	Hs.345805	ESTs, Weakly similar to A47582 B-cell growth	1.55	1.00
	452934	AA581322	Hs.4213	hypothetical protein MGC16207	1.73	1.19
	452946	X95425	Hs.31092	EphA5	1.00	1.00
	452976	R44214	Hs.101189	ESTs	1.58	1.98
	453028	AB006532	Hs.31442	RecQ protein-like 4	1.80	1.60
80	453095	AW295660	Hs.252756	ESTs	0.77	1.50
	453102	NM_007197	Hs.31664	frizzled (Drosophila) homolog 10	1.00	1.00
	453103	AI301052	Hs.153444	ESTs	1.00	1.00
	453120	AA292891	Hs.31773	pregnancy-induced growth inhibitor	1.23	1.20
	453153	N53893	Hs.24360	ESTs	1.00	83.00
85	453160	AI263307	Hs.239884	H2B histone family, member L	1.00	30.00
	453197	AI916269	Hs.109057	ESTs, Weakly similar to ALU5_HUMAN ALU S	1.00	134.00



5	453210	AL133161	Hs.32360	hypothetical protein FLJ10867	1.69	1.93		
	453240	AI969564	Hs.166254	hypothetical protein DKFZp5661133	1.00	1.00		
	453317	NM_002277	Hs.41696	keratin, hair, acidic, 1	1.19	1.27		
	453323	AF034102	Hs.32951	solute carrier family 29 (nucleoside tra	4.90	4.11		
	453331	AI240665	Hs.8860	ESTs	199.42	340.00		
	453392	U23752	Hs.32964	SRV (sex determining region Y)-box 11	1.00	16.00		
	453431	AF094754	Hs.32973	glycine receptor, beta	1.00	1.00		
	453439	AI572438	Hs.32976	guanine nucleotide binding protein 4	3.44	5.17		
	453459	BE047032	Hs.257789	ESTs	2.84	5.58		
10	453563	AW608906.comp		Hs.181163	hypothetical protein MGC5629	4.58	90.00	
	453633	AA357001	Hs.34045	hypothetical protein FLJ20764	1.74	1.60		
	453775	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	19.49	1.00		
	453830	AA534296	Hs.20953	ESTs	24.92	25.00		
15	453857	AL080235	Hs.58661	DKFZP586E1621 protein	167.59	66.00		
	453867	AI929383	Hs.33032	hypothetical protein DKFZp434N185	1.00	39.00		
	453883	AI638516	Hs.347524	cofactor required for Sp1 transcriptiona	1.97	1.58		
	453884	AA355925	Hs.36232	KIAA0186 gene product	63.89	20.00		
	453900	AW003582	Hs.226414	ESTs, Weakly similar to ALU8_HUMAN ALU S	20.41	16.00		
	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1	7.09	22.00		
20	453941	U39817	Hs.36820	Bloom syndrome	29.75	19.00		
	453964	AI961486	Hs.12744	ESTs	1.00	1.00		
	453968	AA847843	Hs.62711	Homo sapiens, clone IMAGE:3351295, mRNA	2.06	1.81		
	453976	BE463830	Hs.163714	ESTs	3.02	131.00		
25	454024	AA993527	Hs.293907	hypothetical protein FLJ23403	1.00	131.00		
	454034	NM_000691	Hs.575	aldehyde dehydrogenase 3 family, member	1.23	1.02		
	454042	T19228	Hs.172572	hypothetical protein FLJ20093	30.63	171.00		
	454059	NM_003154	Hs.37048	statheerin	1.00	1.00		
	454066	X00356	Hs.37058	calcitonin/calcitonin-related polypeptid	1.01	1.45		
30	454098	W27953	Hs.292911	ESTs, Highly similar to S60712 band-6-pr	1.26	1.11		
	454241	BE144666		gb:CM2-HT0176-041099-017-c02 HT0176 Homo	6.33	5.04		
	454417	AI244459	Hs.110826	trinucleotide repeat containing 9	4.30	7.82		
	454439	AW819152	Hs.154320	DKFZP566O1646 protein	1.00	1.00		
	455175	AW993247		gb:RC2-BN0033-180200-014-h09 BN0033 Homo	13.75	103.00		
35	455601	AI368680	Hs.816	SRV (sex determining region Y)-box 2	206.11	1.00		
	456237	AA203682		gb:zx52e07.r1 Soares_fetal_liver_spleen_	1.00	1.00		
	456321	NM_001327	Hs.87225	cancer/testis antigen	1.14	1.10		
	456475	NM_000144	Hs.95998	Friedreich ataxia	1.00	48.00		
	456508	AA502764	Hs.123469	ESTs, Weakly similar to AF208855 1 BM-01	162.25	189.00		
40	456534	X91195	Hs.100623	phospholipase C, beta 3, neighbor pseudo	2.12	1.80		
	456736	AW248217	Hs.1619	achaete-scute complex (Drosophila) homol	1.15	1.94		
	456759	BE259150	Hs.127792	delta (Drosophila)-like 3	1.00	1.00		
	456990	NM_004504	Hs.171545	HIV-1 Rev binding protein	16.42	84.00		
	457200	U33749	Hs.197764	thyroid transcription factor 1	0.57	1.76		
	457234	AW968360	Hs.14355	Homo sapiens cDNA FLJ13207 fis, clone NT	2.71	4.15		
45	457465	AW301344	Hs.122908	DNA replication factor	46.37	47.00		
	457489	AI693815	Hs.127179	cryptic gene	1.12	1.35		
	457646	AA725650	Hs.112948	ESTs	1.55	2.51		
	457733	AW974812	Hs.291971	ESTs	1.00	55.00		
50	457819	AA057484	Hs.35406	ESTs, Highly similar to unnamed protein	4.36	3.18		
	458092	BE545684	Hs.343566	KIAA0251 protein	1.00	1.32		
	458098	BE550224		metallothionein 1E (functional)	1.00	22.00		
	458207	T28472	Hs.7655	U2 small nuclear ribonucleoprotein auxil	2.06	1.88		
	458242	BE299588	Hs.28465	Homo sapiens cDNA: FLJ21869 fis, clone H	1.00	1.00		
55	458247	R14439	Hs.209194	ESTs	7.00	9.85		
	458679	AW975460	Hs.142913	ESTs	1.00	3.00		
	458778	AW451034	Hs.326525	arylsulfatase D	1.31	2.01		
	458933	AI638429	Hs.24763	RAN binding protein 1	1.98	1.71		
	459352	AW810383	Hs.206828	ESTs	12.60	63.00		
60	459670	F01020	Hs.172004	titin	1.00	1.00		
	459702	AI204995		gb:an03c03.x1 Stratagene schizo brain S1	1.00	237.00		

TABLE 9B

65	Pkey:	Unique Eos probeset identifier number	
	CAT number:	Gene cluster number	
	Accession:	Genbank accession numbers	
70	Pkey	CAT Number	Accession
	407746	10125_1	AK001962 R69415 BE464605 AA418699 AA053293 AA149075 AA058396 AW338226 AW272659 AA454607 AI139535 AW469852 AI275461 AW271982 AA730033 AA576507 AA991217 AA782067 AI985851 AA805864 AA505598 AW469857 R69546 AA988279 AW001647 N63320 D82661 T27343 AA306950 AA360989 R58778
	408070	1036688_1	AW148852 BE350895
75	408660	107294_1	AA525775 AA056342 AI538978 AW975281 AA664986
	409522	113735_1	AA075382 AA075431
	409866	1156522_1	AW502152 H41202 H29772
	410032	1170435_1	BE065985 BE065944 BE066008 BE066083 BE066093
	411089	123172_1	AA456454 AA713730 AA091294 AA584921 N86077 AW836781 AA601031 AA579876 AA551106 AA633188 AW905577 AI955808 AI679386 AI679895 AA514764 AA454562 AI082382 AA595822 AA551351 AA586369 AA666384 AA188934 AA666398 AA551297 AA565188
80	411152	1234028_1	BE069199 AW936012 AW877466 AW819782 AW935798 AW835546 AW936042 BE069121 AW835625 AW877536 AW935885 BE069202 AW820019 AW935937 BE160180 AW935946 BE069101 BE069125 AW877527 BE160316 BE160398 AW935794 AW835701 AW935784 AL031778 X59711 NM_002505 M59079 AI870439 AI494259 AW664010 AA405063 AA436132 BE174516 AA412691 AI400314 AA436024 T29403 BE079412 BE079428 N90322 AI631202 AI141758 AI016793 AI167566 AI862075 AI375230 AI208445 AW235763 AL044113 AA382556 AW953918 AA927051 AA889823 BE003094 AW390155 AW360805 AW360823 AW360810 AA425472 AI694282 AL044114 AI684577 AI809865
	412537	1304_1	



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## PCT/US02/12476

			AI478773 AI160445 AI674630 N69088 AW665529 N49278 AI129239 AI457890 AI621264 AW297152 AI268215 AA907787 AI286170 AI017982 AI963541 AI469807 AI969353 BE552356 N66509 AA736741 AA382555 AW075811 AW292026 H06382 AW957730 AA352014 R13591 AA121201 D60420 BE263253 BE047862 Z41952 AI424991 AI693507 AI863108 AA599060 AI091148 AA598689 R39887 AA813482 AW016452 H06383 R41807 AI364268 AA620528 AI241940 AW089149 AW090733 AW088875 Z38240 AA121202 R17734 BE157489 BE157560 AA926960 AA926959 W76521 W24270 W21526 AA037172 BE267636 H83186 AA469909 N86396 AA001348 BE535736 AA081745 BE566245 AA082436 H72525 H77575 N49786 W80565 H78746 BE569085 W04339 R98127 T55938 BE279271 AW960304 T29812 AA476873 BE297387 AA292753 AA177048 NM_001826 X54941 BE314366 AA908783 AI719075 BE270172 BE269819 AA889955 AI204630 W25243 AI935150 AA872039 W72395 T99630 AI422691 H98460 N31428 BE255916 H03265 AI857576 AA776920 AA910644 AA459522 AA293140 AW514667 R75953 AW662396 AA662522 AI865147 AI423153 AW262230 AA584410 AA583187 AW024595 AW069734 AI828996 AA282997 AA876046 AW613002 AA527373 AW972459 AI813360 AA621337 AA100926 AA772418 AA594628 AI033892 W95096 AI034317 AA398727 AI085031 N95210 AI459432 AI041437 AA932124 AA627684 AA935829 AI004827 AI423513 AI094597 H42079 R54703 AI630359 AA617681 AA978045 AA643280 W44561 AI991988 AI537692 AI090262 AA740817 AI312104 AI911822 AA416871 AI185409 AA129784 AA701623 AI075239 AI139549 AA633648 AI339996 AI336880 AA399239 AI078708 AI085351 AI362835 AI346618 AI146955 AI989380 AI348243 N92892 AA765850 AI494230 AI278887 AA962596 AI492600 W80435 AA001979 R97424 AI129015 N24127 AA157451 AA235549 AA459292 AA037114 AA129785 AI494211 AW059601 AW886710 R92790 N59755 AI361128 AW589407 H47725 H97534 H48076 H48450 T99631 AW300758 H03431 R76789 AA954344 H77576 R96823 AI457100 N92845 N49682 H42038 BE220698 BE220715 H99552 AA701624 N74173 R54704 H79520 H72923 H03266 BE261919 AA769633 AA480310 AA507454 AA910586 AI203723 AW104725 W25611 W25071 T88980 H03513 T77589 R99156 W95095 R97470 AA702275 T77551 AA911952 H82956 N83673 AA283672 AI267700 AI720344 AA191424 AI023543 AI469633 AA172056 AW958465 AA172236 AW953397 AA355086 AW265494 AA455904 AA195677 AW265432 AW991605 AA4566370 N28754 N28747 AI568146 AI979339 AA322671 AA322672 AW955043 AI990326 AA776406 AI016250 AA843678 AW451882 N23137 N23129 W70051 AI038748 AA831327 AI925845 AW945895 Z42183 T31621 T97478 D62703 AA242966 D79798 AU076704 T74854 T74860 T72098 T73265 T73873 T69180 T74658 T58786 T60385 T73410 T68781 T67845 T67593 T73952 T67864 T60630 T68367 T68401 T53959 T72360 T72099 T60377 T58961 T71712 T72821 T64738 T74645 T72037 T68688 T72063 T73258 T72826 T64242 T68220 T74673 T71800 T68355 T61227 T62738 T69317 T53850 T64692 T73768 T73962 T73382 T68914 T70975 T73400 T60631 T73277 T73203 T70498 T61409 T58925 NM_000508 M64982 T68301 T73729 T69445 T60424 T67922 T67736 T68716 T67755 T74765 T73819 T58719 T74756 T60477 T74863 T61109 T68329 T58850 T71857 T73425 T53736 T68607 T58898 T64309 T72031 T72079 T64305 T71908 T68107 T71916 T73787 T56035 T64425 T71870 T60476 T61376 T67820 T71895 T41006 T69441 T68170 T74617 T71958 T69440 T61875 R06796 H48353 T71914 T53939 T64121 AA693996 T72525 T67779 T68078 AA011465 AA345378 AV654847 AV654272 AV656001 AI064740 T82897 N33594 AA344542 AW805054 AI207457 T61743 AA026737 H94389 AA382695 AA918409 T68044 S82092 T39959 AI017721 AA312395 AA312919 T40156 H66239 AV652989 H38728 R98521 AV655200 R95790 W03250 W00913 AA344136 AV660126 R97923 AA343595 AW470774 AV651256 N54417 AA812852 AW182929 AI111192 H61463 H72060 AA344503 H38639 AI277511 AV661108 AI207625 T47810 AA235252 T27853 T47778 R95746 H70620 AA701463 AW827166 R98475 C20925 AV657287 T71959 T71313 T73920 T73333 T61618 T69293 T69283 T73931 T72178 T72456 AV645639 AV653476 T72957 T72300 T58906 T71457 T70494 T72956 T70495 T68267 T74407 T85778 AA344726 T27854 T74485 T74101 T73868 T71518 T72304 AA343853 T73909 T68070 T72065 H72149 T73493 T73495 AV645993 R02293 T70475 T64751 AA344441 AA343657 AA345732 AA344328 AI110639 AA344603 AF063513 T64696 T68516 T72223 T60507 T67633 T29500 T72517 R02292 T60599 T69206 T70452 T74677 R29366 T61277 T74914 T60352 R29675 T74843 AV645792 AA344408 T69197 T72057 T69368 T69358 T68258 AV650429 T73341 T61702 T74598 T40095 K02272 T40106 AA343045 AA341908 AA341907 AA342807 AA341964 T53747 T72042 T62764 AI064899 AA343060 T67832 T72440 T71770 T68091 T69108 T72449 T69167 T71289 T68251 AV654844 T64375 AA345234 T67598 AA011414 T68036 H48262 AI207557 T68219 W86031 T69081 T64232 R93196 T62136 AV650539 H67459 T72978 AA344583 T60362 H58121 T95711 T72803 T68055 T71715 R29036 T72793 T69122 T64595 T62888 T69139 T68291 T64652 T67971 T46862 AA693592 AI248502 R29454 T64764 T57001 T73052 T71429 T51176 T58866 AV655414 H90426 AA342489 T73666 T67848 T72512 T53835 T67837 T73317 T74273 T69420 T68245 T74380 T67862 T74474 T56068 AI792788 BE142230 AA252019 AI910275 X00474 X52003 X05030 NM_003225 AA314326 AA308400 AA506787 AA314825 AI571948 AA507595 AA614579 AA587613 R83818 AA568312 AA614409 AA307578 AI925552 AW950155 AI910083 M12075 BE074052 AW004668 AA578674 AA582084 BE074053 BE074126 BE074140 AA514776 AA588034 BE074051 BE074068 AW009769 AW050690 AA858276 R55389 AI001051 AW050700 AW750216 AA614539 BE074045 AI307407 AW602303 BE073575 AI202532 AA524242 AI970839 AI909751 BE076078 AI909749 R55292 AW881145 AA490718 M85637 AA304575 T06067 AA331991 AL119930 AA320696 AW752565 AL031985 AL137241 AI792388 AI733664 AI857654 AI049911 AA337221 AA336756 AW966196 AW953120 R56325 AA349562 AI493134 AI498691 AW771508 AI498457 AI768408 AI783624 AI383985 AI580267 D79813 AA393768 AK001536 AA191092 AW510354 AI554256 AL353968 AA134266 AA663848 AA400100 AA401424 AL038843 AA161338 BE268213 AA425597 N87306 AA092969 BE566038 AA247451 N47392 AI928802 AW182584 AW027872 AI819831 AI936994 W56258 AI653448 AI278611 AI283557 AI824306 AW338658 AW150899 AA687514 N47393 N29885 AA973469 AI038904 AI292064 AI034339 AW674593 N72156 AI079733 AI038683 AI291616 AA491599 AA93675 AA837380 BE006554 AI087090 T33044 AA652043 AI203503 AA583959 W35283 AI129926 Z41844 AW020925 AW575848 AI684603 AA493297 AI140689 AI277175 AA425444 AI932767 W02632 BE396786 R37261 AW207206 AW341473 AA448195 AI951341 AA249027 AL038984 AK001993 AL080066 AV652725 BE566226 AA345557 AA315222 AA090585 AA375688 AA301092 AA298454 W05762 AW607939 H51658 D83880 N84323 BE296821 AW947007 D61461 AW079261 AA329482 AW901780 AI354442 AA772275 R31663 AI354441 AI767525 H92431 AI916735 H93575 AI394255 AW014741 AI573090 C06195 AW612857 AW265195 AI339558 AI377532 AI308821 AI919424 AI589705 AW055215 AI336532 AI338051 AA806547 C75509 C00618 AW071172 AW769904 AA630381 AI678018 AI863985 D79662 BE221049 AW265018 AI589700 AW196655 N76573 AI370908 BE042393 N75017 AI698870 AW960115 AL133561 AL041090 AL117481 AL122069 AW439292 AI968826 AW072916 AI184913 AA489195 AW466994 AW469044 N59350 AI819642 AI280239 AI220572 AA789302 AI473611 AW841126 D60937 BE041395 AA491826 AA621946 AA715980 AA666102 AW970622 AA503009 AA502998 AA502999 AA502805 T92188 AA221036 R87170 BE537068 BE544757 C18935 AW812058 T92565 AA227415 AA233942 AA223237 AA668403 AA601627 AW869639 BE061833 BE000620 AW961170 AW847519 AA308542 AW821833 AW945688 C04699 AA205504 AA377241 AW821667 AA055720 AW817981 AW856468 AA155719 AA179928 T03007 AW754298 AA227407 AA113928 AA307904 C16859 AI788376 S46400 AW811617 AW811616 W00557 BE142245 AW858232 AW861851 AW858362 AA232351 AA218567 AA055556 AW858231 AW857541 AW814172 H66214 AW814398 AF134164 AA243093 AA173345 AA199942 AA223384 AA227092 AA227080 T12379 AA092174 T61139 AA149776 AA699829 AW879188 AW813567 AW813538 AI267168 AA157718 AA157719 AA100472 AA100774 AA130756 AA157705 AA157730 AA157715 AA053524 AW849581 AW854566 C05254 AW882836 T92637 AW812621 AA206583 AA209204 BE156909 AA226824 AI829309 AW991957 N66951 AA527374 H66215 AA045564 AI694265 H60808 AA149726 AW195620 BE081333 BE073424 AW817662 AW817705 AW817703 AW817659 BE081531 H59570 AA628980 AI126603 BE504035
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438091 44964\_1 AW373062 T55662 AI299190 BE174210 AW579001 H01811 W40186 R67100 AI923886 AW952164 AA628440 AW898607 AW898616  
AA709126 AW898628 AW898644 AA947932 AW898625 AW898622 AI276125 AI185720 AW510698 AA987230 T52522 BE467708 AW243400  
AW043642 AI288245 AI186932 D52654 D55017 D52715 D52477 D53933 D54679 AI298739 AI146984 AI922204 N98343 BE174213 AA845571  
AI813854 AI214518 AI635262 AI139455 AI707807 AI698085 AW884528 AI024768 AI004723 AW087420 AI565133 N94964 AI268939  
AW513280 AI061126 AI435818 AI859106 AI360506 AI024767 AA513019 AA757598 X56196 AA902959 AI334784 AI860794 AA010207  
AW890091 AW513771 AI951391 AI337671 T52499 AA890205 AI640908 H75966 AA463487 AA358688 AI961767 AI866295 AA780994  
AI985913 BE174196 AA029094 AW592159 T55581 N79072 AI611201 AA910812 AI220713 AW149306 AI758412 AA045713 R79750 N76096  
AW979121 AA847986 AA829098  
AL133916 N79113 AF086101 N76721 AW950828 AA364013 AW955684 AI346341 AI867454 N54784 AI655270 AI421279 AW014882  
AA775552 N62351 N59253 AA626243 AI341407 BE175639 AA456968 AI358918 AA457077  
AL109688 R23665 R26578  
AA570256 AW014761 AA573721 AI473237 AI022165 AA554071 AA127551 N90525 AW973623 AA447991 AA243852 BE328850 AI148171  
AI359627 AI005068 AI356567 AA232991 AW016855 AA906902 AA233101 AA127550 BE512923  
AI188710 AI032142 AW078833 N30308 AW675632 AI219028 AI341201 N22181 H95390  
W24187 W24194 R17789  
Y10043 NM\_005342 L05085 AL034450 BE614226 AW749053 AA379173 AA248230 BE514634 AA334622 R70656 AA367593 AA214649  
AA369318 AW957081 R05760 AA039903 AI886597 AW630122 AA906264 AA041527 R01145 AI088688 BE463637 AA398795 AI354883  
AI768938 AI569996 AI452952 AI168582 AI189869 AI086670 AW262560 AW613854 AA862839 AA435840 AA670197 AI024032 AI990659  
AI990089 N81095 AA847919 AW960150 AA211075 AA044704 AA367594 AW582587 AW858854 AW818630 AW818281 AW818433 AW582595  
AA096002 N83992  
AI471630 BE540637 BE265481 AW407710 BE513882 BE546739 AA053597 BE140503 BE218514 AW956702 AI656234 AI636283 AI567265  
AW340858 BE207794 AA053085 R69173 AA292343 AA454908 AA293504 AI659741 AI927478 AA399460 AI760441 AA346416 BE047245  
AA730380 AA394063 AA454833 AI982791 AI567270 AI813332 AI767858 AA427705 D20284 AI221458 BE048537 AI263048 AA346417  
AA911497 BE537702  
AI638293 AW813561  
AI761324 AW880941 AW880937  
AW118072 AI631982 T15734 AA224195 AI701458 W20198 F26326 AA890570 N90552 AW071907 AI671352 AI375892 T03517 R88265  
AI124088 AA224388 AI084316 AI354686 T33652 AI140719 AI720211 T03490 AI372637 T15415 AW205836 AA630384 T03515 T33230  
AA017131 AA443303 T33623 AI222556 T33511 T33785 AI419606 D55612  
W52854 AL117600 BE208116 BE208432 BE206239 BE082291 AW953423 AA351619 BE180648 BE140560 W60080 AA865478 N90291  
AW450652 AW449519 AA993634 AI806539 AA351618 AW449522 AI827626 AA904788 AA380381 AA886045 AA774409 BE003229 Z41756  
AI133619 AA468118 AA383064 AI478447 T09430 AI673758 AA524895 AI581345 AI300820 AW498812 AA256162 AI559724 AI685732  
AA602400 AA905453 AI204595 AW166541 AA157458 AA156269 AA383652 AA431072 AW592707 AI435410 AW272464 AI215594 AA622747  
R74039 N35031 AI804128 AW513621 AA868351 AI026826 AI493388 AA614641 W81604 AI567080 AI214351 AA730140 AI125754 AI200813  
AI269603 AI565082 AI807095 AI476629 AA505909 AI368449 AI686077 AI582930 AW085038 AA757863 AA730154 AI767072 AA468316  
AI734130 AI734138 AA426284 AA433997 AI741241 AW043563 AI732741 AI732734 AA437369 AA425820 AA664048 R74130  
BE144666 BE184942 AW238414 BE184946  
AW993247 AW861464  
AA203682 R11958  
BE550224 AA832519 N45402 AW885857 N29245 BE465409 W07677 AW970089 AI299731 AA482971 BE503548 H18151 W79223 AF086393  
AA461301 W74510 R34182 AI090689 N46003 BE071550 R28075 AW134982 AI240204 AI138906 AW026179 AI572316 BE466182 AI206395  
AI276154 AI273269 AI422817 AI371014 AI421274 AI188525 AA939164 BE549810 AW137865 AI694996 BE503841 AA459718 BE327407  
BE467534 BE218421 BE467767 AA989054 BE467063 AI797130 BE327781

## TABLE 9C

Pkey: Unique number corresponding to an Eos probeset  
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.  
Strand: Indicates DNA strand from which exons were predicted.  
NL\_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
400512	9796593	Minus	1439-1615
400517	9796686	Minus	49996-50346
400560	9843598	Plus	94182-94323,97056-97243,101095-101236,102824-103005
400664	8118496	Plus	13558-13721,13942-14090,14554-14679
400665	8118496	Plus	16879-17023
400666	8118496	Plus	17982-18115,20297-20456
400749	7331445	Minus	9162-9293
400763	8131616	Minus	35537-35784
401027	7230983	Minus	70407-70554,71060-71160
401093	8516137	Minus	22335-23166
401203	9743387	Minus	172961-173056,173868-173928
401212	9858408	Plus	87839-88028
401411	7799787	Minus	144144-144329
401435	8217934	Minus	54508-55233
401464	6682291	Minus	170688-170834
401714	6715702	Plus	96484-96681
401747	9789672	Minus	118596-118816,119119-119244,119609-119761,120422-120990,130161-130381,130468-130593,131097-131258,131866-131932,132451-132575,133580-134011
401760	9929699	Plus	83126-83250,85320-85540,94719-95287
401780	7249190	Minus	28397-28617,28920-29045,29135-29296,29411-29567,29705-29787,30224-30573
401781	7249190	Minus	83215-83435,83531-83656,83740-83901,84237-84393,84955-85037,86290-86814
401785	7249190	Minus	165776-165996,166189-166314,166408-166569,167112-167268,167387-167469,168634-168942
401797	6730720	Plus	6973-7118
401961	4581193	Minus	124054-124209
401985	2580474	Plus	61542-61750
401994	4153858	Minus	42904-43124,43211-43336,44607-44763,45199-45281,46337-46732
402075	8117407	Plus	121907-122035,122804-122921,124019-124161,124455-124610,125672-126076
402260	3399665	Minus	113765-113910,115653-115765,116808-116940
402265	3287673	Plus	21059-21168
402297	6598824	Plus	35279-35405,35573-35659
402408	9796239	Minus	110326-110491



	402420	9796339	Plus	129750-129919
	402674	8077108	Minus	39290-39502
	402802	3287156	Minus	53242-53432
5	402994	2996643	Minus	4727-4969
	403137	9211494	Minus	92349-92572,92958-93084,93579-93712,93949-94072,94591-94748,95214-95337
	403306	8099945	Plus	127100-127251
	403329	8516120	Plus	96450-96598
	403381	9438267	Minus	26009-26178
10	403478	9958258	Plus	118458-116564
	403485	9966528	Plus	2888-3001,3198-3532,3655-4117
	403627	8569879	Minus	23868-24342
	403715	7239669	Plus	85128-85292
	404044	9558573	Minus	225757-225939
15	404076	9931752	Minus	3848-3967
	404101	8076925	Minus	125742-125997
	404140	9843520	Plus	37761-38147
	404165	9926489	Minus	69025-69128
	404185	4572584	Minus	129171-129327
20	404210	5006246	Plus	169926-170121
	404253	9367202	Minus	55675-56055
	404287	2326514	Plus	53134-53281
	404298	9944263	Minus	73591-73723
	404347	9838195	Plus	74493-74829
25	404440	7528051	Plus	80430-81581
	404721	9856648	Minus	173763-174294
	404794	4826439	Plus	101619-101898
	404854	7143420	Plus	14260-14537
	404877	1519284	Plus	1095-2107
30	404927	7342002	Plus	68690-69563
	404986	6007890	Plus	37999-38145,38652-38998,39727-39872,40557-40674,42351-42450
	405449	7622497	Plus	42236-42570
	405568	6006906	Plus	35912-36065
	405572	3800891	Plus	85230-85938
35	405646	4914350	Plus	741-969
	405676	4557087	Plus	73195-73917
	405770	2735037	Plus	61057-62075
	405932	7767812	Minus	123525-123713
40	406137	9166422	Minus	30487-31058
	406360	9256107	Minus	7513-7673
	406399	9256288	Minus	63448-63554
	406467	9795551	Plus	182212-182958

TABLE 10A: Potential Therapeutic, Diagnostic and Prognostic targets for Therapy of Lung Cancer and Non-malignant Lung Disease  
 Table 2A shows about 307 genes up-regulated in non-malignant lung disease relative to lung tumors and normal body tissues and/or down-regulated in lung tumors relative to normal lung and non-malignant lung disease. These genes were selected from about 59680 probesets on the Eos/Affymetrix Hu03 Genechip array.

Table 10B show the accession numbers for those Pkey's lacking UnigenelD's for table 10A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Table 10C show the genomic positioning for those Pkey's lacking UnigenelD's and accession numbers in table 10A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

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Pkey:1  
ExAccn:  
UnigenelD:  
Unigene Title:  
R1:  
R2:

Unique Eos probeset identifier number  
Exemplar Accession number, Genbank accession number  
Unigene number  
Unigene gene title  
Average of lung tumors (including squamous cell carcinomas, adenocarcinomas, small cell carcinomas, granulomatous and carcinoid tumors) divided by the average of normal lung samples  
Average of non-malignant lung disease samples (including bronchitis, emphysema, fibrosis, atelectasis, asthma) divided by the average of normal lung samples

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Pkey	ExAccn	UnigenelD	Unigene Title	R1	R2
404394			ENSP00000241075:TRRAP PROTEIN.	0.79	3.10
404916			Target Exon	1.00	159.00
405257			Target Exon	1.00	422.00
407228	M25079	Hs.155376	hemoglobin, beta	0.47	2.33
407568	AA740964	Hs.62699	ESTs	1.00	123.00
408562	AI436323	Hs.31141	Homo sapiens mRNA for KIAA1568 protein,	1.00	230.00
409031	AA376836	Hs.76728	ESTs	1.00	128.00
410434	AF051152	Hs.63668	tol-like receptor 2	39.65	149.00
410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	1.00	109.00
410808	T40326	Hs.167793	ESTs	1.14	13.14
412351	AL135960	Hs.73828	T-cell acute lymphocytic leukemia 1	0.37	2.27
412372	R65998	Hs.285243	hypothetical protein FLJ22029	1.00	173.00
413795	AL040178	Hs.142003	ESTs	0.10	11.90
414154	AW205314	Hs.323060	ESTs	0.62	2.09
414214	D49958	Hs.75819	glycoprotein M6A	0.03	4.55
414998	NM_002543	Hs.77729	oxidised low density lipoprotein (lectin	0.64	2.97
415122	D60708	Hs.22245	ESTs	0.07	8.97
415765	NM_005424	Hs.78824	tyrosine kinase with immunoglobulin and	0.67	1.65
415775	H00747	Hs.29792	ESTs, Weakly similar to I38022 hypothe	0.29	2.64
415910	U20350	Hs.78913	chemokine (C-X3-C) receptor 1	1.00	145.00

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	416319	AI815601	Hs.79197	CD83 antigen (activated B lymphocytes, i	15.32	237.00
	416402	NM_000715	Hs.1012	complement component 4-binding protein,	0.64	4.00
	417355	D13168	Hs.82002	endothelin receptor type B	0.01	3.90
5	417421	AL138201	Hs.82120	nuclear receptor subfamily 4, group A, m	36.30	357.00
	417511	AL049176	Hs.82223	chordin-like	1.00	179.00
	418489	U76421	Hs.85302	adenosine deaminase, RNA-specific, B1 (h	0.02	6.00
	418726	BE241812	Hs.87860	protein tyrosine phosphatase, non-recept	1.00	113.00
	418741	H83265	Hs.8881	ESTs, Weakly similar to S41044 chromosom	0.44	1.90
10	418883	BE387036	Hs.1211	acid phosphatase 5, tartrate resistant	0.96	2.04
	419086	NM_000216	Hs.89591	Kallmann syndrome 1 sequence	0.62	2.74
	419150	T29618	Hs.89640	TEK tyrosine kinase, endothelial (venous	0.03	6.90
	419235	AW470411	Hs.288433	neurotrophin	1.48	5.13
	419407	AW410377	Hs.41502	hypothetical protein FLJ21276	37.55	336.00
15	420556	AA278300	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L	0.80	3.65
	420656	AA279098	Hs.187636	ESTs	1.65	8.07
	420729	AW964897	Hs.290825	ESTs	2.99	25.82
	421177	AW070211	Hs.102415	Homo sapiens mRNA; cDNA DKFZp586N0121 (f	0.46	1.95
	422080	R20893	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A	1.00	156.00
	422426	W79117	Hs.58559	ESTs	0.03	7.44
20	422652	AW967969	Hs.118958	syntrophin 11	0.14	3.62
	423099	NM_002837	Hs.123641	protein tyrosine phosphatase, receptor t	0.01	3.16
	424433	H04607	Hs.9218	ESTs	0.75	141.75
	424585	AA464840	Hs.131987	ESTs	1.00	167.00
25	424711	NM_005795	Hs.152175	calcitonin receptor-like	0.43	3.01
	424973	X92521	Hs.154057	matrix metalloproteinase 19	0.37	19.45
	425023	AW956889	Hs.154210	endothelial differentiation, sphingolipi	0.14	3.35
	425664	AJ006276	Hs.159003	transient receptor potential channel 6	1.00	94.00
	425998	AU076629	Hs.165950	fibroblast growth factor receptor 4	0.68	1.42
30	426657	NM_015865	Hs.171731	solute carrier family 14 (urea transport	0.03	3.74
	426753	T89832	Hs.170278	ESTs	1.00	141.00
	427558	D49493	Hs.2171	growth differentiation factor 10	1.00	117.00
	427983	M17706	Hs.2233	colony stimulating factor 3 (granulocyte	0.75	2.20
	428467	AK002121	Hs.184465	hypothetical protein FLJ11259	0.76	2.25
35	428927	AA441837	Hs.90250	ESTs	0.01	3.62
	429496	AA453800	Hs.192793	ESTs	1.00	138.00
	430468	NM_004673	Hs.241519	angiopoietin-like 1	1.00	132.00
	431385	BE178536	Hs.11090	membrane-spanning 4-domains, subfamily A	1.00	157.00
	431728	NM_007351	Hs.268107	multimerin	1.00	157.00
40	431848	AI378857	Hs.126758	ESTs, Highly similar to AF175283 1 zinc	0.34	2.24
	432128	AA127221	Hs.117037	ESTs	0.00	1.15
	432519	AI221311	Hs.130704	ESTs, Weakly similar to BCHUIA S-100 pro	0.01	2.06
	433043	W57554	Hs.125019	lymphoid nuclear protein (LAF-4) mRNA	1.00	267.00
	433803	AI823593	Hs.27688	ESTs	1.00	105.00
45	434730	AA644669	Hs.193042	ESTs	1.05	3.15
	435472	AW972330	Hs.283022	triggering receptor expressed on myeloid	0.83	1.94
	436532	AA721522	gb:nv54h12.r1 NCLCGAP_Ew1 Homo sapiens	1.00	218.00	
	437119	AI379921	Hs.177043	ESTs	1.00	133.00
	437140	AA312799	Hs.283689	activator of CREM in testis	0.67	122.67
50	437211	AA382207	Hs.5509	ecotropic viral integration site 2B	1.00	142.00
	437960	AI669586	Hs.222194	ESTs	1.00	147.00
	438202	AW169287	Hs.22588	ESTs	1.00	141.00
	438873	AI302471	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L	0.71	3.66
	438875	AA827640	Hs.189059	ESTs	23.32	370.00
55	441048	AA913488	Hs.192102	ESTs	0.77	8.50
	441188	AW292830	Hs.255609	ESTs	3.43	16.36
	441499	AW298235	Hs.101689	ESTs	1.00	167.00
	444513	AL120214	Hs.7117	glutamate receptor, ionotropic, AMPA 1	1.00	151.00
	444527	NM_005408	Hs.11383	small inducible cytokine subfamily A (Cy	46.47	153.00
60	444561	NM_004469	Hs.11392	c-fos induced growth factor (vascular en	0.01	3.08
	445279	R41900	Hs.22245	ESTs	0.60	141.00
	446017	N98238	Hs.55185	ESTs	0.18	2.39
	446984	AB020722	Hs.16714	Rho guanine exchange factor (GEF) 15	0.10	2.16
	446998	N99013	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	0.01	2.53
65	447357	AI375922	Hs.159367	ESTs	0.46	2.64
	448106	AI800470	Hs.171941	ESTs	18.05	296.00
	448253	H25899	Hs.201591	ESTs	1.00	141.00
	449275	AW450848	Hs.205457	periaxin	0.56	1.38
	450400	AI694722	Hs.279744	ESTs	0.88	4.33
70	450696	AI654223	Hs.16026	hypothetical protein FLJ23191	0.52	2.08
	450726	AW204600	Hs.250505	retinoic acid receptor, alpha	0.79	2.01
	451497	H83294	Hs.284122	Wnt inhibitory factor-1	0.35	2.03
	451533	NM_004657	Hs.26530	serum deprivation response (phosphatidyl	0.13	2.25
	453636	R67837	Hs.169872	ESTs	1.00	116.00
75	458332	AI000341	Hs.220491	ESTs	1.00	192.00
	459580	AA022888	Hs.176065	ESTs	0.20	2.98
	400269			Eos Control	0.40	2.40
	403421			NM_016369*:Homo sapiens claudin 18 (CLDN	0.53	1.77
	407570	Z19002	Hs.37096	zinc finger protein 145 (Kruppel-like, e	0.01	3.18
80	412295	AW088826	Hs.117176	poly(A)-binding protein, nuclear 1	0.56	1.74
	414517	M24461	Hs.76305	surfactant, pulmonary-associated protein	0.64	1.50
	417204	N81037	Hs.1074	surfactant, pulmonary-associated protein	0.33	1.16
	418307	U70867	Hs.83974	solute carrier family 21 (prostaglandin	0.53	1.55
	418935	T28499	Hs.89485	carbonic anhydrase IV	0.20	1.28
	421502	AF111856	Hs.105039	solute carrier family 34 (sodium phospho	0.78	1.90
85	421798	N74880	Hs.29877	N-acylsphingosine amidohydrolase (acid c	0.59	1.54



	423354	AB011130	Hs.127436	calcium channel, voltage-dependent, alph	0.59	1.55
	423738	AB002134	Hs.132195	airway trypsin-like protease	10.14	51.00
	425211	M18667	Hs.1867	progastricsin (pepsinogen C)	0.35	1.62
	425438	T62216	Hs.270840	ESTs	0.23	9.45
5	426828	NM_000020	Hs.172670	activin A receptor type II-like 1	0.03	1.71
	427019	AA001732	Hs.173233	hypothetical protein FLJ10970	0.01	1.49
	428043	T92248	Hs.2240	uteroglobin	0.42	1.26
	430280	AA361258	Hs.237868	Interleukin 7 receptor	0.46	2.43
	431433	X65018	Hs.253495	surfactant, pulmonary-associated protein	0.57	1.59
10	431723	AW058350	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	0.29	1.80
	432985	T92363	Hs.178703	ESTs	0.32	2.27
	441835	AB036432	Hs.184	advanced glycosylation end product-speci	0.31	1.51
	442275	AW449467	Hs.54795	ESTs	0.55	1.78
15	443709	AI082692	Hs.134662	ESTs	0.00	3.02
	444325	AW152618	Hs.16757	ESTs	0.32	2.49
	450954	AI904740	Hs.25691	receptor (calcitonin) activity modifying	0.46	1.74
	451558	NM_001089	Hs.26630	ATP-binding cassette, sub-family A (ABC1	0.52	1.87
	453310	X70697	Hs.553	solute carrier family 6 (neurotransmitte	0.00	3.30
	456855	AF035528	Hs.153863	MAD (mothers against decapentaplegic, Dr	0.01	2.31
20	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	0.66	2.20
	400754			Target Exon	1.00	297.00
	401045			C11001883*:gij6753278[ref]NP_033938.1  c	1.00	109.00
	401083			NM_016582*:Homo sapiens peptid transpor	0.89	1.39
	402474			NM_004079:Homo sapiens cathepsin S (CTSS	1.45	4.47
25	402808			ENSP00000235229:SEMB.	1.00	1.87
	403021			C21000030:gij9955960[ref]NP_063957.1  AT	1.00	149.00
	403438			NM_031419*:Homo sapiens molecule possess	1.06	2.96
	403687			NM_007037*:Homo sapiens a disintegrin-li	0.04	4.89
	403764			NM_005463:Homo sapiens heterogeneous nuc	1.00	225.00
30	404277			NM_019111*:Homo sapiens major histocompa	0.97	1.93
	404288			NM_002944*:Homo sapiens v-ros avian UR2	1.00	68.00
	404518	AI815601		CD83 antigen (activated B lymphocytes, i	0.02	1.83
	405106			C11001637*:gij5032241[ref]NP_005732.1  z	1.00	235.00
	405381			Target Exon	1.00	93.00
35	406387			Target Exon	1.37	6.02
	406646	M33600		major histocompatibility complex, class	0.86	2.46
	406714	AI219304	Hs.266959	hemoglobin, gamma G	0.01	3.19
	406753	AA505665	Hs.217493	annexin A2	1.00	147.00
40	406973	M34996	Hs.198253	major histocompatibility complex, class	1.03	2.04
	407248	U82275	Hs.94498	leukocyte immunoglobulin-like receptor,	1.00	64.00
	407510	U96191		gb:Human trophoblast hypoxia-regulated f	1.00	90.00
	407731	NM_000066	Hs.38069	complement component 8, beta polypeptide	1.00	67.00
	407830	NM_001086	Hs.587	arylacetamide deacetylase (esterase)	1.00	102.00
45	408045	AW138959	Hs.245123	ESTs	1.00	70.00
	408074	R20723		ESTs	1.00	112.00
	408374	AW025430	Hs.155591	forkhead box F1	0.07	10.17
	409064	AA062954	Hs.141883	ESTs	0.39	2.31
	409083	AF050083	Hs.673	interleukin 12A (natural killer cell sti	1.00	95.00
50	409153	W03754	Hs.50813	hypothetical protein FLJ20022	0.01	4.55
	409203	AA780473	Hs.687	cytochrome P450, subfamily IVB, polypept	0.01	3.72
	409238	AL049990	Hs.51515	Homo sapiens mRNA; cDNA DKFZp564G112 (fr	1.00	79.00
	409389	AB007979	Hs.301281	Homo sapiens mRNA, chromosome 1 specific	0.14	27.35
	409718	D86640	Hs.56045	src homology three (SH3) and cysteine ri	1.00	113.00
55	410798	BE178622	Hs.16291	gb:PM3-HT0605-270200-001-a02 HT0605 Homo	0.64	2.47
	411020	NM_006770	Hs.67726	macrophage receptor with collagenous str	0.55	2.40
	411667	BE160198		gb:QV1-HT0413-010200-059-h03 HT0413 Homo	1.00	111.00
	412000	AW576555	Hs.15780	ATP-binding cassette, sub-family A (ABC1	1.00	95.00
	412358	BE047490	Hs.24172	ESTs	1.00	87.00
60	412420	AL035668	Hs.73853	bone morphogenetic protein 2	1.43	8.07
	412564	X83703	Hs.31432	cardiac ankyrin repeat protein	0.02	3.07
	412869	AA290712	Hs.82407	CXC chemokine ligand 16	0.93	1.72
	412870	N22788	Hs.82407	CXC chemokine ligand 16	0.97	1.51
	413529	U11874	Hs.846	interleukin 8 receptor, beta	0.02	2.42
	413533	BE146973		gb:QV4-HT0222-011199-019-e05 HT0222 Homo	0.65	1.50
65	413689	BE157286	Hs.20631	zinc finger protein, subfamily 1A, 5 (Pe	20.87	232.00
	413724	AA131466	Hs.23767	hypothetical protein FLJ12666	1.00	80.00
	413800	AI129238	Hs.192235	ESTs	1.00	85.00
	413802	AW964490	Hs.32241	ESTs, Weakly similar to S65657 alpha-1C-	1.00	213.00
70	413829	NM_001872	Hs.75572	carboxypeptidase B2 (plasma)	0.02	3.93
	414376	BE393856	Hs.66915	ESTs, Weakly similar to 16.7Kd protein [	1.00	115.00
	414577	AI056548	Hs.72116	hypothetical protein FLJ20992 similar to	0.49	1.94
	414700	H63202	Hs.38163	ESTs	0.03	3.75
	415078	AA311223	Hs.283091	found in inflammatory zone 3	0.86	1.95
75	415120	N64464	Hs.34950	ESTs	1.00	120.00
	415323	BE269352	Hs.949	neutrophil cytosolic factor 2 (65kD, chr	0.60	2.48
	415335	AA847758	Hs.111030	ESTs	1.00	95.00
	415582	W92445	Hs.165195	Homo sapiens cDNA FLJ14237 fis, clone NT	1.00	136.00
	416030	H15261	Hs.21948	ESTs	0.02	8.07
	416427	BE244050	Hs.79307	Rac/Cdc42 guanine exchange factor (GEF)	1.00	73.00
80	416464	NM_000132	Hs.79345	coagulation factor VIII, procoagulant co	0.70	3.36
	416585	X54162	Hs.79386	leiomodulin 1 (smooth muscle)	0.06	6.56
	416847	L43821	Hs.80261	enhancer of filamentation 1 (cas-like do	0.70	3.66
	417148	AA359896	Hs.293885	hypothetical protein FLJ14902	1.00	114.00
	417370	T28651	Hs.82030	tryptophanyl-tRNA synthetase	0.85	1.30
85	417673	T87281	Hs.16355	ESTs	0.15	15.54



	418067	AI127958	Hs.83393	cystatin E/M	0.81	1.74
	418296	C01566	Hs.86671	ESTs	1.00	99.00
	418643	J03798	Hs.86948	small nuclear ribonucleoprotein D1 polyp	1.00	60.00
	418832	X04011	Hs.88974	cytochrome b-245, beta polypeptide (chro	2.40	14.74
5	418945	BE246762	Hs.89499	arachidonate 5-lipoxygenase	0.67	3.16
	419261	X07876	Hs.89791	wingless-type MMTV integration site fami	1.00	73.00
	419564	U08989	Hs.91139	solute carrier family 1 (neuronal/epithe	1.00	192.00
	419574	AK001989	Hs.91165	hypothetical protein	1.00	94.00
10	419968	X04430	Hs.93913	interleukin 6 (Interferon, beta 2)	61.16	500.00
	420256	U84722	Hs.76206	cadherin 5, type 2, VE-cadherin (vascula	0.52	1.70
	420285	AA258124	Hs.293878	ESTs, Moderately similar to ZN91_HUMAN Z	1.00	172.00
	420577	AA278436	Hs.186649	ESTs	1.00	97.00
	421262	AA286746	Hs.9343	Homo sapiens cDNA FLJ14265 fis, clone PL	1.00	64.00
15	421445	AA913059	Hs.104433	Homo sapiens, clone IMAGE:4054868, mRNA	0.88	1.51
	421470	R27496	Hs.1378	annexin A3	0.05	11.26
	421478	AI683243	Hs.97258	ESTs, Moderately similar to S29539 ribos	1.00	73.00
	421563	NM_006433	Hs.105806	granulysin	0.82	2.42
	421566	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	5.50	31.57
20	421855	F06504	Hs.27384	ESTs, Moderately similar to ALU4_HUMAN A	1.00	129.00
	421913	AI934365	Hs.109439	osteoglycin (osteoinductive factor, mime	1.00	101.00
	421952	AA300900	Hs.98849	ESTs, Moderately similar to AF161511 1 H	0.60	63.60
	422232	D43945	Hs.113274	transcription factor EC	1.00	148.00
	422386	AF105374	Hs.115830	heparan sulfate (glucosamine) 3-O-sulfot	1.40	3.98
25	423168	R34385	Hs.124940	GTP-binding protein	0.34	3.59
	423196	AK001866	Hs.125139	hypothetical protein FLJ11004	0.55	2.00
	423387	AJ012074		vasoactive intestinal peptide receptor 1	0.09	2.13
	423424	AF150241	Hs.128433	prostaglandin D2 synthase, hematopoietic	1.00	141.00
	423456	AL110151	Hs.128797	DKFZP586D0824 protein	1.00	66.00
30	423696	Z92546		Sushi domain (SCR repeat) containing	0.73	1.27
	424027	AW337575	Hs.201591	ESTs	0.54	2.58
	424212	NM_005814	Hs.143131	glycoprotein A33 (transmembrane)	0.77	2.47
	425087	R62424	Hs.126059	ESTs	1.00	74.00
	425175	AF020202	Hs.155001	UNC13 (C. elegans)-like	0.85	1.96
35	425771	BE561776	Hs.159494	Bruton agammaglobulinemia tyrosine kinas	1.18	2.56
	426486	BE178285	Hs.170056	Homo sapiens mRNA; cDNA DKFZp586B0220 (f	1.00	76.00
	427507	AF240467	Hs.179152	toll-like receptor 7	1.00	63.00
	427618	NM_000760	Hs.2175	colony stimulating factor 3 receptor (gr	0.60	2.19
	427732	NM_002980	Hs.2199	secretin receptor	0.97	1.42
40	427952	AA765368	Hs.293941	ESTs, Moderately similar to A53959 throm	1.00	105.00
	428709	BE268717	Hs.104916	hypothetical protein FLJ21940	1.00	80.00
	428769	AW207175	Hs.106771	ESTs	0.09	2.55
	428780	AI478578	Hs.50636	ESTs	1.00	98.00
	428833	AI928355	Hs.185805	ESTs	1.00	113.00
45	429657	D13626	Hs.2465	KIAA0001 gene product; putative G-protei	1.00	52.00
	430212	AA469153		gb:nc67f04.s1 NCI_CGAP_Pr1 Homo sapiens	1.00	132.00
	430226	BE245562	Hs.2551	adrenergic, beta-2-, receptor, surface	0.11	15.60
	430376	AW292053	Hs.12532	chromosome 1 open reading frame 21	1.00	103.00
50	430414	AW365665	Hs.120388	ESTs	0.50	6.96
	430656	AA482900	Hs.162080	ESTs	1.00	70.00
	430843	AI734149	Hs.119514	ESTs	1.00	90.00
	430998	AF128847	Hs.204038	indolethylamine N-methyltransferase	0.29	1.84
	431217	NM_013427	Hs.250830	Rho GTPase activating protein 6	1.00	79.00
	431921	N46466	Hs.58879	ESTs	0.91	1.67
55	432176	AW090386	Hs.112278	arrestin, beta 1	0.66	2.63
	432203	AA305745	Hs.49	macrophage scavenger receptor 1	1.00	76.00
	432231	AA339977	Hs.274127	CLST 11240 protein	0.46	1.46
	432485	N90866	Hs.276770	CDW52 antigen (CAMPATH-1 antigen)	0.79	2.25
	432522	D11466	Hs.51	phosphatidylinositol glycan, class A (pa	1.93	4.83
60	432596	AJ224741	Hs.278461	mairilin 3	0.04	5.79
	432850	X87723	Hs.3110	angiotensin receptor 2	1.00	167.00
	433138	AB029496	Hs.59729	semaphorin sem2	0.04	9.16
	433563	AI732637	Hs.277901	ESTs	1.00	91.00
	433588	AI056872	Hs.133386	ESTs	120.16	315.00
	434445	AI349306	Hs.11782	ESTs	0.60	1.84
65	435496	AW840171	Hs.265398	ESTs, Weakly similar to transformation-r	1.00	128.00
	435974	U29690	Hs.37744	Homo sapiens beta-1 adrenergic receptor	1.00	108.00
	436061	AI248584	Hs.190745	Homo sapiens cDNA: FLJ21326 fis, clone C	1.00	91.00
	437157	BE048860	Hs.120655	ESTs	1.00	87.00
70	437207	T27503	Hs.15929	hypothetical protein FLJ12910	1.00	105.00
	437311	AA370041	Hs.9456	SWI/SNF related, matrix associated, acti	1.00	71.00
	437439	H29796	Hs.269622	ESTs	1.00	115.00
	438199	AW016531	Hs.122147	ESTs	1.00	80.00
	439551	W72062	Hs.11112	ESTs	0.30	3.10
75	440515	AJ131245	Hs.7239	SEC24 (S. cerevisiae) related gene famil	1.00	77.00
	440887	AI799488	Hs.135905	ESTs	1.00	85.00
	441025	AA913880	Hs.176379	ESTs	1.00	82.00
	441384	AA447849	Hs.288660	Homo sapiens cDNA: FLJ22182 fis, clone H	0.79	1.89
	441735	AI738675	Hs.127346	ESTs	1.00	75.00
80	442200	AW590572	Hs.235768	ESTs	0.78	5.83
	442832	AW206560	Hs.253569	ESTs	0.03	10.88
	442957	AI949952	Hs.49397	ESTs	1.00	70.00
	443282	T47764	Hs.132917	ESTs	1.00	197.00
	443547	AW271273	Hs.23767	hypothetical protein FLJ12666	1.00	253.00
	443951	F13272	Hs.111334	ferritin, light polypeptide	0.55	2.09
85	444330	AI597655	Hs.49265	ESTs	1.00	90.00



	444515	AW204908	Hs.169979	ESTs	1.00	84.00
	445769	AI741471	Hs.23666	ESTs	0.02	4.38
	445908	R13580	Hs.13436	Homo sapiens clone 24425 mRNA sequence	1.00	97.00
5	446291	BE397753	Hs.14623	interferon, gamma-inducible protein 30	0.93	1.69
	446917	AI347863	Hs.156672	ESTs	1.00	106.00
	447261	NM_006691	Hs.17917	extracellular link domain-containing 1	0.40	47.20
	447432	AW958473	Hs.301957	nudix (nucleoside diphosphate linked moi	1.00	100.00
	447482	AB033059	Hs.18705	KIAA1233 protein	0.05	8.21
10	447997	H00656	Hs.29792	ESTs, Weakly similar to I38022 hypotheti	0.02	5.42
	448299	AA497044	Hs.20887	hypothetical protein FLJ10392	1.00	79.00
	448782	AL050295	Hs.22039	KIAA0758 protein	0.42	1.56
	450575	NM_005859	Hs.29117	purine-rich element binding protein A	0.17	11.33
	450584	AA040403	Hs.60371	ESTs	1.00	94.00
	450693	AW450461	Hs.203965	ESTs	1.00	91.00
15	450715	AI266484	Hs.31570	ESTs, Weakly similar to KIAA1324 protein	1.00	152.00
	451103	R52804	Hs.25956	DKFZP564D206 protein	1.00	86.00
	451220	AF124251	Hs.26054	novel SH2-containing protein 3	0.60	1.30
	451668	Z43948	Hs.326444	cartilage acidic protein 1	0.54	1.91
20	452197	AW023595	Hs.232048	ESTs	1.00	67.00
	452331	AA598509	Hs.29117	purine-rich element binding protein A	4.53	11.07
	452353	C18825	Hs.29191	epithelial membrane protein 2	0.72	2.24
	453049	BE537217	Hs.30343	ESTs	1.00	68.00
	453107	NM_016113	Hs.279746	vanilloid receptor-like protein 1	0.83	1.70
25	453355	AW295374	Hs.31412	Homo sapiens cDNA FLJ11422 fis, clone HE	1.00	132.00
	453390	AA862496	Hs.28482	ESTs	1.00	72.00
	453531	AA417940		ESTs, Weakly similar to JC5795 CDEP prot	1.00	68.00
	454741	BE154396		gb:CM2-HT0342-091299-050-b05 HT0342 Homo	0.57	2.89
	456579	AA287827	Hs.284205	up-regulated by BCG-CWS	1.00	82.00
30	456672	AK002016	Hs.114727	Homo sapiens, clone MGC:16327, mRNA, com	0.79	1.96
	457400	AF032906	Hs.252549	cathepsin Z	1.03	3.25
	457718	F18572	Hs.22978	ESTs, Weakly similar to ALU4_HUMAN ALU S	1.00	113.00
	459696	F03027		gb:HSC1KA072 normalized infant brain cDN	1.00	544.00

TABLE 10B

Pkey: Unique Eos probeset identifier number  
CAT number: Gene cluster number  
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
408074	103684_1	R20723 AA263003 AA333976 AA334725 AA334151 AW965490 AA310513 AI810530 D31302 AW134897 AA830127 AA046953 AI668930 C06094 AW104534
411667	1253334_1	BE160198 AW935898 T11520 AW935930 AW856073 AW861034
413533	1375344_1	BE146973 BE146972 BE147042 BE147018 BE146783 BE147020 BE146781 BE147019 BE146766 BE147021 BE146952 BE146767 BE147044 BE146797 BE146776 BE146985 BE146793 BE146768 BE146771 BE146954 BE146760 BE147048 BE147025 BE147030
423387	22779_1	AJ012074 U11087 L13288 X75299 L20295 AW630780 H14880 T28037 AI872991 R72136 AW449839 T81622 T79697 T29519 R94105 T83923 R73300 AI797007 R73390 AA961010 H74168 AI689932 BE045543 AI808418 AI608912 AI806573 AW884084 AW872978 AW872985 AA565655 AI022915 R50647 R73210 H45098 R46451 AW166269 T71132 AI264547 R52146 AI304920 R73391 AW884059 AW884085 H73241 T60038 T79612 R73145 R50549 AI094557 AI668793 R72302 AI564366 W01956 AA418962 W32571 R72840 H45409 R72085 R46356 R46758 AA508805 AA418798 T83751 R94072 T16182 AA928785 AA903896
423696	23112_1	Z92546 AA330586 AI570568 AW341487 AI827050 AW298668 AI792189 AI015693 AI733599 AI572251 AI672488 AW193262 AI244716 AI864375 AI206100 AA912444 AI269365 AI640254 AW72466 AI867336 AA627604 H16914 AA358477 AA338009
430212	314437_1	AA469153 AI718503 AA469225
436532	421802_1	AA721522 AW975443 T93070
453531	97026_1	AA417940 AA036735 T07025
454741	1232559_1	BE154396 AW817959 BE154393

TABLE 10C

Pkey: Unique number corresponding to an Eos probeset  
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.  
Strand: Indicates DNA strand from which exons were predicted.  
Nt\_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400754	7331445	Plus	144559-144684
401045	8117619	Plus	90044-90184,91111-91345
401083	3242744	Plus	33192-33360
402474	7547175	Minus	53526-53628,55755-55920,57530-57757
402808	6456148	Minus	114964-115136,115461-115585,115931-116047,117666-117771,118004-118102
403021	7547270	Plus	120799-120966
403421	9665041	Minus	126609-126773,139986-140205
403438	9719679	Plus	90792-90938
403687	7387384	Plus	9009-9534
403764	7717105	Minus	118692-118853
404277	1834458	Minus	91665-91946
404288	2769644	Plus	3512-3691
404394	3135305	Minus	37121-37205,37491-37762,41053-41140,41322-41593,41773-41919
404518	8151988	Plus	84494-84603
404916	7341826	Plus	91057-91188
405106	8079395	Minus	80877-81418
405257	7329310	Plus	73121-73273
405381	6006920	Minus	7636-8054







TABLE 11A: Genes Distinguishing Adenocarcinoma from Other Lung Diseases and Normal Lung

Table 11A shows about 84 genes upregulated in lung adenocarcinomas relative to other lung tumors, non-malignant lung disease, and normal lung. These genes were selected from about 59680 probesets on the Eos/Atfytmatrix Hu03 Genechip array.

Table 11B show the accession numbers for those Pkey's lacking UnigenelD's for table 11A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Table 11C show the genomic positioning for those Pkey's lacking UnigenelD's and accession numbers in table 11A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Pkey: Unique Eos probeset identifier number  
 ExAccn: Exemplar Accession number, Genbank accession number  
 UnigenelD: Unigene number  
 Unigene Title: Unigene gene title  
 R1: Average of lung tumors (including squamous cell carcinomas, adenocarcinomas, small cell carcinomas, granulomatous and carcinoid tumors) divided by the average of normal lung samples  
 R2: Average of non-malignant lung disease samples (including bronchitis, emphysema, fibrosis, atelectasis, asthma) divided by the average of normal lung samples

Pkey	ExAccn	UnigenelD	Unigene Title	R1	R2
403329			Target Exon	1.00	61.00
408399			NM_003122*:Homo sapiens serine protease	1.00	39.00
406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad	226.37	350.00
407869	AI827976	Hs.24391	hypothetical protein FLJ13612	0.77	1.18
407881	AW072003	Hs.40968	heparan sulfate (glucosamine) 3-O-sulfot	1.00	10.00
408908	BE296227	Hs.250822	serine/threonine kinase 15	7.76	1.00
409103	AF251237	Hs.112208	XAGE-1 protein	80.44	40.00
409187	AF154830	Hs.50966	carbamoyl-phosphate synthetase 1, mitoch	1.00	1.00
409269	AA576953	Hs.22972	hypothetical protein FLJ13352	1.00	1.00
410076	T05387	Hs.7991	ESTs	1.12	1.50
410102	AW248508	Hs.279727	Homo sapiens cDNA FLJ14035 fis, clone HE	9.89	1.00
410399	BE068889		synuclein, gamma (breast cancer-specific	0.92	1.06
411908	L27943	Hs.72924	cytidine deaminase	1.00	1.00
412612	NM_000047	Hs.74131	arylsulfatase E (chondrodysplasia puncta	1.02	1.03
414075	U11862	Hs.75741	amiloride binding protein 1 (amine oxida	0.84	1.07
416208	AW291168	Hs.41295	ESTs, Weakly similar to MUC2_HUMAN MUCIN	3.67	1.00
417542	J04129	Hs.82269	progesterone-associated endometrial prote	1.28	1.35
419183	U60669	Hs.89663	cytochrome P450, subfamily XXIV (vitamin	1.00	1.00
419502	AU076704		fibrinogen, A alpha polypeptide	13.05	115.00
419631	AW188117	Hs.303154	popeye protein 3	1.00	13.00
420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	1.00	8.00
421155	H87879	Hs.102267	lysyl oxidase	1.00	15.00
421190	U95031	Hs.102482	mucin 5, subtype B, tracheobronchial	1.17	1.55
421474	U76362	Hs.104637	solute carrier family 1 (glutamate trans	1.46	1.76
421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialyltransferase 1, l	1.00	3.00
421582	AI910275		trefoil factor 1 (breast cancer, estroge	1.23	1.00
422026	U80736	Hs.110826	trinucleotide repeat containing 9	1.00	52.00
422095	AI868872	Hs.282804	hypothetical protein FLJ22704	4.37	2.34
422311	AF073515	Hs.114948	cytokine receptor-like factor 1	1.15	1.78
422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	1.69	3.17
423472	AF041260	Hs.129057	breast carcinoma amplified sequence 1	48.13	72.00
423554	M90516	Hs.1674	glutamine-fructose-6-phosphate transamin	1.00	50.00
424502	AF242388	Hs.149585	lengsin	1.00	1.00
424544	M88700	Hs.150403	dopa decarboxylase (aromatic L-amino aci	1.00	59.00
424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	21.35	1.00
424960	BE245380	Hs.153952	5' nucleotidase (CD73)	1.00	1.00
425523	AB007948	Hs.158244	KIAA0479 protein	1.00	35.00
426230	AA367019	Hs.241395	protease, serine, 1 (trypsin 1)	1.00	83.00
427701	AA411101	Hs.243886	nuclear autoantigenic sperm protein (his	7.41	34.00
428585	AB007863	Hs.185140	KIAA0403 protein	1.00	6.00
428758	AA433988	Hs.98502	hypothetical protein FLJ14303	1.06	1.13
429170	NM_001394	Hs.2359	dual specificity phosphatase 4	16.18	105.00
429263	AA019004	Hs.198396	ATP-binding cassette, sub-family A (ABC1	1.07	1.00
429610	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas	1.59	1.69
430508	AI015435	Hs.104637	ESTs	4.75	7.27
430985	AA490232	Hs.27323	ESTs, Weakly similar to I78885 serine/th	0.94	1.28
431548	AI834273	Hs.9711	novel protein	5.66	15.00
431566	AF176012	Hs.260720	J domain containing protein 1	49.76	37.00
431986	AA536130	Hs.149018	Novel human gene mapping to chromosome 20	1.19	1.47
432375	BE536069	Hs.2962	S100 calcium-binding protein P	1.65	1.06
432677	NM_004482	Hs.278611	UDP-N-acetyl-alpha-D-galactosamine:polyp	1.00	48.00
433556	W56321	Hs.111460	calcium/calmodulin-dependent protein kin	1.00	19.00
433819	AW511097	Hs.112765	ESTs	3.71	8.00
434001	AW950905	Hs.3697	serine (or cysteine) proteinase inhibito	29.31	72.00
434424	AI811202	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L	1.00	64.00
434792	AA649253	Hs.132458	ESTs	8.52	44.00
436217	T53925	Hs.107	fibrinogen-like 1	57.97	31.00
436749	AA584890	Hs.5302	lectin, galactoside-binding, soluble, 4	1.10	1.41
436972	AA284679	Hs.25640	claudin 3	1.59	1.46
437866	AA156781		metallothionein 1E (functional)	3.62	101.00
437935	AW939591	Hs.5940	mucin 13, epithelial transmembrane	1.60	1.39
438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regi	1.00	1.00
439451	AF086270	Hs.278554	heterochromatin-like protein 1	23.28	52.00



439759	AL359055	Hs.67709	Homo sapiens mRNA full length insert cDN	1.00	21.00
441031	AI110684	Hs.7645	fibrinogen, B beta polypeptide	1.41	99.00
441377	BE218239	Hs.202656	ESTs	22.03	1.00
443614	AV655386	Hs.7645	fibrinogen, B beta polypeptide	1.00	16.00
443813	AA876372	Hs.93961	Homo sapiens mRNA; cDNA DKFZp667D095 (fr	1.20	1.99
443991	NM_002250	Hs.10082	potassium intermediate/small conductance	5.71	6.87
444670	H58373	Hs.332938	hypothetical protein MGC5370	1.98	38.00
444931	AV652066	Hs.75113	general transcription factor IIIA	1.00	54.00
446102	AW168067	Hs.317694	ESTs	1.00	1.00
446163	AA026880	Hs.25252	Homo sapiens cDNA FLJ13603 fis, clone PL	1.00	36.00
446469	BE094848	Hs.15113	homogentisate 1,2-dioxygenase (homogenti	1.00	11.00
447388	AW630534	Hs.76277	Homo sapiens, clone MGC:9381, mRNA, comp	1.24	1.16
447532	AK000614	Hs.18791	hypothetical protein FLJ20607	1.23	1.63
448243	AW369771	Hs.52620	integrin, beta 8	15.84	1.00
448844	AI581519	Hs.177164	ESTs	1.00	31.00
449444	AW818436	Hs.23590	solute carrier family 16 (monocarboxylic	1.00	83.00
451807	W52854		hypothetical protein FLJ23293 similar to	1.55	35.00
452689	F33868	Hs.284176	transferrin	1.54	1.44
453392	U23762	Hs.32964	SRV (sex determining region Y)-box 11	1.00	16.00
453464	AI884911	Hs.32989	receptor (calcitonin) activity modifying	1.55	2.45
453735	AI066629	Hs.125073	ESTs	1.01	1.30

TABLE 11B

Pkey: Unique Eos probeset identifier number  
 CAT number: Gene cluster number  
 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
410399	11995_1	BE068889 BE068882 AF044311 AF017256 NM_003087 AF037207 AF010126 AA633976 AA872836 BE298825 BE299899 AI016464 AI684600 AI936527 AA804675 AA394097 AI139933 AA946606 BE171313 AA722407 AA293803 AI468480 AA056035 AA055968 AW796957 AI637713 AA410737 H49348 AA486472 AA411094 AA235594 AA402624 AA443638 AW452137 AA421708 AW265211 AI493266 AA365132 AW966044 AU076704 T74854 T74860 T72098 T73265 T73873 T69180 T74658 T58786 T60385 T73410 T68781 T67845 T67593 T73952 T67864 T60630 T68367 T68401 T53959 T72360 T72099 T60377 T58961 T71712 T72821 T64738 T74645 T72037 T68688 T72063 T73258 T72826 T64242 T68220 T74673 T71800 T68355 T61227 T62738 T69317 T53850 T64692 T73768 T73962 T73382 T68914 T70975 T73400 T60631 T73277 T73203 T70498 T61409 T58925 NM_000508 M64982 T68301 T73729 T69445 T60424 T67922 T67736 T68716 T67755 T74765 T73819 T58719 T74756 T60477 T74863 T61109 T68329 T58850 T71857 T73425 T53736 T68607 T58898 T64309 T72031 T72079 T64305 T71908 T68107 T71916 T73787 T56035 T64425 T71870 T60476 T61376 T67820 T71895 T41006 T69441 T68170 T74617 T71958 T69440 T61875 R06796 H48353 T71914 T53939 T64121 AA693996 T72525 T67779 T68078 AA011465 AA345378 AV654847 AV654272 AV656001 AI064740 T82897 N33594 AA344542 AW805054 AI207457 T61743 AA026737 H94389 AA382695 AA918409 T68044 S82092 T39959 AI017721 AA312395 AA312919 T40156 H66239 AV652989 H38728 R98521 AV655200 R95790 W03250 W00913 AA344136 AV660126 R97923 AA343596 AW470774 AV651256 N54417 AA812862 AW182929 AI111192 H61463 H72060 AA344503 H38639 AI277511 AV661108 AI207625 T47810 AA235252 T27853 T47778 R95746 H70620 AA701463 AW827166 R98475 C20925 AV657287 T71959 T71313 T73920 T73333 T61618 T69293 T69283 T73931 T72178 T72456 AV645639 AV653476 T72957 T72300 T58906 T71457 T70494 T72956 T70495 T68267 T74407 T85778 AA344726 T27854 T74485 T74101 T73868 T71518 T72304 AA343853 T73909 T68070 T72065 H72149 T73493 T73495 AV645993 R02293 T70475 T64751 AA344441 AA343657 AA345732 AA344328 AI110639 AA344603 AF063513 T64696 T68516 T72223 T60507 T67633 R29500 T72517 R02292 T60599 T69206 T70452 T74677 R29366 T61277 T74914 T60352 R29675 T74843 AV645792 AA344408 T69197 T72057 T69368 T69358 T68258 AV650429 T73341 T61702 T74598 T40095 K02272 T40106 AA343045 AA341908 AA341907 AA342807 AA341964 T53747 T72042 T62764 AI064899 AA343080 T67832 T72440 T71770 T68091 T69108 T72449 T69167 T71289 T68251 AV654844 T64375 AA345234 T67598 AA011414 T68036 H48262 AI207557 T68219 W86031 T69081 T64232 R93196 T62136 AV650539 H67459 T72978 AA344583 T60362 H58121 T95711 T72803 T68055 T71715 R29036 T72793 T69122 T64595 T62888 T69139 T68291 T64652 T67971 T46862 AA693592 AI248502 R29454 T64764 T57001 T73052 T71429 T51176 T58866 AV655414 H90426 AA342489 T73666 T67848 T72512 T53835 T67837 T73317 T74273 T69420 T68245 T74380 T67862 T74474 T56068 AI910275 X00474 X52003 X05030 NM_003225 AA314326 AA308400 AA506787 AA314825 AI571948 AA507595 AA614579 AA587613 R83818 AA568312 AA614409 AA307578 AI925552 AW950155 AI910083 M12075 BE074052 AW004668 AA578674 AA582084 BE074053 BE074126 BE074140 AA514776 AA588034 BE074051 BE074068 AW009769 AW050690 AA858276 R55389 AI001051 AW050700 AW750216 AA614539 BE074045 AI307407 AW602303 BE073575 AI202532 AA524242 AI970839 AI909751 BE076078 AI909749 R55292 AA156781 AW293839 U52054 AA024963 AA778446 BE073977 AW444904 AW602574 BE164040 BE164012 BE163972 BE163974 BE163992 AA837481 AW468444 BE185091 AW468002 AA687333 AA811830 AA581806 AI866686 AI572124 AA043777 AA040926 D20160 AI536733 AA812489 AW874142 AI471883 W84421 AA156850 W52854 AL117600 BE208116 BE208432 BE206239 BE082291 AW953423 AA351619 BE180648 BE140560 W60080 AA865478 N90291 AW450652 AW449519 AA993634 AI806539 AA351618 AW449522 AI827626 AA904788 AA380381 AA886045 AA774409 BE003229 Z41756

TABLE 11C

Pkey: Unique number corresponding to an Eos probeset  
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., *Nature* (1999) 402:489-495.  
 Strand: Indicates DNA strand from which exons were predicted.  
 Nt\_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
403329	8516120	Plus	96450-96598
406399	9256288	Minus	63448-63554



TABLE 12A: Genes Distinguishing Squamous Cell Carcinoma from Other Lung Diseases and Normal Lung

Table 12A shows about 72 genes upregulated in squamous cell carcinomas of the lung relative to other lung tumors, non-malignant lung disease, and normal lung. These genes were selected from about 59680 probesets on the Eos/Affymetrix Hu03 Genechip array.

Table 12B show the accession numbers for those Pkey's lacking UnigenelD's for table 12A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Table 12C show the genomic positioning for those Pkey's lacking Unigene ID's and accession numbers in table 12A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Pkey: Unique Eos probeset identifier number  
 ExAccn: Exemplar Accession number, Genbank accession number  
 UnigenelD: Unigene number  
 Unigene Title: Unigene gene title  
 R1: Average of lung tumors (including squamous cell carcinomas, adenocarcinomas, small cell carcinomas, granulomatous and carcinoid tumors) divided by the average of normal lung samples  
 R2: Average of non-malignant lung disease samples (including bronchitis, emphysema, fibrosis, atelectasis, asthma) divided by the average of normal lung samples

Pkey	ExAccn	UnigenelD	Unigene Title	R1	R2
400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	132.45	4.00
400666			NM_002425:Homo sapiens matrix metallopro	3.26	3.22
401780			NM_005557*:Homo sapiens keratin 16 (foca	26.47	10.50
401781			Target Exon	10.33	4.61
401785			NM_002275*:Homo sapiens keratin 15 (KRT1	4.13	2.70
401994			Target Exon	61.84	47.00
402075			ENSP00000251056*:Plasma membrane calcium	1.00	1.00
404996			Target Exon	1.00	1.00
407839	AA045144	Hs.161566	ESTs	173.91	108.00
408000	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	151.17	8.00
408522	AI541214	Hs.46320	Small proline-rich protein SPRK (human,	1.98	1.24
410561	BE540255	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone H	10.04	1.00
415091	AL044872	Hs.77910	3-hydroxy-3-methylglutaryl-Coenzyme A sy	1.00	30.00
415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	24.30	1.00
416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	53.29	51.00
417034	NM_006183	Hs.80962	neurotensin	1.00	1.00
417366	BE185289	Hs.1076	small proline-rich protein 1B (cornifin)	8.97	3.27
418663	AK001100	Hs.41690	desmocollin 3	112.17	19.00
418678	NM_001327	Hs.87225	cancer/testis antigen	1.18	1.10
419121	AA374372	Hs.89626	parathyroid hormone-like hormone	1.00	1.00
420783	AI659838	Hs.99923	lectin, galactoside-binding, soluble, 7	3.04	1.25
421773	W69233	Hs.112457	ESTs	1.12	1.14
421948	L42583	Hs.334309	keratin 6A	51.83	20.25
421978	AJ243662	Hs.110196	NICE-1 protein	1.01	0.91
422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	2.37	1.10
422440	NM_004812	Hs.116724	aldo-keto reductase family 1, member B10	47.53	32.00
423634	AW959908	Hs.1690	heparin-binding growth factor binding pr	76.02	1.00
423725	AJ403108	Hs.132127	hypothetical protein LOC57822	4.20	1.00
423738	AB002134	Hs.132195	airway trypsin-like protease	10.14	51.00
424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	233.42	68.00
424046	AF027866	Hs.138202	serine (or cysteine) proteinase inhibito	1.00	1.00
424098	AF077374	Hs.139322	small proline-rich protein 3	137.82	54.00
424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT	56.19	12.00
425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen	33.45	1.00
427099	AB032953	Hs.173560	odd Oz/ten-m homolog 2 (Drosophila, mous	4.24	17.00
427335	AA448542	Hs.251677	G antigen 7B	51.83	4.00
428182	BE386042	Hs.293317	ESTs, Weakly similar to GGC1_HUMAN G ANT	1.00	1.00
428645	AA431400	Hs.98729	ESTs, Weakly similar to 2017205A dihydro	1.00	16.00
428748	AW593206	Hs.98785	Ksp37 protein	1.00	87.00
429259	AA420450	Hs.292911	ESTs, Highly similar to S60712 band-6-pr	2.01	1.18
429538	BE182592	Hs.11261	small proline-rich protein 2A	4.43	2.90
429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	11.80	1.00
430486	BE062109	Hs.241551	chloride channel, calcium activated, fam	12.28	41.00
430890	X54232	Hs.2699	glypican 1	1.58	1.40
431009	BE149762	Hs.48956	gap junction protein, beta 6 (connexin 3	60.25	28.00
431846	BE019924	Hs.271580	uroplakin 1B	4.49	2.51
433091	Y12642	Hs.3185	lymphocyte antigen 6 complex, locus D	1.20	1.09
434360	AW015415	Hs.127780	ESTs	40.98	27.00
434880	U02388	Hs.101	cytochrome P450, subfamily IVF, polypept	1.00	1.00
435505	AF200492	Hs.211238	interleukin-1 homolog 1	1.00	38.00
435793	AB037734	Hs.4993	KIAA1313 protein	23.68	42.00
436511	AA721252	Hs.291502	ESTs	16.76	14.00
438403	AA806607	Hs.292206	ESTs	1.00	1.00
439285	AL133916		hypothetical protein FLJ20093	46.23	139.00
439606	W79123	Hs.58561	G protein-coupled receptor 87	33.61	1.00
439670	AF088076	Hs.59507	ESTs, Weakly similar to AC004858 3 U1 sm	1.00	1.00
439706	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	86.55	11.00
440325	NM_003812	Hs.7164	a disintegrin and metalloproteinase doma	62.88	147.00
441525	AW241867	Hs.127728	ESTs	1.53	1.42
443162	T49951	Hs.9029	DKFZP434G032 protein	31.11	38.00
444378	R41339	Hs.12569	ESTs	1.00	1.00



446292	AF081497	Hs.279682	Rh type C glycoprotein	1.55	1.26
447078	AW885727	Hs.9914	ESTs	47.24	24.00
447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	28.63	1.00
449003	X76342	Hs.389	alcohol dehydrogenase 7 (class IV), mu o	1.00	1.00
449101	AA205847	Hs.23016	G protein-coupled receptor	2.58	27.00
450832	AW970602	Hs.105421	ESTs	25.17	36.00
452240	AI591147	Hs.61232	ESTs	13.42	1.00
453317	NM_002277	Hs.41696	keratin, hair, acidic,1	1.19	1.27
453830	AA534296	Hs.20953	ESTs	24.92	25.00
454098	W27953	Hs.292911	ESTs, Highly similar to S60712 band-6-pr	1.26	1.11
455601	AI368680	Hs.816	SRY (sex determining region Y)-box 2	206.11	1.00

TABLE 12B

Pkey: Unique Eos probeset identifier number  
CAT number: Gene cluster number  
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
439285	47065_1	AL133916 N79113 AF086101 N76721 AW950828 AA364013 AW955684 AI346341 AI867454 N54784 AI655270 AI421279 AW014882 AA775552 N62351 N59253 AA626243 AI341407 BE175639 AA456968 AI358918 AA457077

TABLE 12C

Pkey: Unique number corresponding to an Eos probeset  
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.  
Strand: Indicates DNA strand from which exons were predicted.  
Nt\_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400666	8118496	Plus	17982-18115,20297-20456
401780	7249190	Minus	28397-28617,28920-29045,29135-29296,29411-29567,29705-29787,30224-30573
401781	7249190	Minus	83215-83435,83531-83656,83740-83901,84237-84393,84955-85037,86290-86814
401785	7249190	Minus	165776-165996,166189-166314,166408-166569,167112-167268,167387-167469,168634-168942
401994	4153858	Minus	42904-43124,43211-43336,44607-44763,45199-45281,46337-46732
402075	8117407	Plus	121907-122035,122804-122921,124019-124161,124455-124610,125672-126076
404996	6007890	Plus	37999-38145,38652-38998,39727-39872,40557-40674,42351-42450



TABLE 13A: Genes Distinguishing Non-Malignant Lung Disease from Lung Tumors and Normal lung

Table 13A shows about 23 genes upregulated in non-malignant lung disease relative to lung tumors and normal lung. These genes were selected from about 59680 probesets on the Eos/Affymetrix Hu03 Genechip array.

Table 13B show the accession numbers for those Pkey's lacking UnigenelD's for table 13A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Table 13C show the genomic positioning for those Pkey's lacking Unigene ID's and accession numbers in table 13A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Pkey: Unique Eos probeset identifier number  
 ExAccn: Exemplar Accession number, Genbank accession number  
 UnigenelD: Unigene number  
 Unigene Title: Unigene gene title  
 R1: Average of lung tumors (including squamous cell carcinomas, adenocarcinomas, small cell carcinomas, granulomatous and carcinoid tumors) divided by the average of normal lung samples  
 R2: Average of non-malignant lung disease samples (including bronchitis, emphysema, fibrosis, atelectasis, asthma) divided by the average of normal lung samples

Pkey	ExAccn	UnigenelD	Unigene Title	R1	R2
408562	AI436323	Hs.31141	Homo sapiens mRNA for KIAA1568 protein,	1.00	230.00
409031	AA376836	Hs.76728	ESTs	1.00	128.00
412372	R65998	Hs.285243	hypothetical protein FLJ22029	1.00	173.00
415910	U20350	Hs.78913	chemokine (C-X3-C) receptor 1	1.00	145.00
417511	AL049176	Hs.82223	chordin-like	1.00	179.00
418819	AA228776	Hs.191721	ESTs	1.00	140.00
422060	R20893	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A	1.00	156.00
424585	AA464840	Hs.131987	ESTs	1.00	167.00
426753	T89832	Hs.170278	ESTs	1.00	141.00
429496	AA453800	Hs.192793	ESTs	1.00	138.00
430719	AA488988	Hs.293796	ESTs	1.00	133.00
431089	BE041395		ESTs, Weakly similar to unknown protein	23.32	941.00
431385	BE178536	Hs.11090	membrane-spanning 4-domains, subfamily A	1.00	157.00
431728	NM_007351	Hs.268107	multimerin	1.00	157.00
436532	AA721522		gb:nv54h12.r1 NCL_CGAP_Ew1 Homo sapiens	1.00	218.00
437960	AI669586	Hs.222194	ESTs	1.00	147.00
438202	AW169287	Hs.22588	ESTs	1.00	141.00
441499	AW298235	Hs.101689	ESTs	1.00	167.00
444513	AL120214	Hs.7117	glutamate receptor, ionotropic, AMPA 1	1.00	151.00
448253	H25899	Hs.201591	ESTs	1.00	141.00
453636	R67837	Hs.169872	ESTs	1.00	116.00
458332	AI000341	Hs.220491	ESTs	1.00	192.00
459587	AA031956		gb:zk15e04.s1 Soares_pregnant_uterus_NbH	1.00	154.00

TABLE 13B

Pkey: Unique Eos probeset identifier number  
 CAT number: Gene cluster number  
 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
431089	327825_1	BE041395 AA491826 AA621946 AA715980 AA666102
436532	421802_1	AA721522 AW975443 T93070

TABLE 13C

Pkey: Unique number corresponding to an Eos probeset  
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.  
 Strand: Indicates DNA strand from which exons were predicted.  
 Nt\_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
402075	8117407	Plus	121907-122035,122804-122921,124019-124161,124455-124610,125672-126076



TABLE 14A: Preferred Utility and Subcellular Localization for Potential Lung Disease Targets

Table 14A shows the subcellular localization and preferred utility for the genes appearing in Tables 9A and 10A. mAb symbolizes monoclonal antibody, diag symbolizes diagnostic, s.m. symbolizes small molecule, and CTL symbolizes cytotoxic lymphocytic ligand. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array.

Table 14B show the accession numbers for those Pkey's lacking UnigenelD's for table 14A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Table 14C show the genomic positioning for those Pkey's lacking Unigene ID's and accession numbers in table 14A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Pkey: Unique Eos probeset identifier number

ExAccn: Exemplar Accession number, Genbank accession number

UnigenelD: Unigene number

Unigene Title: Unigene gene title

Pref.Utility: Preferred Utility

Pred.Loc: Predicted subcellular localization

Pkey	ExAccn	UnigenelD	Unigene Title	Pref Utility	Pred. Loc
400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	mAb & diag & s.m.	extracellular
400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	mAb	plasma membrane
402075			ENSP00000251056*:Plasma membrane calcium	mAb & diag	secreted
407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagonist	diag	secreted
408243	Y00787	Hs.624	interleukin 8	diag	secreted
408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,	mAb & s.m.	plasma membrane
408908	BE296227	Hs.250822	serine/threonine kinase 15	s.m.	cytoplasm
409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	CTL & diag	secreted
409103	AF251237	Hs.112208	XAGE-1 protein	CTL	nuclear
409420	Z15008	Hs.54451	laminin, gamma 2 (nicein (100kD), kalini	diag	secreted
409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibito	diag	secreted
409757	NM_001898	Hs.123114	cystatin SN	diag	extracellular
409893	AW247090	Hs.57101	minichromosome maintenance deficient (S.	CTL	nuclear
409956	AW103364	Hs.727	inhibin, beta A (activin A, activin AB a	diag	extracellular
410001	AB041036	Hs.57771	kallikrein 11	diag	extracellular
410407	X66839	Hs.63287	carbonic anhydrase IX	mAb & s.m.	plasma membrane
410418	D31382	Hs.63325	transmembrane protease, serine 4	mAb & diag & s.m.	plasma membrane
412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	s.m.	
412719	AW016610	Hs.816	ESTs	s.m.	nuclear
414774	X02419	Hs.77274	plasminogen activator, urokinase	diag	extracellular
414883	AA926960		CDC28 protein kinase 1	s.m.	
415138	C18356	Hs.295944	tissue factor pathway inhibitor 2	CTL & diag	extracellular
415669	NM_005025	Hs.78589	serine (or cysteine) proteinase inhibito	mAb & diag & s.m.	secreted
415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	mAb & s.m.	plasma membrane
416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	diag	extracellular
417034	NM_006183	Hs.80962	neurotensin	diag	extracellular
417079	U65590	Hs.81134	Interleukin 1 receptor antagonist	diag	extracellular
417308	H60720	Hs.81892	KIAA0101 gene product	s.m.	mitochondrial
417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor	mAb & diag	secreted
417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	mAb	plasma membrane
417933	X02308	Hs.82962	thymidylate synthetase	s.m.	endoplasmic reticulum
418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	s.m.	cytoplasm
418506	AA084248	Hs.85339	G protein-coupled receptor 39	mAb & s.m.	plasma membrane
418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-1)	CTL	cytoplasmic
419121	AA374372	Hs.89626	parathyroid hormone-like hormone	diag	secreted
419171	NM_002846	Hs.89655	protein tyrosine phosphatase, receptor t	mAb & s.m.	plasma membrane
419183	U60689	Hs.89663	cytochrome P450, subfamily XXIV (vitamin	CTL & s.m.	mitochondrial
419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy	diag	secreted
419235	AW470411	Hs.288433	neurotrimin	mAb & diag	plasma membrane
419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7	mAb & s.m.	plasma membrane
419556	U29615	Hs.91093	chitinase 1 (chitotriosidase)	mAb & diag	extracellular*
420610	AI683183	Hs.99348	distal-less homeo box 5	CTL	nuclear
421110	AJ250717	Hs.1355	calthepin E	sm & diag	extracellular
421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	diag	secreted
421474	U76362	Hs.104637	solute carrier family 1 (glutamate trans	mAb & s.m.	plasma membrane
421552	AF026692	Hs.105700	secreted frizzled-related protein 4	diag	secreted
421753	BE314828	Hs.107911	ATP-binding cassette, sub-family B (MDR/	mAb & s.m.	plasma membrane
421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR	mAb & s.m.	plasma membrane
422109	S73265	Hs.1473	gastrin-releasing peptide	diag	secreted
422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	diag	secreted
422282	AF019225	Hs.114309	apolipoprotein L	diag	secreted
422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis	s.m.	nuclear
422424	AI186431	Hs.296638	prostate differentiation factor	diag	extracellular
422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	s.m.	cytoplasm
422809	AK001379	Hs.121028	hypothetical protein FLJ10549	s.m.	nuclear
422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	diag	extracellular
422956	BE545072	Hs.122579	ECT2 protein (Epithelial cell transformi	CTL & s.m.	
423634	AW959908	Hs.1690	heparin-binding growth factor binding pr	diag	
423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	mAb & diag & s.m.	secreted
423961	D13666	Hs.136348	perostin (OSF-2os)	mAb & diag	extracellular
424046	AF027866	Hs.138202	serine (or cysteine) proteinase inhibito	diag	secreted
424381	AA285249	Hs.146329	protein kinase Chk2	s.m.	nuclear



5	424502	AF242388	Hs.149585	lengsin	s.m.	cytoplasmic
	424503	NM_002205	Hs.149609	integrin, alpha 5 (fibronectin receptor,	mAb & s.m.	plasma membrane
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	diag	extracellular
	425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin	mAb & diag & s.m.	secreted
	425322	U63630	Hs.155637	protein kinase, DNA-activated, catalytic	s.m.	cytoplasmic
	425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen	mAb	plasma membrane
	425734	AF056209	Hs.159396	peptidylglycine alpha-amidating monooxyg	s.m.	
	425776	U25128	Hs.159499	parathyroid hormone receptor 2	mAb & diag	plasma membrane
10	425852	AK001504	Hs.159651	death receptor 6, TNF superfamily member	mAb & s.m.	plasma membrane
	426215	AW963419	Hs.155223	stanniocalcin 2	mAb & diag	secreted
	426427	M86699	Hs.169840	TTK protein kinase	CTL & s.m.	nuclear
	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic	mAb & diag	secreted
	427335	AA448542	Hs.251677	G antigen 7B	CTL	cytoplasmic
15	427747	AW411425	Hs.180655	serine/threonine kinase 12	s.m.	cytoplasmic
	428242	H55709	Hs.2250	leukemia inhibitory factor (cholinergic	diag	
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	mAb & diag & s.m.	extracellular
	428450	NM_014791	Hs.184339	KIAA0175 gene product	s.m.	nuclear
	428479	Y00272	Hs.334562	cell division cycle 2, G1 to S and G2 to	s.m.	nuclear
20	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino	mAb & s.m.	plasma membrane
	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	CTL & s.m.	nuclear
	428698	AA852773	Hs.334838	KIAA1866 protein	mAb	
	428748	AW593206	Hs.98785	Ksp37 protein	diag	extracellular
	428758	AA433988	Hs.98502	CA125 antigen; mucin 16	diag	mitochondria*
25	428969	AF120274	Hs.194689	artemin	diag	extracellular
	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3	mAb & s.m.	plasma membrane
	429263	AA019004	Hs.198396	ATP-binding cassette, sub-family A (ABC1	mAb & s.m.	plasma membrane
	429547	AW009166	Hs.99376	ESTs	diag	secreted
	429610	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas	mAb & diag	secreted
30	429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	s.m.	
	430486	BE062109	Hs.241551	chloride channel, calcium activated, fam	mAb & s.m.	plasma membrane
	431462	AW583672	Hs.256311	granin-like neuroendocrine peptide precu	diag	extracellular
	431515	NM_012152	Hs.258583	endothelial differentiation, lysophospha	mAb & s.m.	plasma membrane
	431846	BE019924	Hs.271580	uroplakin 1B	mAb & diag	plasma membrane
35	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	mAb & diag	plasma membrane
	432201	AI538613	Hs.298241	Transmembrane protease, serine 3	mAb & diag & s.m.	plasma membrane
	433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	s.m.	nuclear
	435505	AF200492	Hs.211238	interleukin-1 homolog 1	diag	secreted
40	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	s.m.	
	437016	AU076916	Hs.5398	guanine monophosphate synthetase	s.m.	cytoplasm
	437044	AL035864	Hs.69517	differentially expressed in Fanconi's an	CTL	ER
	437789	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheti	CTL	nuclear
	437852	BE001836	Hs.256897	ESTs, Weakly similar to dJ365012.1 [H.sa	mAb & s.m.	plasma membrane
	439223	AW238299	Hs.250618	UL16 binding protein 2	mAb	plasma membrane
45	439477	W69813	Hs.58042	ESTs, Moderately similar to GFR3_HUMAN G	mAb & s.m.	
	439606	W79123	Hs.58561	G protein-coupled receptor 87	mAb & s.m.	plasma membrane
	439738	BE246502	Hs.9598	sema domain, immunoglobulin domain (Ig),	mAb & s.m.	plasma membrane
	440006	AK000517	Hs.6844	NALP2 protein; PYRIN-Containing APAF1-li	s.m.	nuclear
	441362	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re	s.m.	
50	442117	AW664954	Hs.128899	ESTs; hypothetical protein for IMAGE:447	mAb & s.m.	plasma membrane
	443247	BE614387	Hs.333893	c-Myc target JPO1	CTL	extracellular*
	443426	AF098158	Hs.9329	chromosome 20 open reading frame 1	CTL	
	443859	NM_013409	Hs.9914	folliculin	diag	extracellular
55	444006	BE395085	Hs.10086	type I transmembrane protein Fn14	mAb	plasma membrane
	444371	BE540274	Hs.239	forkhead box M1	s.m.	nuclear
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	diag	secreted
	444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote	mAb & diag	plasma membrane
	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	mAb & diag	secreted
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	diag	secreted
60	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	diag	extracellular
	447033	AI357412	Hs.157601	ESTs	CTL & diag	secreted
	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	CTL	
	448243	AW369771	Hs.52620	Integrin, beta 8	mAb & s.m.	plasma membrane
	448844	AI581519	Hs.177164	ESTs	mAb & s.m.	
65	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	mAb	plasma membrane
	449722	BE280074	Hs.23960	cyclin B1	s.m.	cytoplasm
	450001	NM_001044	Hs.406	solute carrier family 6 (neurotransmitte	mAb & s.m.	plasma membrane
	450375	AA009647		a disintegrin and metalloproteinase doma	mAb & diag & s.m.	plasma membrane
70	450701	H39960	Hs.288467	hypothetical protein XP_098151 (leucine-	mAb & diag	plasma membrane
	450983	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	diag	secreted
	451668	Z43948	Hs.326444	cartilage acidic protein 1	mAb & diag	plasma membrane
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	diag	
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	diag	extracellular
	452747	BE153855	Hs.61460	Ig superfamily receptor LNIR	mAb	plasma membrane
75	452838	U65011	Hs.30743	preferentially expressed antigen in mela	CTL	nuclear
	453968	AA847843	Hs.62711	High mobility group (nonhistone chromoso	CTL & s.m.	nuclear
	457489	AI693815	Hs.127179	cryptic gene	diag	secreted

TABLE 14B

Pkey: Unique Eos probeset identifier number  
 CAT number: Gene cluster number  
 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
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414883 15024\_1 AA926960 AA926959 W76521 W24270 W21526 AA037172 BE267636 H83186 AA469909 N86396 AA001348 BE535736 AA081745 BE566245  
 AA082436 H72525 H77575 N49786 W80565 H78746 BE569085 W04339 R98127 T55938 BE279271 AW960304 T29812 AA476873 BE297387  
 AA292753 AA177048 NM\_001826 X54941 BE314366 AA908783 AI719075 BE270172 BE269819 AA889955 AI204630 W25243 AI935150  
 5 AA872039 W72395 T99630 AI422691 H98460 N31428 BE255916 H03265 AI857576 AA776920 AA910644 AA459522 AA293140 AW514667  
 R75953 AW662396 AA662522 AI865147 AI423153 AW262230 AA584410 AA583187 AW024595 AW069734 AI828996 AA282997 AA876046  
 AW613002 AA527373 AW972459 AI831360 AA621337 AA100926 AA772418 AA594628 AI033892 W95096 AI034317 AA398727 AI085031  
 10 N95210 AI459432 AI041437 AA932124 AA627684 AA935829 AI004827 AI423513 AI094597 H42079 R54703 AI630359 AA617681 AA978045  
 AA643280 W44561 AI991988 AI537692 AI090262 AA740817 AI312104 AI911822 AA416871 AI185409 AA129784 AA701623 AI075239  
 AI139549 AA633648 AI339996 AI336880 AA399239 AI078708 AI085351 AI362835 AI346618 AI146955 AI989380 AI348243 N92892 AA765850  
 AI494230 AI278887 AA962596 AI492600 W80435 AA001979 R97424 AI129015 N24127 AA157451 AA235549 AA459292 AA037114 AA129785  
 AI494211 AW059601 AW886710 R92790 N59755 AI361128 AW589407 H47725 H97534 H48076 H48450 T99631 AW300758 H03431 R76789  
 AA954344 H77576 R96823 AI457100 N92845 N49682 H42038 BE220698 BE220715 H99552 AA701624 N74173 R54704 H79520 H72923  
 H03266 BE261919 AA769633 AA480310 AA507454 AA910586 AI203723 AW104725 W25611 W25071 T88980 H03513 T77589 R99156  
 15 W95095 R97470 AA702275 T77551 AA911952 H82956 N83673 AA283672  
 450375 83327\_1 AA009647 AA131254 AA374293 AW954405 H04410 AW606284 AA151166 BE157467 BE157601 H04384 W46291 AW663674 H04021 H01532  
 AA190993 H03231 H59605 H01642 AA852876 AA113758 AA626915 AA746952 AI161014 AA099554 R69067

TABLE 14C

Pkey: Unique number corresponding to an Eos probaset  
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA  
 sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.  
 Strand: Indicates DNA strand from which exons were predicted.  
 25 Nt\_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
402075	8117407	Plus	121907-122035,122804-122921,124019-124161,124455-124610,125672-126076



TABLE 15A: Information for all sequences in Table 16

Table 15A shows the Seq ID No, Pkey, ExAccn, UnigenelD, and Unigene Title for all of the sequences in Table 16.

Table 15B show the accession numbers for those Pkey's lacking UnigenelD's for table 15A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Table 15C show the genomic positioning for those Pkey's lacking Unigene ID's and accession numbers in table 15A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Seq ID No: Sequence ID number  
 Pkey: Unique Eos probeset identifier number  
 ExAccn: Exemplar Accession number, Genbank accession number  
 UnigenelD: Unigene number  
 Unigene Title: Unigene gene title

Seq ID No:	Pkey	ExAccn	UnigenelD	Unigene Title
Seq ID No: 1 & 2	410407	X66839	Hs.63287	carbonic anhydrase IX
Seq ID No: 3 & 4	412719	AW016610	Hs.816	ESTs
Seq ID No: 5 & 6	417034	NM_006183	Hs.80962	neurotensin
Seq ID No: 7 & 8	430486	BE062109	Hs.241551	chloride channel, calcium activated, fam
Seq ID No: 9 & 10	407788	BE514982	Hs.38991	S100 calcium-binding protein A2
Seq ID No: 11 & 12	407788	BE514982	Hs.38991	S100 calcium-binding protein A2
Seq ID No: 13 & 14	407788	BE514982	Hs.38991	S100 calcium-binding protein A2
Seq ID No: 15 & 16	407788	BE514982	Hs.38991	S100 calcium-binding protein A2
Seq ID No: 17 & 18	439285	AL133916		hypothetical protein FLJ20093
Seq ID No: 19 & 20	413753	U17760	Hs.75517	laminin, beta 3 (nicein (125kD), kalinin
Seq ID No: 21 & 22	120486	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog
Seq ID No: 23 & 24	425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen
Seq ID No: 25 & 26	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines
Seq ID No: 27 & 28	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage
Seq ID No: 29 & 30	452838	U65011	Hs.30743	preferentially expressed antigen in mela
Seq ID No: 31 & 32	418663	AK001100	Hs.41690	desmocollin 3
Seq ID No: 33 & 34	418663	AK001100	Hs.41690	desmocollin 3
Seq ID No: 35 & 36	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibito
Seq ID No: 37 & 38	429610	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas
Seq ID No: 39 & 40	406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad
Seq ID No: 41 & 42	431846	BE019924	Hs.271580	uropod 1B
Seq ID No: 43 & 44	418830	BE513731	Hs.88959	hypothetical protein MGC4816
Seq ID No: 45 & 46	424098	AF077374	Hs.139322	small proline-rich protein 3
Seq ID No: 47 & 48	443648	AI085377	Hs.143610	ESTs
Seq ID No: 49	311034	BE567130	Hs.311369	ESTs, Highly similar to NKGD_HUMAN NKG2-
Seq ID No: 50 & 51	408522	AI541214	Hs.46320	Small proline-rich protein SPRK [human,
Seq ID No: 52 & 53	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL
Seq ID No: 54 & 55	435505	AF200492	Hs.211238	interleukin-1 homolog 1
Seq ID No: 56 & 57	417366	BE185289	Hs.1076	small proline-rich protein 1B (cornifin)
Seq ID No: 58 & 59	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta
Seq ID No: 60 & 61	441020	W79283	Hs.35962	ESTs
Seq ID No: 62 & 63	423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys
Seq ID No: 64 & 65	429538	BE182592	Hs.11261	small proline-rich protein 2A
Seq ID No: 66 & 67	448733	NM_005629	Hs.187958	solute carrier family 6 (neurotransmitte
Seq ID No: 68 & 69	444371	BE540274	Hs.239	forkhead box M1
Seq ID No: 70 & 71	444371	BE540274	Hs.239	forkhead box M1
Seq ID No: 72 & 73	444371	BE540274	Hs.239	forkhead box M1
Seq ID No: 74 & 75	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias
Seq ID No: 76 & 77	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias
Seq ID No: 78 & 79	429259	AA420450	Hs.292911	Plakophilin
Seq ID No: 80 & 81	426440	BE382756	Hs.169902	solute carrier family 2 (facilitated glu
Seq ID No: 82 & 83	437044	AL035864	Hs.69517	differentially expressed in Fanconi's an
Seq ID No: 84 & 85	423662	AK001035	Hs.130881	B-cell CLL/lymphoma 11A (zinc finger pro
Seq ID No: 86 & 87	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino
Seq ID No: 88 & 89	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3
Seq ID No: 90 & 91	417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor
Seq ID No: 92 & 93	423634	AW959908	Hs.1690	heparin-binding growth factor binding pr
Seq ID No: 94 & 95	417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated
Seq ID No: 96 & 97	441362	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E. coli Re
Seq ID No: 98 & 99	425322	U63630	Hs.155637	protein kinase, DNA-activated, catalytic
Seq ID No: 100 & 101	449003	X76342	Hs.389	alcohol dehydrogenase 7 (class IV), mu o
Seq ID No: 102 & 103	431009	BE149762	Hs.48956	gap junction protein, beta 6 (connexin 3
Seq ID No: 104 & 105	409103	AF251237	Hs.112208	XAGE-1 protein
Seq ID No: 106 & 107	417542	J04129	Hs.82269	progesterone-associated endometrial prote
Seq ID No: 108 & 109	428471	X57348	Hs.184510	stratiferin
Seq ID No: 110 & 111	418004	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member
Seq ID No: 112 & 113	414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2
Seq ID No: 114 & 115	418203	X54942	Hs.83758	CDC28 protein kinase 2
Seq ID No: 116	447343	AA256641	Hs.236894	ESTs, Highly similar to S02392 alpha-2-m
Seq ID No: 117 & 118	437016	AU076916	Hs.5398	guanine monophosphate synthetase
Seq ID No: 119 & 120	449230	BE613348	Hs.211579	melanoma cell adhesion molecule
Seq ID No: 121 & 122	446989	AK001898	Hs.16740	hypothetical protein FLJ11036
Seq ID No: 123 & 124	457819	AA057484	Hs.35406	ESTs, Highly similar to unnamed protein
Seq ID No: 125 & 126	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B



	Seq ID No: 127 & 128	414430	AI346201	Hs.76118	ubiquitin carboxyl-terminal esterase L1
	Seq ID No: 129 & 130	418462	BE001596	Hs.85266	integrin, beta 4
	Seq ID No: 131 & 132	100668	L05424	Hs.169610	CD44 antigen (homing function and Indian
5	Seq ID No: 133 & 134	458933	AI638429	Hs.24763	RAN binding protein 1
	Seq ID No: 135 & 136	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me
	Seq ID No: 137 & 138	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me
	Seq ID No: 139 & 140	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me
	Seq ID No: 141 & 142	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me
10	Seq ID No: 143 & 144	446269	AW263155	Hs.14559	hypothetical protein FLJ10540
	Seq ID No: 145 & 146	422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur
	Seq ID No: 147 & 148	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con
	Seq ID No: 149 & 150	440325	NM_003812	Hs.7164	a disintegrin and metalloproteinase doma
	Seq ID No: 151 & 152	439606	W79123	Hs.58561	G protein-coupled receptor 87
15	Seq ID No: 153 & 154	453884	AA355925	Hs.36232	KIAA0186 gene product
	Seq ID No: 155 & 156	453884	AA355925	Hs.36232	KIAA0186 gene product
	Seq ID No: 157 & 158	453884	AA355925	Hs.36232	KIAA0186 gene product
	Seq ID No: 159 & 160	453884	AA355925	Hs.36232	KIAA0186 gene product
	Seq ID No: 161 & 162	404877			NM_005365:Homo sapiens melanoma antigen,
20	Seq ID No: 163 & 164	413129	AF292100	Hs.104613	RP42 homolog
	Seq ID No: 165 & 166	413281	AA861271	Hs.222024	transcription factor BMAL2
	Seq ID No: 167 & 168	444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote
	Seq ID No: 169 & 170	416819	U77735	Hs.80205	pim-2 oncogene
	Seq ID No: 171 & 172	451320	AW118072		diacylglycerol kinase, zeta (104kD)
25	Seq ID No: 173 & 174	418543	NM_005329	Hs.85962	hyaluronan synthase 3
	Seq ID No: 175 & 176	454034	NM_000691	Hs.575	aldehyde dehydrogenase 3 family, member
	Seq ID No: 177 & 178	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)
	Seq ID No: 179 & 180	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
	Seq ID No: 181 & 182	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
30	Seq ID No: 183 & 184	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
	Seq ID No: 185 & 186	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
	Seq ID No: 187 & 188	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
	Seq ID No: 189 & 190	419121	AA374372	Hs.89626	parathyroid hormone-like hormone
	Seq ID No: 191 & 192	448993	AI471630	Hs.8127	KIAA0144 gene product
35	Seq ID No: 193 & 194	421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR
	Seq ID No: 195 & 196	430393	BE185030	Hs.241305	estrogen-responsive B box protein
	Seq ID No: 197 & 198	425057	AA826434	Hs.1619	achaete-scute complex (Drosophila) homol
	Seq ID No: 199 & 200	420462	AF050147	Hs.97932	chondromodulin I precursor
40	Seq ID No: 201 & 202	102963	X02404	Hs.274534	calcitonin-related polypeptide, beta
	Seq ID No: 203 & 204	100576	X00356	Hs.37058	calcitonin/calcitonin-related polypeptid
	Seq ID No: 205 & 206	101175	U82671	Hs.36980	melanoma antigen, family A, 2
	Seq ID No: 207 & 208	429038	AL023513	Hs.194766	seizure related gene 6 (mouse)-like
	Seq ID No: 209 & 210	418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-1)
	Seq ID No: 211 & 212	418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-1)
45	Seq ID No: 213 & 214	131927	AJ003112	Hs.34780	doublecortin; lissencephaly, X-linked (d
	Seq ID No: 215 & 216	428182	BE386042	Hs.293317	ESTs, Weakly similar to GGC1_HUMAN G ANT
	Seq ID No: 217 & 218	427335	AA448542	Hs.251677	G antigen 7B
	Seq ID No: 219 & 220	409420	Z15008	Hs.54451	laminin, gamma 2 (nicein (100kD), kalini
	Seq ID No: 221 & 222	114346	AL137256	Hs.130489	ATPase, aminophospholipid transporter-II
50	Seq ID No: 223 & 224	438956	W00847	Hs.135056	Human DNA sequence from clone RP5-850E9
	Seq ID No: 225 & 226	404440			NM_021048:Homo sapiens melanoma antigen,
	Seq ID No: 227 & 228	415669	NM_005025	Hs.78589	serine (or cysteine) proteinase inhibito
	Seq ID No: 229 & 230	103312	Y12642	Hs.3185	lysosomal
	Seq ID No: 231 & 232	320843	BE069288	Hs.34744	Homo sapiens mRNA; cDNA DKFZp547C136 (fr
55	Seq ID No: 233	429065	AI753247	Hs.29643	Homo sapiens cDNA FLJ13103 fis, clone NT
	Seq ID No: 234 & 235	446102	AW168067	Hs.317694	ESTs
	Seq ID No: 236 & 237	330495	U47924	Hs.71642	guanine nucleotide binding protein (G pr
	Seq ID No: 238	413573	AI733859	Hs.149089	ESTs
	Seq ID No: 239 & 240	428479	Y00272	Hs.334562	cell division cycle 2, G1 to S and G2 to
60	Seq ID No: 241 & 242	428479	Y00272	Hs.334562	cell division cycle 2, G1 to S and G2 to
	Seq ID No: 243 & 244	332180	AF134160	Hs.7327	claudin 1
	Seq ID No: 245	437915	AI637993	Hs.202312	Homo sapiens clone N11 NTERA2D1 teratoca
	Seq ID No: 246 & 247	441553	AA281219	Hs.121296	ESTs
	Seq ID No: 248 & 249	331692	AI683487	Hs.152213	wingless-type MMTV integration site fami
65	Seq ID No: 250 & 251	429413	NM_014058	Hs.201877	DESC1 protein
	Seq ID No: 252 & 253	422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis
	Seq ID No: 254 & 255	448357	N20169	Hs.108923	RAB38, member RAS oncogene family
	Seq ID No: 256 & 257	446292	AF081497	Hs.279682	Rh type C glycoprotein
	Seq ID No: 258 & 259	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h
70	Seq ID No: 260 & 261	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1
	Seq ID No: 262 & 263	424046	AF027866	Hs.138202	serine (or cysteine) proteinase inhibito
	Seq ID No: 264 & 265	439223	AW238299	Hs.250618	UL16 binding protein 2
	Seq ID No: 266 & 267	429228	AI553633	Hs.326447	ESTs
	Seq ID No: 268 & 269	409757	NM_001898	Hs.123114	cystatin SN
75	Seq ID No: 270 & 271	411089	AA456454	Hs.214291	cell division cycle 2-like 1 (PITSLRE pr
	Seq ID No: 272 & 273	436511	AA721252	Hs.291502	ESTs
	Seq ID No: 274 & 275	428969	AF120274	Hs.194689	artemin
	Seq ID No: 276 & 277	428969	AF120274	Hs.194689	artemin
	Seq ID No: 278 & 279	428969	AF120274	Hs.194689	artemin
80	Seq ID No: 280 & 281	428969	AF120274	Hs.194689	artemin
	Seq ID No: 282	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen
	Seq ID No: 283 & 284	412723	AA648459	Hs.335951	hypothetical protein AF301222
	Seq ID No: 285 & 286	450701	H39960	Hs.288467	hypothetical protein XP_098151 (leucine-
	Seq ID No: 287 & 288	405770			NM_002362:Homo sapiens melanoma antigen,
	Seq ID No: 289 & 290	4394574	BE264974	Hs.6566	thyroid hormone receptor interactor 13
85	Seq ID No: 291 & 292	414774	X02419	Hs.77274	plasminogen activator, urokinase



	Seq ID No: 293 & 294	424629	M90656	Hs.151393	glutamate-cysteine ligase, catalytic sub
	Seq ID No: 295 & 296	437789	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheti
	Seq ID No: 297 & 298	437789	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheti
5	Seq ID No: 299 & 300	437789	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheti
	Seq ID No: 301 & 302	437789	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheti
	Seq ID No: 303 & 304	437789	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheti
	Seq ID No: 305 & 306	453968	AA847843	Hs.62711	High mobility group (nonhistone chromoso
	Seq ID No: 307 & 308	403478			NM_022342:Homo sapiens kinesin protein 9
10	Seq ID No: 309	441525	AW241867	Hs.127728	ESTs
	Seq ID No: 310 & 311	434105	AW952124	Hs.13094	presenilins associated rhomboid-like pro
	Seq ID No: 312 & 313	428810	AF068236	Hs.193788	nitric oxide synthase 2A (inducible, hep
	Seq ID No: 314 & 315	413691	AB023173	Hs.75478	ATPase, Class VI, type 11B
	Seq ID No: 316 & 317	423934	U89995	Hs.159234	forkhead box E1 (thyroid transcription f
15	Seq ID No: 318 & 319	409228	R16811	Hs.22010	ESTs, Weakly similar to 2109260A B cell
	Seq ID No: 320 & 321	425734	AF056209	Hs.159396	peptidylglycine alpha-amidating monooxyg
	Seq ID No: 322 & 323	413582	AW295647	Hs.71331	hypothetical protein MGC5350
	Seq ID No: 324 & 325	438403	AA806607	Hs.292206	ESTs
	Seq ID No: 326 & 327	403329			unnamed protein product [Homo sapiens]
20	Seq ID No: 328 & 329	409893	AW247090	Hs.57101	minichromosome maintenance deficient (S.
	Seq ID No: 330 & 331	119073	BE245360	Hs.279477	v-ets erythroblastosis virus E26 oncogen
	Seq ID No: 332 & 333	113195	H83265	Hs.8881	ESTs, Weakly similar to S41044 chromosom
	Seq ID No: 334 & 335	102283	AW161552	Hs.83381	guanine nucleotide binding protein 11
	Seq ID No: 336 & 337	101345	NM_005795	Hs.152175	calcitonin receptor-like
25	Seq ID No: 338 & 339	103280	U84722	Hs.76206	cadherin 5, type 2, VE-cadherin (vascula
	Seq ID No: 340 & 341	102012	BE259035	Hs.118400	singed (Drosophila)-like (sea urchin fas
	Seq ID No: 342 & 343	105729	H46612	Hs.293815	Homo sapiens HSPC285 mRNA, partial cds
	Seq ID No: 344 & 345	134299	AW580939	Hs.97199	complement component C1q receptor
	Seq ID No: 346 & 347	412719	AW016610	Hs.816	ESTs
30	Seq ID No: 348 & 349	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL
	Seq ID No: 350 & 351	128924	BE279383	Hs.26557	plakophilin 3
	Seq ID No: 352 & 353	100486	T19006	Hs.10842	RAN, member RAS oncogene family
	Seq ID No: 354 & 355	419121	AA374372	Hs.89626	parathyroid hormone-like hormone
	Seq ID No: 356 & 357	409459	D86407	Hs.54481	low density lipoprotein receptor-related
35	Seq ID No: 358 & 359	330493	M27826		endogenous retroviral protease
	Seq ID No: 360 & 361	417866	AW067903	Hs.82772	collagen, type XI, alpha 1
	Seq ID No: 362 & 363	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4
	Seq ID No: 364 & 365	437016	AU076916	Hs.5398	guanine monophosphate synthetase
	Seq ID No: 366 & 367	429612	AF062649	Hs.252587	pituitary tumor-transforming 1
40	Seq ID No: 368 & 369	440704	M69241	Hs.162	insulin-like growth factor binding prote
	Seq ID No: 370 & 371	431221	AA449015	Hs.286145	SRB7 (suppressor of RNA polymerase B, ye
	Seq ID No: 372 & 373	431565	AF161470	Hs.260622	butyrate-induced transcript 1
	Seq ID No: 374 & 375	431565	AF161470	Hs.260622	butyrate-induced transcript 1
	Seq ID No: 376 & 377	132354	BE185289	Hs.1076	small proline-rich protein 1B (cornifin)
45	Seq ID No: 378 & 379	424441	X14850	Hs.147097	H2A histone family, member X
	Seq ID No: 380 & 381	103768	AF086009	Hs.296398	gb:Homo sapiens full length insert cDNA
	Seq ID No: 382 & 383	417512	X76534	Hs.82226	glycoprotein (transmembrane) nmb
	Seq ID No: 384 & 385	425266	J00077	Hs.155421	alpha-fetoprotein
	Seq ID No: 386 & 387	424503	NM_002205	Hs.149609	integrin, alpha 5 (fibronectin receptor,
50	Seq ID No: 388 & 389	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin
	Seq ID No: 390 & 391	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial
	Seq ID No: 392 & 393	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial
	Seq ID No: 394 & 395	418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino
	Seq ID No: 396 & 397	415138	C18356	Hs.295944	tissue factor pathway inhibitor 2
55	Seq ID No: 398 & 399	418506	AA084248	Hs.85339	G protein-coupled receptor 39
	Seq ID No: 400 & 401	423961	D13666	Hs.136348	periostin (OSF-2os)
	Seq ID No: 402 & 403	414812	X72755	Hs.77367	monokine induced by gamma interferon
	Seq ID No: 404 & 405	417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein
	Seq ID No: 406 & 407	417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein
60	Seq ID No: 408 & 409	422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse
	Seq ID No: 410 & 411	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy
	Seq ID No: 412 & 413	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti
	Seq ID No: 414 & 415	400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated
	Seq ID No: 416 & 417	411789	AF245505	Hs.72157	Adlcan
65	Seq ID No: 418 & 419	428698	AA852773	Hs.334838	KIAA1866 protein
	Seq ID No: 420 & 421	450098	W27249	Hs.8109	hypothetical protein FLJ21080
	Seq ID No: 422 & 423	421552	AF026692	Hs.105700	secreted frizzled-related protein 4
	Seq ID No: 424 & 425	452747	BE153855	Hs.61460	Ig superfamily receptor LNIR
	Seq ID No: 426 & 427	450375	AA009647		a disintegrin and metalloproteinase doma
70	Seq ID No: 428 & 429	426215	AW963419	Hs.155223	stanniocalcin 2
	Seq ID No: 430 & 431	425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin
	Seq ID No: 432 & 433	432201	AI538613	Hs.298241	Transmembrane protease, serine 3
	Seq ID No: 434 & 435	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph
	Seq ID No: 436 & 437	442117	AW664964	Hs.128899	ESTs; hypothetical protein for IMAGE:447
75	Seq ID No: 438 & 439	431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn
	Seq ID No: 440 & 441	447033	AI357412	Hs.157601	ESTs
	Seq ID No: 442 & 443	447033	AI357412	Hs.157601	ESTs
	Seq ID No: 444 & 445	447033	AI357412	Hs.157601	ESTs
	Seq ID No: 446 & 447	115522	BE614387	Hs.333893	c-Myc target JPO1
80	Seq ID No: 448 & 449	410418	D31382	Hs.63325	transmembrane protease, serine 4
	Seq ID No: 450 & 451	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119
	Seq ID No: 452 & 453	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119
	Seq ID No: 454 & 455	452461	N78223	Hs.108106	transcription factor
	Seq ID No: 456 & 457	412420	AL035668	Hs.73853	bone morphogenetic protein 2
	Seq ID No: 458 & 459	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara
85	Seq ID No: 460 & 461	407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagone



	Seq ID No: 462 & 463	437852	BE001836	Hs.256897	ESTs, Weakly similar to dJ365O12.1 [H.sa
	Seq ID No: 464 & 465	402075			ENSP00000251056*:Plasma membrane calcium
	Seq ID No: 466 & 467	421110	AJ250717	Hs.1355	cathepsin E
5	Seq ID No: 468 & 469	451668	Z43948	Hs.326444	cartilage acidic protein 1
	Seq ID No: 470 & 471	451668	Z43948	Hs.326444	cartilage acidic protein 1
	Seq ID No: 472 & 473	451668	Z43948	Hs.326444	cartilage acidic protein 1
	Seq ID No: 474 & 475	422282	AF019225	Hs.114309	apolipoprotein L
	Seq ID No: 476 & 477	425852	AK001504	Hs.159651	death receptor 6, TNF superfamily member
10	Seq ID No: 478 & 479	439738	BE246502	Hs.9598	sema domain, immunoglobulin domain (Ig),
	Seq ID No: 480 & 481	427747	AW411425	Hs.180655	serine/threonine kinase 12
	Seq ID No: 482 & 483	420281	AI623693	Hs.323494	Predicted cation efflux pump
	Seq ID No: 484 & 485	405932			C15000305:gil3806122[gb]AAC69198.1) (AF0
	Seq ID No: 486 & 487	405932			C15000305:gil3806122[gb]AAC69198.1) (AF0
15	Seq ID No: 488 & 489	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane
	Seq ID No: 490 & 491	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy
	Seq ID No: 492 & 493	417079	U65590	Hs.81134	interleukin 1 receptor antagonist
	Seq ID No: 494 & 495	430890	X54232	Hs.2699	glypican 1
	Seq ID No: 496 & 497	419721	NM_001650	Hs.288650	aquaporin 4
20	Seq ID No: 498 & 499	444471	AB020684	Hs.11217	KIAA0877 protein
	Seq ID No: 500 & 501	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote
	Seq ID No: 502 & 503	433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly
	Seq ID No: 504 & 505	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro
	Seq ID No: 506 & 507	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro
25	Seq ID No: 508 & 509	450001	NM_001044	Hs.406	solute carrier family 6 (neurotransmitte
	Seq ID No: 510 & 511	410407	X66839	Hs.63287	carbonic anhydrase IX
	Seq ID No: 512 & 513	309931	AW341683		gb:hd13d01.x1 Soares_NFL_T_GBC_S1 Homo s
	Seq ID No: 514 & 515	412719	AW016610	Hs.816	ESTs
	Seq ID No: 516 & 517	417034	NM_006183	Hs.80962	neurotensin
30	Seq ID No: 518 & 519	430486	BE062109	Hs.241551	chloride channel, calcium activated, fam
	Seq ID No: 520 & 521	413753	U17760	Hs.75517	laminin, beta 3 (nicein (125kD), kalinin
	Seq ID No: 522 & 523	425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen
	Seq ID No: 524 & 525	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage
	Seq ID No: 526 & 527	418663	AK001100	Hs.41690	desmocollin 3
35	Seq ID No: 528 & 529	418663	AK001100	Hs.41690	desmocollin 3
	Seq ID No: 530 & 531	429610	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas
	Seq ID No: 532 & 533	406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad
	Seq ID No: 534 & 535	431846	BE019924	Hs.271580	uroplakin 1B
	Seq ID No: 536 & 537	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL
40	Seq ID No: 538 & 539	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta
	Seq ID No: 540 & 541	437044	AL035864	Hs.69517	differentially expressed in Fanconi's an
	Seq ID No: 542 & 543	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino
	Seq ID No: 544 & 545	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3
	Seq ID No: 546 & 547	417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor
45	Seq ID No: 548 & 549	431009	BE149762	Hs.48956	gap junction protein, beta 6 (connexin 3
	Seq ID No: 550 & 551	417542	J04129	Hs.82269	progesterone-associated endometrial prote
	Seq ID No: 552 & 553	449230	BE613348	Hs.211579	melanoma cell adhesion molecule
	Seq ID No: 554 & 555	410555	U92649	Hs.64311	a disintegrin and metalloproteinase doma
	Seq ID No: 556 & 557	410555	U92649	Hs.64311	a disintegrin and metalloproteinase doma
50	Seq ID No: 558 & 559	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B
	Seq ID No: 560 & 561	418462	BE001596	Hs.85266	integrin, beta 4
	Seq ID No: 562 & 563	410274	AA381807	Hs.61762	hypoxia-inducible protein 2
	Seq ID No: 564 & 565	439606	W79123	Hs.58561	G protein-coupled receptor 87
	Seq ID No: 566 & 567	404877			NM_005365:Homo sapiens melanoma antigen,
55	Seq ID No: 568 & 569	444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote
	Seq ID No: 570 & 571	418543	NM_005329	Hs.85962	hyaluronan synthase 3
	Seq ID No: 572 & 573	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
	Seq ID No: 574 & 575	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
	Seq ID No: 576 & 577	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
60	Seq ID No: 578 & 579	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
	Seq ID No: 580 & 581	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
	Seq ID No: 582 & 583	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
	Seq ID No: 584 & 585	421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR
	Seq ID No: 586 & 587	418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-1)
65	Seq ID No: 588 & 589	418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-1)
	Seq ID No: 590 & 591	409420	Z15008	Hs.54451	laminin, gamma 2 (nicein (100kD), kalini
	Seq ID No: 592 & 593	332180	AF134160	Hs.7327	claudin 1
	Seq ID No: 594 & 595	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,
	Seq ID No: 596 & 597	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,
70	Seq ID No: 598 & 599	439223	AW238299	Hs.250618	UL16 binding protein 2
	Seq ID No: 600 & 601	409757	NM_001898	Hs.123114	cystatin SN
	Seq ID No: 602 & 603	428969	AF120274	Hs.194689	artemin
	Seq ID No: 604 & 605	428969	AF120274	Hs.194689	artemin
	Seq ID No: 606 & 607	428969	AF120274	Hs.194689	artemin
75	Seq ID No: 608 & 609	428969	AF120274	Hs.194689	artemin
	Seq ID No: 610 & 611	450701	H39960	Hs.288467	hypothetical protein XP_098151 (leucine-
	Seq ID No: 612 & 613	450701	H39960	Hs.288467	hypothetical protein XP_098151 (leucine-
	Seq ID No: 614 & 615	414774	X02419	Hs.77274	plasminogen activator, urokinase
	Seq ID No: 616 & 617	407944	R34008	Hs.239727	desmocollin 2
	Seq ID No: 618 & 619	407944	R34008	Hs.239727	desmocollin 2
80	Seq ID No: 620 & 621	457489	AI693815	Hs.127179	cryptic gene
	Seq ID No: 622 & 623	429547	AW009166	Hs.99376	ESTs
	Seq ID No: 624 & 625	407242	M18728		gb:Human nonspecific crossreacting anti
	Seq ID No: 626 & 627	407242	M18728		gb:Human nonspecific crossreacting anti
	Seq ID No: 628 & 629	407242	M18728		gb:Human nonspecific crossreacting anti
85	Seq ID No: 630 & 631	444006	BE395085	Hs.10086	type 1 transmembrane protein Fn14



Seq ID No: 632 & 633	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma
Seq ID No: 634 & 635	422109	S73265	Hs.1473	gastrin-releasing peptide
Seq ID No: 636 & 637	419235	AW470411	Hs.288433	neurotrimin
Seq ID No: 638 & 639	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc
Seq ID No: 640 & 641	419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy
Seq ID No: 642 & 643	431462	AW583672	Hs.256311	granin-like neuroendocrine peptide precu
Seq ID No: 644 & 645	448243	AW369771	Hs.52620	integrin, beta 8
Seq ID No: 646 & 647	426427	M86699	Hs.169840	TTK protein kinase
Seq ID No: 648 & 649	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6
Seq ID No: 650 & 651	422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6
Seq ID No: 652 & 653	428450	NM_014791	Hs.184339	KIAA0175 gene product
Seq ID No: 654 & 655	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,
Seq ID No: 656 & 657	453392	U23752	Hs.32964	SRY (sex determining region Y)-box 11
Seq ID No: 658 & 659	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic
Seq ID No: 660 & 661	425776	U25128	Hs.159499	parathyroid hormone receptor 2
Seq ID No: 662 & 663	425776	U25128	Hs.159499	parathyroid hormone receptor 2
Seq ID No: 664 & 665	431515	NM_012152	Hs.258583	endothelial differentiation, lysophospha
Seq ID No: 666 & 667	419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7
Seq ID No: 668 & 669	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci
Seq ID No: 670 & 671	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci
Seq ID No: 672 & 673	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci
Seq ID No: 674 & 675	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci
Seq ID No: 676 & 677	410001	AB041036	Hs.57771	kalikrein 11
Seq ID No: 678 & 679	426501	AW043782	Hs.293616	ESTs
Seq ID No: 680 & 681	408369	R38438	Hs.182575	solute carrier family 15 (H??? transport
Seq ID No: 682 & 683	445413	AA151342	Hs.12677	CGI-147 protein
Seq ID No: 684 & 685	422424	AI186431	Hs.296638	prostate differentiation factor
Seq ID No: 686 & 687	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,
Seq ID No: 688 & 689	420610	AI683183	Hs.99348	distal-less homeo box 5

TABLE 15B

Pkey: Unique Eos probeset identifier number  
CAT number: Gene cluster number  
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
309931	AW341683	
330493	33264_5	M27826 R78416 AA307645 AW957879 AW957800 AA633529 H03662
439285	47065_1	AL133916 N79113 AF086101 N76721 AW950828 AA364013 AW955684 AI346341 AI867454 N54784 AI655270 AI421279 AW014882
		AA775552 N62351 N59253 AA626243 AI341407 BE175639 AA456968 AI358918 AA457077
450375	83327_1	AA009647 AA131254 AA374293 AW954405 H04410 AW606284 AA151166 BE157467 BE157601 H04384 W46291 AW663674 H04021 H01532
		AA190993 H03231 H59605 H01642 AA852876 AA113758 AA626915 AA746952 AI161014 AA099554 R69067
451320	86576_1	AW118072 AI631982 T15734 AA224195 AI701458 W20198 F26326 AA890570 N90552 AW071907 AI671352 AI375892 T03517 R88265
		AI124088 AA224388 AI084316 AI354686 T33652 AI140719 AI720211 T03490 AI372637 T15415 AW205836 AA630384 T03515 T33230
		AA017131 AA443303 T33623 AI222556 T33511 T33785 AI419606 D56612

TABLE 15C

Pkey: Unique number corresponding to an Eos probeset  
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.  
Strand: Indicates DNA strand from which exons were predicted.  
Nt\_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
402075	8117407	Plus	121907-122035,122804-122921,124019-124161,124455-124610,125672-126076
403329	8516120	Plus	96450-96598
403478	9958258	Plus	116458-116564
404440	7528051	Plus	80430-81581
404877	1519284	Plus	1095-2107
405770	2735037	Plus	61057-62075
405932	7767812	Minus	123525-123713



Table 16

Seq ID NO: 1 DNA sequence  
Nucleic Acid Accession #: NM\_001216  
Coding sequence: 43..1422

	1	11	21	31	41	51	
10	GCCCGTACAC	ACCGTGTGCT	GGGACACCCC	ACAGTCAGCC	GCATGGCTCC	CCTGTGCCCC	60
	AGCCCTGGC	TCCCTCTGTT	GATCCCGGCC	CCTGCTCCAG	GCCTCACTGT	GCAACTGCTG	120
	CTGTCACTGC	TGCTTCTGAT	GCCTGTCCAT	CCCCAGAGGT	TGCCCCGGAT	GCAGGAGGAT	180
	TCCCCCTTGG	GAGGAGGCTC	TTCTGGGGAA	GATGACCCAC	TGGCGCAGGA	GGATCTGCCC	240
	AGTGAAGAGG	ATTCAACCAG	AGAGGAGGAT	CCACCCGGAG	AGGAGGATCT	ACCTGGAGAG	300
15	GAGGATCTAC	CTGGAGAGGA	GGATCTACCT	GAAGTTAAGC	CTAAATCAGA	AGAAGAGGGC	360
	TCCCTGAAGT	TAGAGGATCT	ACCTACTGTT	GAGGCTCCTG	GAGATCCTCA	AGAACCCAG	420
	AATAATGCC	ACAGGGACAA	AGAAGGGGAT	GACCAGAGTC	ATTGGCGCTA	TGGAGGCGAC	480
	CCGCCCTGGC	CCCGGGTGTG	CCCAGCCTGC	CGCGGCCGCT	TCCAGTCCCC	GGTGGATATC	540
	CGCCCCAGC	TCGGCCGCTT	CTGCCCGGCC	CTGCGCCCCC	TGGAACCTCT	GGGCTTCCAG	600
20	CTCCCGCCGC	TCCGAGAATC	CGCGCTCGGC	AACAATGGCC	ACAGTGTGCA	ACTGACCTTG	660
	CCTCTGCGG	TAGAGATGGC	TCTGGGTCCC	GGGCGGGAGT	ACCGGGCTCT	GCAGCTGCAT	720
	CTGCACTGGG	GGGCTGCAGG	TCGTCGGGCG	TCGGAGCACA	CTGTGGAAGG	CCACCGTTTC	780
	CCTGCCGAGA	TCCACGTGGT	TCACCTCAGC	ACCGCCTTTG	CCAGAGTTGA	CGAGGCCCTT	840
	GGGCGCCCGG	GAGGCCTGGC	CGTGTGGGCC	GCCTTCTGCG	AGGAGGGCCC	GGAAGAAAAC	900
	AGTGCCTATG	AGCAGTTGCT	GTCCTGCTTG	GAAGAAATCG	CTGAGGAAGG	CTCAGAGACT	960
25	CAGGTCCCAG	GACTGGACAT	ATCTGCACCT	CTGCCCTCTG	ACTTCAGCCG	CTACTTCCAA	1020
	TATGAGGGGT	CTCTGACTAC	ACCGCCCTGT	GCCAGGGGTG	TCATCTGGAC	TGTGTTTAAAC	1080
	CAGACAGTGA	TGCTGAGDQSH	TAAGCAGCTC	CACACCTCT	CTGACACCTT	GTGGGGACCT	1140
	GGTGACTCTC	GGCTACAGCT	GAATTCCTGA	CGCAGCAGC	CTTTGAATGG	GCGAGTGATT	1200
	GAGGCCTCCT	TCCCTGCTGG	AGTGGACAGC	AGTCTCTGGG	CTGCTGAGCC	AGTCCAGCTG	1260
30	AATTCCTGCC	TGGCTGCTGG	TGACATCCTA	GCCCTGGTTT	TTGGCCTCCT	TTTTGCTGTC	1320
	ACCAGCGTCC	CGTTCCTTGT	GCAGATGAGA	AGGCAGCACA	GAAGGGGAAC	CAAGGGGGGT	1380
	GTGAGCTACC	GCCAGCAGCA	GGTAGCCGAG	ACTGGAGCCT	AGAGGCTGGA	TCTTGAGAGAA	1440
	TGTGAGAAGC	CAGCCAGAGG	CATCTGAGGG	GGAGCCGGTA	ACTGTCTCTG	CCTGCTCATT	1500
35	ATGCCACTTC	CTTTTAACTG	CCAAGAAATT	TTTAAAATA	AATATTATATA	AT	

Seq ID NO: 2 Protein sequence:  
Protein Accession #: NP\_001207

	1	11	21	31	41	51	
40	MAPLCPSFWL	PLLIPAPAPG	LTVQLLSLL	LLMPVHPQRL	PRMQEDSPLG	GGSSGEDDPL	60
	GEEDLPSEED	SPREEDPPGE	EDLPGEEDLP	GEEDLPPEVKP	KSEBEGSLKL	EDLPTVEAPG	120
	DFQEFQNNAH	RDKEGDDQSH	WRYGGDPPWP	RVSPACAGRF	QSPVDIRPQL	AAFPCALRPL	180
45	ELLGFQLEPL	PELLRLNNGH	SVQLTLPPGL	EMALGPGRFY	RALQLHLHWG	AAGRPGSEHT	240
	VEGHRFPAEI	HVVHLSTAFD	RVDBALGRPG	GLAVLAAPLE	EGPEENSAYE	QLLSRLEIEIA	300
	EGSETQVPG	LDISALLPSD	FSRYFYQYEGS	LTPPPCAQGV	IWTVFNQIVM	LSAKQLHTLS	360
	DTLWPGDSR	LQLNFRATQP	LNGRVIEASF	PAGVDSSPRA	AEPVQLNSCL	AAGDILALVF	420
	GLLFAVTSVA	FLVQMRRQHR	RGTGKGVSYR	PAEVAETGA			

Seq ID NO: 3 DNA sequence  
Nucleic Acid Accession #: BC013923  
Coding sequence: 438-1391

	1	11	21	31	41	51	
55	AGCGGGGTTG	TCTATTAAGT	TGTTCAAAAA	GTATCAGGAG	TTGTCAAGGC	AGAGAAGAGA	60
	GTGTTTGCAA	AAGGGGGAAA	GTAGTTTGCT	GCCTCTTTAA	GACTAGGACT	GAGAGAAAGA	120
	AGAGGAGAGA	GAAAGAAAGG	GAGAGAAGTT	TGAGCCCCAG	GCTTAAGCCT	TTCCAAAAAA	180
60	TAATAATAAC	AATCATCGGC	GGCGGCAGGA	TCGGCCAGAG	GAGGAGGGAA	GCGCTTTTTT	240
	TGATCCTGAT	TCCAGTTTGC	CTCTCTCTTT	TTTTCCCCCA	AATATTCTT	CGCCTGATTT	300
	TCCTCGCGGA	GCCCTGCGCT	CCCGACACC	CCGCGCGCCT	CCCCTCTCTC	TCTCCCCCG	360
	CCCGCGGGCC	CCCCAAAGTC	CCGCGCGGGC	CGAGGGTCGG	CGGCGCGCGG	CGGGCCGGGC	420
	CCGCGCACAG	CGCCCGCATG	TACAACATGA	TGGAGACGGA	GCTGAAGCCG	CCGGGCCCGC	480
65	AGCAAACTTC	GGGGGGCGGC	GGCGGCAACT	CCACCGCGGC	GGCGGCCGGC	GGCAACCAGA	540
	AAAACAGCCC	GGACCGCTC	AAGCGGCCCA	TGAATGCCTT	CATGGTGTGG	TCCCGCGGGC	600
	AGCGGCGCAA	GATGGCCAG	GAGAACCCCA	AGATGCACAA	CTCGGAGATC	AGCAAGCGCC	660
	TGGGCGCCGA	GTGGAACCTT	TTGTGCGAGA	CGGAGAAGCG	GCCGTTTCATC	GACGAGGCTA	720
	AGCGGCTGCG	AGCGCTGCAC	ATGAAGGAGC	ACCCGGATTA	TAAATACCGG	CCCGCGCGGA	780
70	AAACCAAGAC	GCTCATGAAG	AAGGATAAGT	ACACGCTGCC	CGGCGGGCTG	CTGGCCCCCG	840
	GCGGCAATAG	CATGGCGAGC	GGGGTCGGGG	TGGGCGCCGG	CCTGGGCGCG	GGCGTGAACC	900
	AGCGCATGGA	CAGTTACCGC	CACATGAACG	GCTGGAGCAA	CGGCAGCTAC	AGCATGATGC	960
	AGGACCAAGT	GGGCTACCCG	CAGCACCCGG	GCCTCAATGC	GCACGGCGCA	GCGCAGATGC	1020
	AGCCCATGCA	CCGTACGAC	GTGAGCGCCC	TGCAGTACAA	CTCCATGACC	AGCTCGCAGA	1080
75	CCTACATGAA	CGGCTCGCCC	ACCTACAGCA	TGTCCTACTC	GCAGCAGGGC	ACCCCTGGCA	1140
	TGGCTCTTGG	CTCCATGGGT	TCGGTGGTCA	AGTCCGAGGC	CAGCTCCAGC	CCCCTGTGG	1200
	TTACCTCTTC	CTCCCACTTC	AGGGCGCCCT	GCCAGGCCGG	GGACCTCCGG	GACATGATCA	1260
	GCATGATCTC	CCCGGCGGCC	GAGGTGCGCG	AACCGCGCGC	CCCCAGCAGA	CTTCACATGT	1320
	CCCAGCACTA	CCAGAGCGGC	CCGGTGCCCG	GCACGGCCAT	TAACGGCACA	CTGCCCTCT	1380
80	CACACATGTG	AGGGCCGAGC	AGCGAACTGG	AGGGGGGAGA	AATTTTCAAA	GAAAAACGAG	1440
	GGAAATGGGA	GGGGTGCAAA	AGAGGAGAGT	AAGAAACAGC	ATGGAGAAAA	CCCGGTACGC	1500
	TCAAAAAAAA	AAAAAATAAA	AAAATCCCAT	CACCCACAGC	AAATGACAGC	TGCAAAAGAG	1560
	AACACCAATC	CCATCCACAC	TCACGCAAAA	ACCGCGATGC	CGACAAGAAA	ACTTTTATGA	1620
	GAGAGATCCT	GGACTTCTTT	TKGGGGGACT	ATTTTGTGAC	AGAGAAAAAC	TGGGGAGGGT	1680
	GGGGAGGGCG	GGGGAATGGA	CCTTGATAG	ATCTGGAGGA	AAGAAAGCTA	CGAAAAACTT	1740
85	TTTAAAGATT	CATGTGGTCA	TTGAGGAGCT	TTGCAGGAAG	TTTGCAAAAG	TCTTTACCAA	1800
	TAATATTTAG	AGCTAGTCTC	CAAGCGACGA	AAAAAATGTT	TTAATATTTG	CAAGCAACTT	1860
	TTGTACAGTA	TTTATCGAGA	TAAACATGGC	AATCAAAATG	TCCATTGTTT	ATAAGCTGAG	1920



AATTGGCCAA TATTTTTCAA GGAGAGGCTT CTTGCTGAAT TTTGATTCTG CAGCTGAAAT 1980  
 TTAGGACAGT TGCAGACGTG AAAAGAAGAA AATTATTCAA ATTTGGACAT TTTAATTGTT 2040  
 TAAAAATTGT ACAAAGGAA AAAATTAGAA TAAGTACTGG CGAACCATCT CTGTGGTCTT 2100  
 GTTTAAAAAG GGCAGAAAGT TTAGACTGTA CTAAATTTTA TAACCTACTG TTTAAAGCAA 2160  
 AAATGGCCAT GCAGGTTGAC ACCGTTGGTA ATTTATAATA GCTTTTGTTC GATCCCAACT 2220  
 TTCCATTTTG TTCAGATAAA AAAAACCATG AAATTACTGT GTTTGAAATA TTTTCTTATG 2280  
 GTTTGTAAATA TTTCTGTAAT TTTATTGTGA TATTTTAAAG TTTTCCCCC TTTATTTTCC 2340  
 GTAGTTGTAT TTTAAAAGAT TCGGCTCTGT ATTATTTGAA TCAGTCTGCC GAGAATCCAT 2400  
 GTATATATTT GAACTAATAT CATCCTTATA ACAGGTACAT TTTCAACTTA AGTTTCTACT 2460  
 CCATTATGCA CAGTTTGAGA TAAATAAATT TTTGAAATAT GGACACTGAA AAAAAAATAA 2520  
 AAAAAACAA AACAAAAAAA CAAAAACAA AACACAGAAA AACAAAAAAA AAAACAAAAA 2580  
 CACAACACAA AACAAAAAAA AAAAAAAGA AACAAACACA CAACACAACA CAACACAAAA 2640  
 CCACAACACA AACACAACA CACAGAGGG

Seq ID NO: 4 Protein sequence:  
 Protein Accession #:CAA83435.1

1 11 21 31 41 51  
 MYNMMETELK PPGPQQTSGG GGNSTAAAA GGNQKNSPDR VKRPMNAFMV WSRGQRRKMA 60  
 QENPKMHNSE ISKRLGAEWK LLETETKRPF IDEAKRLRAL HMKEHPDYKY RPRRKTKTLM 120  
 KKDKYTLPGG LLAPGGNSMA SGVGVGAGLG AGVNQRMDSY AHMNGWSNGS YSMMDQDLGY 180  
 PQHPGLNAHG AAQMPPMHRY DVSALQVNSM TSSQTYMNGS PTYSMSYSQQ GTPGMALGSM 240  
 GSVVKSEASS SPPVVTSSSH SRAPCQAGDL RDMISMYLPG AEPPEPAAPS RLHMSQHYQS 300  
 GPVPGTAING TLPLSHM

Seq ID NO: 5 DNA sequence  
 Nucleic Acid Accession #: U91618  
 Coding sequence: 29-541

1 11 21 31 41 51  
 CGGACTTGGC TTGTTAGAAG GCTGAAAGAT GATGGCAGGA ATGAAAATCC AGCTTGTTATG 60  
 CATGCTACTC CTGGCTTTCA GCTCCTGGAG TCTGTGCTCA GATTTCAGAAG AGGAAATGAA 120  
 AGCATTAGAA GCAGATTCTT TGACCAATAT GCATACATCA AAGATTAGTA AAGCACATGT 180  
 TCCCTCTTGG AAGATGACTC TGCTAAATGT TTGCAGTCTT GTAAATAATT TGAACAGCCC 240  
 AGCTGAGGAA ACAGGAGAAG TTCATGAAGA GGAGCTTGTT GCAAGAAGGA AACTTCCTAC 300  
 TGCTTTAGAT GGCTTTAGCT TGGAGCAAT GTTGACAATA TACCAGCTCC ACAAATCTG 360  
 TCACAGCAGG GCTTTTCAAC ACTGGGAGTT AATCCAGGAA GATATTCTTG ATACTGGAAA 420  
 TGACAAAAAT GCAAGGAAG AAGTCATAAA GAGAAAAATT CCTTATATTC TGAAACGGCA 480  
 GCTGTATGAG AATAAACCCA GAAGACCTTA CATACTCAA AGAGATTCTT ACTATTACTG 540  
 AGAGAATAAA TCTTTTATTT ACATGTGATT GTGATTTCATC ATCCCTTAAT TAAATATCAA 600  
 ATTATATTTG TGTGAAATG TGACAAACAC ACTTATCTGT CTCTTCTACA ATTGTGGTTT 660  
 ATTGAATGTG TTTTCTGCA CTAATAGAAA TTAGACTAAG TGTTTTCAA TAAATCTAAA 720  
 TCTTCAAAAA AAAAAAATAA AAATGGGGCC GCAATT

Seq ID NO: 6 Protein sequence:  
 Protein Accession #: AAB50564

1 11 21 31 41 51  
 MMAGMKIQLV CMLLLAFSSW SLCSDSSEEM KALEADFLTN MHTSKISKAH VPSWKMTLLN 60  
 VCSLVNLLNS PAETGVEVHE EELVARRKLP TALDGFSLTA MLTIYQLHKI CHSRAFQHWE 120  
 LIQEDILDG NDKNGKEEVI KRKIPYILKR QLYENKPRRP YILKRDSYVV

Seq ID NO: 7 DNA sequence  
 Nucleic Acid Accession #: NM\_006536.2  
 Coding sequence: 109-2940

1 11 21 31 41 51  
 ACCTAAAACC TTGCAAGTTC AGGAAGAAAC CATCTGCATC CATATTGAAA ACCTGACACA 60  
 ATGTATGCAG CAGGCTCAGT GTGAGTGAAC TGGAGGCTTC TCTACAACAT GACCCAAAGG 120  
 AGCATTGCAG GTCCTATTTC CAACCTGAAG TTTGTGACTC TCCTGGTTGC CTTAAGTTCA 180  
 GAACCTCCAT TCCTGGGAGC TGGAGTACAG CTTCAAGACA ATGGGTATAA TGGATTGCTC 240  
 ATTGCAATTA ATCCTCAGGT ACCTGAGAAT CAGAACCCTA TCTCAAACAT TAAGGAAATG 300  
 ATAACTGAAG CTTCAATTTA CCTATTTAAT GCTACCAAGA GAAGAGTATT TTTGAGAAAT 360  
 ATAAAGATTT TAATACCTGC CACATGGAAA GCTAATAATA ACAGCAAAAT AAAACAAGAA 420  
 TCATATGAAA AGGCAGATGT CATAGTGACT GACTGGTATG GGGCACATGG AGATGATCCA 480  
 TACACCTTAC AATACAGAGG GTGTGGAAAA GAGGGAAAAA ACATTCAATTT CACACCTAAT 540  
 TTCCTACTGA ATGATAACTT AACAGCTGGC TACGGATCAC GAGGCCGAGT GTTTGTCCAT 600  
 GAATGGGGCC ACCCTCCGTTG GGGTGTGTTT GATGAGTATA ACAATGACAA ACCTTTCTAC 660  
 ATAAATGGGC AAAATGCAAT TAAAGTGACA AGGTGTTTCA CTGACATCAC AGGCATTTT 720  
 GTGTGTGAAA AAGGTCTCTG CCCCAGAGAA AACTGTATTA TTAGTAAGCT TTTTAAAGAA 780  
 GGATGCACCT TTATCTACAA TAGCACCCAA AATGCAACTG CATCAATAAT GTTCATGCAA 840  
 AGTTTATCTT CTGTGGTTGA ATTTTGTAAAT GCAAGTACCC ACAACCAAGA AGCACCAAAC 900  
 CTACAGAACCC AGATGTGCAG CCTCAGAAGT GCATGGGATG TAATCACAGA CTCTGCTGAC 960  
 TTTTACCACA GCTTTCCCAT GAATGGGACT GAGCTTCCAC CTCCTCCCAC ATTCTCGCTT 1020  
 GTACAGGCTG GTGACAAAGT GGTCTGTTTA GTGCTGGATG TGTCAGCAAA GATGGCAGAG 1080  
 GCTGACAGAC TCCTTCAACT ACAACAAGCC CAGAAATTTT ATTTGATGCA GATTGTTGAA 1140  
 ATTATACCTT TCGTGGGCAT TGCCAGTTTC GACAGCAAAG GAGAGATCAG AGCCCAGCTA 1200  
 CACCAAAATTA ACAGCAATGA TGATCGAAAG TTGCTGTTTT CATATCTGCC CACCACTGTA 1260  
 TCAGCTAAAA CAGACATCAG CATTGTTTCA GGGCTTAAAG AAGGATTGGA GGTGGTTGAA 1320  
 AAACCTGAATG GAAAAGCTTA TGGCTCTGTG ATGATATTAG TGACCAGCGG AGATGATAAG 1380  
 CTTCTTGCCA ATTGCTTACC CACTGTGCTC AGCAGTGGTT CAACAATTCA CTCATTGGCC 1440



CTGGGTTTCAT CTGCAGCCCC AAATCTGGAG GAATTATCAC GTCTTACAGG AGGTTTAAAG 1500  
 TTCTTTTGTTC CAGATATATC AAATCTCCAAT AGCATGATTG ATGCTTTCAG TAGAATTTC 1560  
 TCTGGAACTG GAGACATTTT CCAGCAACAT ATTCAGCTTG AAAGTACAGG TGAAAAATGTC 1620  
 AAACCTCACC ATCAATTGAA AAACACAGTG ACTGTGGATA ATACTGTGGG CAACGACACT 1680  
 5 ATGTTTCTAG TTACGTGGCA GGCCAGTGGT CCTCCTGAGA TTATATTATT TGATCCTGAT 1740  
 GGACGAAAAAT ACTACACAAA TAATTTTATC ACCAATCTAA CTTTTCGGAC AGCTAGTCTT 1800  
 TGGATCCAG GAACAGCTAA GCCTGGGCAC TGGACTTACA CCCTGAAACAA TACCCATCAT 1860  
 TCTCTGCAAG CCTGAAAGT GACAGTGACC TCTCGCGCTT CCAACTCAGC TGTGCCCCCA 1920  
 10 GCCACTGTGG AAGCCTTTGT GGAAGAGAC AGCCTCCATT TTCCTCATCC TGTGATGATT 1980  
 TATGCCAATG TGAACACAGG ATTTTATCCC ATTCCTTAATG CCACTGTCCAC TGCCACAGTT 2040  
 GAGCCAGAGA CTGGAGATCC TGTACGCTG AGACTCCTTG ATGATGGAGC AGGTGCTGAT 2100  
 GTTATAAAAA ATGATGGAAT TTACTCGAGG TATTTTTTCT CCTTGTCTGC AAATGGTAGA 2160  
 TATAGCTTGA AAGTGCATGT CAATCACTCT CCCAGCATAA GCACCCCAAC CCACTCTATT 2220  
 15 CCAGGGAGTC ATGCTATGTA TGTACAGGT TACACAGCAA ACGGTAATAT TCAGATGAAT 2280  
 GCTCCAAGGA AATCAGTAGG CAGAAAATGAG GAGGAGCGAA AGTGGGGCTT TAGCCGAGTC 2340  
 AGCTCAGGAG GCTCCTTTTC AGTGCTGGGA GTTCCAGCTG GCCCCACCC TGATGTGTTT 2400  
 CCACCATGCA AAATTATTGA CCTGGAAGCT GTAAAAGTAG AAGAGGAATT GACCCTATCT 2460  
 TGGACAGCAC CTGGAGAAGA CTTTGATCAG GGCCAGGCTA CAAGCTATGA AATAAGAATG 2520  
 20 AGTAAAGTC TACAGAAATAT CCAAGATGAC TTTAACAATG CTATTTTAGT AAATACATCA 2580  
 AAGCGAAATC CTAGCAAGC TGGCATCAGG GAGATATTGA CGTCTCACC CCAGATTTC 2640  
 ACGAATGGAC CTGAACATCA GCCAAATGGA GAAACACATG AAAGCCACAG AATTATGTT 2700  
 GCAATACGAG CAATGGATAG GAATCCTTA CAGTCTGCTG TATCTAACAT TGCCACAGCG 2760  
 CCTCTGTTTA TTCCCCCAA TTCTGATCCT GTACCTGCCA GAGATTATCT TATATTGAAA 2820  
 25 GGAGTTTAA CAGCAATGGG TTTGATAGGA ATCATTTGCC TTATTATAGT TGTGACACAT 2880  
 CATACTTTAA GCAGGAAAAA GAGAGCAGAC AAGAAAGAGA ATGGAACAAA ATTATTATAA 2940  
 ATAAATATCC AAGTGTCTT CCTTCTTAGA TATAAGACCC ATGGCCTTCG ACTACAAAAA 3000  
 CACTATAACA AAGTCAAAAT AACATCAAAA CTGTATTAAA ATGCATTGAG TTTTGTGACA 3060  
 ATACAGATAA GATTTTACA TGGTAGATCA ACAATCTTTT TTGGGGGTAG ATTAGAAAAA 3120  
 30 CCTTACACTT TGGCTATGAA CAAATAATAA AAATTATCTT TTAAGTAAT GTCTTTAAAG 3180  
 GCAAGGGGAA GGGTAAAGTC GGACCAAGTG CAAGGAAAGT TTGTTTTATT GAGGTGGAAA 3240  
 AATAGCCCCA AGCAGAGAAA AGGAGGGTAG GTCTGCATTA TAAGTGTCTG TGTGAAGCAA 3300  
 TCATTAGATT ACCTTTGATTA ATTTTCTTTT TCTCCTTATC TGTGCAGTAC AGGTTGCTGT 3360  
 35 TTTACATGAA GATCATGCTA TATTTTATAT ATGTAGCCCC TAATGCAAAG CTCTTTACCT 3420  
 CTTGCTATTT TGTATATAT ATTTTCAGATG ACATCTCCCT GCTAATGCTC AGAGATCTTT 3480  
 TTTCACTGTA AGAGGTAACC TTTAACAATA TGGGTATTAC CTTTGTCTCT TCATACCGGT 3540  
 TTTATGACAA AGGTCTATTG AATTATTTTG TNTGTAAGTT TCTACTCCCA TCAAAGCAGC 3600  
 TTTCTAAGTT TATGCCCTTG GGTATTATAT GAATGATAGT TATAGCCCN TATAATGCCT 3660  
 TACCTAGGAA A

Seq ID NO: 8 Protein sequence:  
 Protein Accession #: NP\_006527.1

1 11 21 31 41 51  
 45 MTQRSIAGPI CNLKFTVLLV ALSSELPFLG AGVQLQDNGY NGLLIAINPQ VPENQNLISS 60  
 IKEMITEASF YLFNATKRRV FFRNIKILIP ATWKANNNSK IKQESYEKAN VIVTDWYGAAH 120  
 GDDPYTLQYR GCGKEGYIHF FTFNELLNDN LTAGYGSRRR VFVHEWAHLR WGVFDEYNND 180  
 KPFIYINGQNR IKVTRCSSDI TGIIVCEKGP CPQENCLISK LFKEGCTFIY NSTQNATASI 240  
 50 MFMQSLSSVV EFCNASTHNQ EAPNLQNMCM SLRSAWDVIT DSADEFHHSFP MNGTELEPPPP 300  
 TFSLVQAGDK VVCLVLDVSS KMAEADRLLO LQQAEEFYLM QIVEIHTFVG IASFDSKGEI 360  
 RAQLHQINSN DDRKLLVSYL PTTVSAKTDI SICSLKKGF EVVEKLNGKA YGSVMILVTS 420  
 GDDKLLGNCL PTVLSSSGSTI HSIALLGSSAA PNLEELSRIT GGLKFFVPDI SNSNSMIDAF 480  
 55 SRISSTIGDI FQQHIGLEST GENVKPHQL KNTVTVDNTV GNDTMFLVTW QASGPPBIL 540  
 FDPDRKYYT NNFITNLTFR TASLWIPGTA KPGHWYTYLN NTHHSLQALK VTVTSRASNS 600  
 AVPPATVEAF VERDSLHFFH PVMYIANVKQ GFYPILNATV TATVEPETGD PVTLRLRDDG 660  
 60 AGADVINDSG IYSRYFFSFA ANGRYSKLVH VNHSPSISTP AHSIPGSHAM YVPGYTANGN 720  
 IQMNAPRKSV GRNEEERKVG FSRVSSGGSF SVLGVPAGEH PDVFPPCKII DLEAVKVEEE 780  
 LTLSTWAPGE DFDQGQATSY EIRMSKSLQN IQDDFNNAIL VNTSKRNPQQ AGIREIIFTS 840  
 PQISTNGPEH QPNGETHESH RIYVAIRAMD RNSLQSAVSN IAQAPLFIPP NSDPVPARDY 900  
 LILKGVLTAM GLIGIICLII VVTHHTLSRK KRADKKENG T KLL

Seq ID NO: 9 DNA sequence  
 Nucleic Acid Accession #: Eos sequence  
 Coding sequence: 336-632

1 11 21 31 41 51  
 70 CTCCCTCAC CCCGGTCCAG GATGCCAGT CCCCACGACA CCTCCACTT CCCACTGTGG 60  
 CCTGGGTGGG CTCAGGGGCT GCCCTTGACC TGGCCTAGAG CCCTCCCCCA GCTGGTGGTG 120  
 GAGCTGGCAC TCTCTGGGAG GGAGGGGGCT GGGAGGGAAT GAGTGGGAAT GGCAAGAGGC 180  
 CAGGGTTTGG TGGGATCAGG TTGAGGCAGG TTTGGTTTCC TTAATAATGCC AAGTTGGGGG 240  
 CCAGTGGGGC CCACATATAA ATCTCTACCC TGGGAGCCTG GCTGCCTTGC TCTCCTTCCT 300  
 75 GGGTCTGTCT CTGCCACCTG GTCTGCCACA GATCCATGAT GTGCAGTTCT CTGGAGCAGG 360  
 CGCTGGCTGT GCTGCTCACT ACCTTCCACA AGTACTCCTG CCAAGAGGGC GACAAGTTCA 420  
 AGCTGAGTAA GGGGGAATG AAGGAACCTT TGCACAAGGA GCTGCCAGC TTTGTGGGGG 480  
 AGAAAGTGGA TGAGGAGGGG CTGAAGAAGC TGATGGGCAG CCTGGATGAG AACAGTGACC 540  
 AGCAGGTGGA CTTCCAGGAG TATGCTGTTT TCCTGGCACT CATCACTGTC ATGTGCAATG 600  
 80 ACTTCTTCCA GGGCTGCCCA GACCGACCTT GAAGCAGAAC TCTTGACTTC CTGCCATGGA 660  
 TCTCTGGGC CAGGACTGTG TGATGCCCTT GAGTTTGTG TTAATAAAC TTTTGTGTC 720  
 TGTGATAAT ATTTTAATTG CTCAGTGATG TTCCATAACC CGGCTGGCTC AGCTGGAGTG 780  
 CTGGGAGATG AGGGCTCTCT GGATCCTGCT CTTTCTGGG CTCTGACTCT CCTGGAATC 840  
 TCTCCAAGGC CAGAGCTAGT CTTTAGTCT CAATTTTGGG ATTTCAACA CAGCAAAAA 900  
 85 ATTGGAATC GAGATAGGTT GCTGACTTTT ATTTTGTCAA ATAAAGATAT TAAAAAGGC 960  
 AAATACCA

Seq ID NO: 10 Protein sequence:



Protein Accession #: NP\_005969.1

5                   11                   21                   31                   41                   51  
 |                   |                   |                   |                   |                   |  
 MMCSSLEQAL AVLVTTFFHKY SCQEGDKFKL SKGEMKELLH KELPSFVGEK VDEEGLKKLM 60  
 GSLDENSQQ VDFQEYAVFL ALITVMCNDF FQGCPRDP

Seq ID NO: 11 DNA sequence  
 Nucleic Acid Accession #: Eos sequence  
 Coding sequence: 336-626

15                   11                   21                   31                   41                   51  
 |                   |                   |                   |                   |                   |  
 CTCCCTCAC CCCGGTCCAG GATGCCAGT CCCACGACA CCTCCACTT CCCACTGTGG 60  
 CTTGGGTGGG CTCAGGGGCT GCCCTTGACC TGGCTAGAG CCTCCCCCA GCTGGTGGTG 120  
 GAGCTGGCAC TCTCTGGGAG GGAGGGGGCT GGGAGGGAAT GAGTGGGAAT GGCAAGAGGC 180  
 CAGGGTTTGG TGGGATCAGG TTGAGGCAGG TTTGGTTTCC TTAATAATGCC AAGTTGGGGG 240  
 CCAGTGGGGC CCACATATAA ATCCTCACCC TGGGAGCCTG GCTGCCTTGC TCTCCTTCTT 300  
 20 GGGTCTGTCT CTGCCACCTG GTCTGCCACA GATCCATGAT GTGCAGTTCT CTGGAGCAGG 360  
 CGCTGGCTGT GCTGGTCACT ACCTTCCACA AGTACTCCTG CCAAGAGGGC GACAAGTTCA 420  
 AGCTGAGTAA GGGGGAATATG AAGGAACTTC TGCACAAGGA GCTGCCAGC TTTGTGGGGC 480  
 ATTCAGAGA ACCATGTGCT GTGAGGGCCT TCCGAGTCCA TCTGTTTAACT CCTGTCTATTG 540  
 GAGACTTGAG AAACACAGAG CCAGAAGGGA AAAGTGATTG TCCCAAGATC ACACAGCACT 600  
 25 GGAGAAAGTG GATGAGGAGG GGTGAAGAA GCTGATGGGC AGCCTGGATG AGAACAGTGA 660  
 CCAGCAGGTG GACTTCCAGG AGTATGCTGT TTTCTGGCA CTCATCACTG TCATGTGCAA 720  
 TGACTTCTTC CAGGGCTGCC CAGACCGACC CTGAAGCAGA ACTCTTGACT TCCTGCCATG 780  
 GATCTCTTGG GCCCAGGACT GTTGATGCCT TTGAGTTTTC TATTCAATAA ACTTTTTTTG 840  
 30 TCTGTTGATA ATATTTTAAT TGCTCAGTGA TGTTCCTATA CCGGCTGGC TCAGCTGGAG 900  
 TGCTGGGAGA TGAGGGCCTC CTGGATCCTG CTCCTTCTG GGCCTGACT CTCCTGGAAA 960  
 TCTCTCAAG GCCAGAGCTA TGCTTTAGGT CTCATTTTG GAATTTCAA CACCAGCAA 1020  
 AAATTGGAAA TCGAGATAGG TTGCTGACTT TTATTTTGT CAAATAAGAT ATTAATAAAG 1080  
 GCAATACCA

Seq ID NO: 12 Protein sequence:  
 Protein Accession #: Eos sequence

40                   11                   21                   31                   41                   51  
 |                   |                   |                   |                   |                   |  
 MMCSSLEQAL AVLVTTFFHKY SCQEGDKFKL SKGEMKELLH KELPSFVGH S REPCA VRAFR 60  
 VHLNPFVIGD LRNQSPGK S DCPKITQHWR KWMRRG

Seq ID NO: 13 DNA sequence  
 Nucleic Acid Accession #: Eos sequence  
 Coding sequence: 58-354

50                   11                   21                   31                   41                   51  
 |                   |                   |                   |                   |                   |  
 GTGAGCTCAC CATGTGGGGG TGAGGCTGAG AGAAAACAAG TACACAGCCA CAGATCCATG 60  
 ATGTGCAGTT CTCTGGAGCA GGCGCTGGCT GTGCTGGTCA CTACCTTCCA CAAGTACTCC 120  
 TGCCAAGAGG GCGACAAGTT CAAGCTGAGT AAGGGGGAAA TGAAGGAAT TCTGCACAAG 180  
 GAGCTGCCCA GCTTTGTGGG GGAGAAAGTG GATGAGGAGG GGCTGAAGAA GCTGATGGGC 240  
 55 AGCCTGGATG AGAACAGTGA CCAGCAGGTG GACTTCCAGG AGTATGCTGT TTTCTGGCA 300  
 CTCATCACTG TCATGTGCAA TGACTTCTTC CAGGGCTGCC CAGACCGACC CTGAAGCAGA 360  
 ACTCTTGACT TCCTGCCATG GATCTCTTGG GCCCAGGACT GTTGATGCCT TTGAGTTTTC 420  
 TATTCAATAA ACTTTTTTTG TCTGTTGATA ATATTTTAAT TGCTCAGTGA TGTTCCTATA 480  
 CCCGGCTGGC TCAGCTGGAG TGCTGGGAGA TGAGGGCCTC CTGGATCCTG CTCCTTCTG 540  
 60 GGCTCTGACT CTCCTGGAAA TCTCTCCAAG GCCAGAGCTA TGCTTTAGGT TCCAATTTTG 600  
 GAATTTCAA CACCAGCAA AAATTGGAAA TCGAGATAGG TTGCTGACTT TTATTTTGT C 660  
 AAATAAGAT ATTAATAAAG GCAATACCA

Seq ID NO: 14 Protein sequence:  
 Protein Accession #: NP\_005969.1

65                   11                   21                   31                   41                   51  
 |                   |                   |                   |                   |                   |  
 MMCSSLEQAL AVLVTTFFHKY SCQEGDKFKL SKGEMKELLH KELPSFVGEK VDEEGLKKLM 60  
 GSLDENSQQ VDFQEYAVFL ALITVMCNDF FQGCPRDP

Seq ID NO: 15 DNA sequence  
 Nucleic Acid Accession #: Eos sequence  
 Coding sequence: 62-358

75                   11                   21                   31                   41                   51  
 |                   |                   |                   |                   |                   |  
 GGAGGGTGTG CCGCTGAGTC ACTGCCTGGG CATCTGGGCC TGAACCTCG GCCACAGATC 60  
 CATGATGTGC AGTTCTCTGG AGCAGGCGCT GGCTGTGCTG GTCCTACCT TCCACAAGTA 120  
 CTCCTGCCAA GAGGGCGACA AGTTCAAGCT GAGTAAGGGG GAAATGAAGG AACTTCTGCA 180  
 80 CAAGGAGCTG CCCAGCTTTG TGGGGGAGAA AGTGGATGAG GAGGGGCTGA AGAAGCTGAT 240  
 GGGCAGCCTG GATGAGAACA GTGACCAGCA GGTGGACTTC CAGGAGTATG CTGTTTTCTT 300  
 GGCCTCATC ACTGTCATGT GCAATGACTT CTTCCAGGCG TGCCAGACC GACCTGAAG 360  
 CAGAACTCTT GACTTCTGTC CATGGATCTC TTGGGCCCAG GACTGTTGAT GCCTTTGAGT 420  
 TTTGTATTCA ATAAACTTTT TTTGTCTGTT GATAATATT TAATTGCTCA GTGATGTTCC 480  
 85 ATAACCCGGC TGGCTCAGCT GGAGTGCTGG GAGATGAGGG CCTCTGGAT CCTGCTCCTT 540  
 TCTGGGCTCT GACTCTCCTG GAAATCTCTC CAAGGCCAGA GCTATGCTTT AGGTCTCAAT 600  
 TTTGGAATTT CAAACACCAG CAAAAAATTG GAAATCGAGA TAGGTTGCTG ACTTTTATT 660



TGTCAAATAA AGATATTAAA AAAGGCAAAT ACCA

Seq ID NO: 16 Protein sequence:  
Protein Accession #: NP\_005969.1

1	11	21	31	41	51	
MMCSSLEQAL	AVLVTTTFHKY	SCQEGDKFKL	SKGEMKELLH	KELPSFVGEK	VDEEGLKKLM	60
GSLDENSQQ	VDFQYAVFL	ALITVMCNDF	FQGCPCDRP			

Seq ID NO: 17 DNA sequence  
Nucleic Acid Accession #: Eos sequence  
Coding sequence: 939-2372

1	11	21	31	41	51	
AAGACGGATT	CTCAGACAAG	GCTTGGCAAAT	GCCCCGCAGC	CATCATTAA	CTGCACCCGC	60
AGAATAGTTA	CGGTTTGTC	CCCAGACCTC	CCGGATCGCC	TAATTTGTCC	CTAGTGAGAC	120
CCCGAGGCTC	TGCCCGCGCC	TGGCTTCTTC	GTAGCTGGAT	GCATATCGTG	CTCCGGGCAG	180
CGCGGGCGCA	GGGCACGCGT	TCGCGCACAC	CCTAGCACAC	ATGAACACGC	GCAAGAGCTG	240
AACCAAGCAC	GGTTTCCATT	TCAAAAAGGG	AGACAGCCTC	TACCGCGATT	GTAGAAGAGA	300
CTGTGGTGTG	AATTAGGGAC	CGGGAGGCGT	CGAACGGAGG	AACGGTTCAT	CTTAGAGACT	360
AATTTTCTGG	AGTTTCTGCC	CCTGCTCTGC	GTCAGCCCTC	ACGTCACCTC	GCCAGCAGTA	420
GCAGAGGCGG	CGGCGGCGGC	TCCGGAATT	GGGTGGAGC	AGGAGCCTCG	CTGGCTGCTT	480
CGCTCGCGCT	CTACGCGCTC	AGTCCCCGGC	GGTAGCAGGA	GCCTGGACCC	AGGCGCGGCC	540
GGCGGGCGTG	AGGCGCGGGA	GCCCGGCCCTC	GAGGTGCATA	CCGGACCCCC	ATTGCGCATCT	600
AACAAGGAAT	CTGCGCCCCA	GAGAGTCCCG	GGAGCGCCGC	CGGTCGGTGC	CCGCGCGGCC	660
GGGCCATGCA	GCGAGCGCGC	CCGCGGAGCT	CCGAGCAGCG	GTAGCGCCCC	CCTGTAAAGC	720
GGTTCCGTAT	GCCGGGGGCA	CTGTGAACCC	TGCCGCCTGC	CGAACACTCT	TTGCTCCGG	780
ACCAGCTCAG	CCTCTGATAA	GCTGGACTCG	GCACGCCCCG	AACAAGCACC	GAGGAGTTAA	840
GAGAGCCGCA	AGCCGAGGGA	AGGCCTCCCC	GCACGGGTGG	GGGAAAGCGG	CCGGTGCAGC	900
GCGGGGACAG	GCACCTCGGC	TGGCACTGGC	TGCTAGGGAT	GTCTGCTGG	ATAAGGTGGC	960
ATGGACCCGC	CATGGCGCGG	CTCTGGGCT	TCTGCTGGCT	GGTTGTGGGC	TTCTGGAGGG	1020
CCGCTTTGCG	CTGTCCACAG	TCCGTGCAAAT	GCAGTGCCTC	TCCGATCTGG	TGCAGCGACC	1080
CTTCTCCTGG	CATCGTGGCA	TTTCCGAGAT	TGGAGCCTAA	CAGTGTAGAT	CCTGAGAACA	1140
TCACCGAAAT	TTTTCATCGA	AACCAGAAAA	GGTTAGAAAT	CATCAACGAA	GATGATGTTG	1200
AAGCTTATGT	GGGACTGAGA	AATCTGACAA	TTGTGGATT	TGGATTAAAA	TTTGTGGCTC	1260
ATAAAGCATT	TCTGAAAAAC	AGCAACCTGC	AGCACATCAA	TTTTACCCGA	AACAACTGA	1320
CGAGTTTGTC	TAGGAAACAT	TTCCGTCAAC	TTGACTTGTC	TGAACTGATC	CTGGTGGGCA	1380
ATCCATTTAC	ATGCTCCTGT	GACATTATGT	GGATCAAGAC	TCTCCAAGAG	GCTAAATCCA	1440
GTCCAGACAC	TCAGGATTG	TACTGCCTGA	ATGAAGCAG	CAAGAATATT	CCCCTGGCAA	1500
ACCTGCAGAT	ACCCAATTGT	GGTTTGCCAT	CTGCAATCT	GGCCGCACCT	AACCTCACTG	1560
TGGAGGAAGG	AAAGTCTATC	ACATTTATCT	GTAGTGTGGC	AGGTGATCCG	GTTCCTAATA	1620
TGTATTGGGA	TGTTGGTAAC	CTGTTTCCA	AACATATGAA	TGAACACAGC	CACACACAGG	1680
GCTCCTTAAG	GATAACTAAC	ATTTTCATCCG	ATGACAGTGG	GAAGCAGATC	TCTTGTGTGG	1740
CGGAAAAATCT	TGTAGGAGAA	GATCAAGATT	CTGTCAACCT	CACGTGTGAT	TTTGCACCAA	1800
CTATCACATT	TCTCGAATCT	CCAACCTCAG	ACCACCCTG	GTGCATTCCA	TTCACTGTGA	1860
AAGGCAACCC	CAAACCCAGC	CTTCAGTGGT	TCTATAACGG	GGCAATATTG	AATGAGTCCA	1920
AATACATCTG	TACTAAAAAT	CATGTTACCA	ATCACACGGA	GTACCACGGC	TGCCTCCAGC	1980
TGGATAATCC	CACCTCACATG	AACAATGGGG	ACTACACTCT	AATAGCCAAG	AATGAGTATG	2040
GGAAAGGATGA	GAAACAGATT	TCTGCTCACT	TCATGGGCTG	GCCTGGAATT	GACGATGGTG	2100
CAAAACCCAAA	TTATCCTGAT	GTAATTTATG	AAGATTATGG	AACTGCAGCG	AATGACATCG	2160
GGGACACCCAC	GAACAGAAAT	AATGAAATCC	CTTCCACAGA	CGTCACTGAT	AAAACCGGCT	2220
GGGAACATCT	CTCGGTCTAT	GCTGTGGTGG	TGATTGCGTC	TGTGGTGGGA	TTTTGCCTTT	2280
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CCAGCAGCAA	AGAGGTGACA	GGTCGCTAAT	GAATATATGC	TTTATAATGT	CTTCTTCAT	3540
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Seq ID NO: 18 Protein sequence:  
 Protein Accession #: CAA53571

1 11 21 31 41 51  
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 SKNIPLANLQ IPNCLPSAN LAAPNLVVEE GKSTILSCSV AGDPVPMYMW DVGNLVSKHM 240  
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Seq ID NO: 20 Protein sequence:  
 Protein Accession #: NP\_000219

1 11 21 31 41 51  
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Seq ID NO: 21 DNA sequence  
 Nucleic Acid Accession #: NM\_003722  
 Coding sequence: 145-1491

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Seq ID NO: 22 Protein sequence:  
 Protein Accession #: NP\_003713

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 Coding sequence: 84-3083

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 CAGGAGGCTC GGGGCTGCCC GCCATCGGCC TGCTGCTCCT TGGTCTCCTG CTGCTGCTGT 1980  
 TGGCCCCCCT TCTGTGTTG ACCTGTGACT GTGGGCGAGG TTCTACTGGG GGAGTGACAG 2040  
 GTGGTTTTAT CCCAGTTCCT GATGGCTCAG AAGGAACAAT TCATCAGTGG GGAATTGAAG 2100  
 GAGCCCATCC TGAAGACAAG GAAATCACAA ATATTGTGT GCCTCCTGTA ACAGCCAATG 2160  
 GAGCCGATTT CATGGAAGT TCTGAAGTT GTACAAATAC GTATGCCAGA GGCACAGCGG 2220  
 TGGAAGGCAC TTCAGGAATG GAAATGACCA CTAAGCTTGG AGCAGCCACT GAATCTGGAG 2280  
 GTGCTGACAG CTTTCAACA GGGACAGTGT CAGGAGCTGC TTCAGGATTC GGAGCAGCCA 2340  
 CTGGAGTTGG CATCTGTTCC TCAGGGCAGT CTGGAACCAT GAGAACAAGG CATTCACATG 2400  
 GAGGAACCAA TAAGGACTAC GCTGATGGGG CGATAAGCAT GAATTTTCTG GACTCCTACT 2460  
 TTTCTCAGAA AGCATTTGCC TGTGCGGAGG AAGACGATGG CCAGGAAGCA AATGACTGCT 2520  
 TGTGATCTA TGATAATGAA GGCGCAGATG CCACTGGTTC TCCTGTGGGC TCCGTGGGTT 2580  
 GTTGCAAGTT TATTGCTGAT GACCTGGATG ACAGCTTCTT GGACTCACAT GGACCCAAT 2640  
 TTAATAAACT TGCAGAGATA AGCCTTGGTG TTGATGGTGA AGGCAAGAA GTTCAGCCAC 2700  
 CCTCTAAGA CAGCGTTTAT GGGATTGAAT CCTGTGGCCA TCCCATAGAA GTCCAGCAGA 2760  
 CAGGATTTGT TAAGTGCCAG ACTTTGTGAG GAAGTCAAGG AGCTTCTGCT TTGTCCGCCT 2820  
 CTGGGTCTGT CCAGCCAGCT GTTTCATCC CTGACCCCTC GCAGCATGGT AACTATTTAG 2880  
 TAACGGAGAC TTACTCGGGT TCTGGTTCCT TCGTGCAACC TTCCACTGCA GGCTTTGATC 2940  
 CACTTCTCAC ACAAATGTG ATAGTGACAG AAAGGGTGAT CTGTCCCAT TCCAGTGTTC 3000  
 CTGGCAACCT AGCTGGCCCA ACGCAGCTAC GAGGGTCACA TACTATGCTC TGTACAGAGG 3060  
 ATCCTTGCTC CCGTCTAATA TGACCAGAAT GAGCTGGAAT ACCACACTGA CCAATCTGG 3120  
 ATCTTTGGAC TAAAGTATTC AAAATAGCAT AGCAAGGCTC ACTGTATTGG GCTAATAATT 3180  
 TGGCACTTAT TAGCTTCTCT CATAAAGTGA TCACGATTAT AAATAAATG TTTGGGTTCA 3240  
 TACCCAAAAA GCAATATGTT GTCACTCCTA ATTCTCAAGT ACTATTCAAA TTGTAGTAAA 3300  
 TCTTAAAGTT TTTCAAAACC CTAATATCAT ATTCGC

Seq ID NO: 24 Protein sequence:  
 Protein Accession #: NP\_001935.1

1 11 21 31 41 51



	MMGLFPRTTG	ALAIFVVVIL	VHGELEIETK	GQYDEEEMTM	QQAARRQKRE	VVKFAKPCRE	60
	GEDNSKRNP	AKITSDYQAT	QKITYRISGV	GIDQPPFGIF	VVDKNTGDI	ITAIVDREET	120
	PSFLTTCRAL	NAQGLDVEKP	LILTVKILDI	NDNPPVFSQQ	IFMGEIEBNS	ASNSLVMILN	180
5	ATDADEPNHL	NSKIAFKIVS	QEPAGTMMFL	LSRNTGEVRT	LTNSLDREQA	SSYRLVVSQA	240
	DKDGBGLSTQ	CECNKVKDV	NDNPFMFRDS	QYSARIEENI	LSSLLRFQV	TDLDEEYTDN	300
	WLAVYFFSTG	NEGNWFEIQT	DPRTNEGILK	VVKALDYEQ	QSVKLSIAVK	NKAEFHQSVI	360
	SRIRVQSTPV	TIQVINVREG	IAFRPASKTF	TVQKGISSKK	LVDYILGTQ	AIDEDTNKAA	420
10	SNVYVYVGRN	DGGYLMDSK	TAEIKFVKNM	NRDSTFIVNK	TITAEVLAI	BYTGKTSTGT	480
	VYVRVPDFND	NCPTAVLEKD	AVCSSSPSVV	VSARTLNNRY	TGPYTFALD	QPVKLPAVWS	540
	ITTLNATSAL	LRAQEQIPFG	VYHISLVLT	SQNNRCCEMR	SLTLEVQCQD	NRGICGTSYP	600
	TTSPGTRYGR	PHSGRLGPAA	IGLLLLGLLL	LLLAPLLLLT	CDCGAGSTGG	VTGGFIPVPD	660
	GSEGTIHQWG	IEGAHPEDKE	ITNICVPVPT	ANGADFMESS	EVCTNTYARG	TAVEGTSME	720
15	MTTKLGAATE	SGGAAGFATG	TVSGAASGFG	AATGVGICSS	GQSGTMRTRH	STGGTNKYA	780
	DGAISMNPLD	SYFSQKAFAC	AEEDDGQEAN	DCLLIYDNEG	ADATGSPVGS	VGCCSFIADD	840
	LDDSFLLDSL	PKFKKLAELS	LGVDEGEGKEV	QPPSKDSGYG	IESCGHPIEV	QQTGFVKCQT	900
	LSGSQGSASL	SASGSVQPAV	SIPDPLQHGN	YLVTTETYSAS	GSLVQPSLAG	FDPLLTQNV	960
	VTERTVICPIS	SVPGNLAGPT	QLRGSHTMLC	TEDPCSRLLI			

Seq ID NO: 25 DNA sequence  
Nucleic Acid Accession #: Eos sequence  
Coding sequence: 56-1642

	1	11	21	31	41	51	
25	AGTATCCAG	GAGGAGCAAG	TGGCAGCTCT	TCGGACCTAG	GCTGCCCCCTG	CCGTCAATGTC	60
	GCAAGGGATC	CTTTCTCCGC	CAGCGGGCTT	GCTGTCCGAT	GACGATGTCG	TAGTTTCTCC	120
	CATGTTTGAG	TCCACAGCTG	CAGATTGCGG	GTCTGTGGTA	CGCAAGAAC	TGCTATCAGA	180
	CTGCTCTGTC	GTCTCTACCT	CCCTAGAGGA	CAAGCAGCAG	GTTCCATCTG	AGGACAGTAT	240
30	GGAGAAAGTG	AAAGTATACT	TGAGGGTTAG	GCCCTTGTTA	CCTTCAGAGT	TGGAACGACA	300
	GGAAAGATCAG	GGTTGTGTCC	GTATTGAGAA	TGTGGAGACC	CTTGTTCTAC	AAGCACCCAA	360
	GGACTCTTTT	GCCCTGAAGA	GCAATGAACG	GGGAATTGGC	CAAGCCACAC	ACAGGTTTAC	420
	CTTTTCCAG	ATCTTTGGGC	CAGAAGTGGG	ACAGGCATCC	TTCTTCAACC	TAAGTGTGAA	480
	GGAGATGGTA	AAGGATGTAC	TCAAAGGGCA	GAAGTGGCTC	ATCTATACAT	ATGGAGTCAC	540
35	TAAGTCAAGG	AAAAACCCCA	CGATTCAAGG	TACCATCAAG	GATGGAGGGA	TTCTCCCCCG	600
	GTCCCTGGCG	CTGATCTTCA	ATAGCCTCCA	AGGCCAACTT	CATCCAACAC	CTGATCTGAA	660
	GCCCTTGCTC	TCCAATGAGG	TAATCTGGCT	AGACAGCAAG	CAGATCCGAC	AGGAGGAAAT	720
	GAAGAAGCTG	TCCCTGCTAA	ATGGAGGCTT	CCAAGAGGAG	GAGCTGTCCA	CTTCTTTGAA	780
	GAGGAGTGTC	TACATCGAAC	GTCCGATAGG	TACAGCAGCC	AGCTTCGACA	GTGGCATTGC	840
40	TGGGCTCTCT	CTATCATGCT	AGTGTACCAG	CAGTAGCCAG	CTGGATGAAA	CAAGTCATGC	900
	ATGGGCACAG	CCAGACACTG	CCCCACTACC	TGTCCCGGCA	AACATTCGCT	TCTCCATCTG	960
	GATCTCATTC	TTTGAGATCT	ACAACGAACT	GCTTTATGAC	CTATTAGAAC	CGCCTAGCCA	1020
	ACAGCGCAAG	AGGCGAGACT	TGCGGCTATG	CGAGGATCAA	AATGGCAATC	CCTATGTGAA	1080
	AGATCTCAAC	TGGATTCAATG	TGCAAGATGC	TGAGGAGGCC	TGGAAGCTCC	TAAAGTGGG	1140
45	TCGTAAAGAA	CAGAGCTTTG	CCAGCACCCA	CCTCAACCAG	AACTCCAGCC	GCAGTCACAG	1200
	CATCTTCTCA	ATCAGGATCC	TACACCTTCA	GGGGGAAGGA	GATATAGTCC	CCAAGATCAG	1260
	CGAGCTGTCA	CTCTGTGATC	TGGCTGGCTC	AGAGCGCTGC	AAAGATCAGA	AGAGTGGTGA	1320
	ACGGTTGAAG	GAAGCAGGAA	ACATTAAACAC	CTCTCTACAC	ACCCCTGGGC	GCTGTATTGC	1380
	TGCCCTTCCT	CAAAACCAAG	AGAACCGGTC	AAAGCAGAAC	CTGGTTCCCT	TCCGTGACAG	1440
50	CAAGTTGACT	CGAGTGTTC	AAGGTTTCTT	CACAGGCCGA	GGCCGTTTCT	GCATGATTGT	1500
	CAATGTGAAT	CCCTGTGCAT	CTACCTATGA	TGAAACTCTT	CATGTGGCCA	AGTTCTCAGC	1560
	CATTGCTAGC	CAGGTGACTT	GTGCTAGCCC	CACCTATGCA	ACTGGGATTC	CCATCCCTGC	1620
	ACTCGTTCAT	CAAGGAACAT	AGTCTTCAGG	TATCCCCCAG	CTTAGAGAAA	GGGGCTAAGG	1680
	CAGACACAGG	CCTTGATGAT	GATATTGAAA	ATGAAGCTGA	CATCTCCATG	TATGGCAAAG	1740
55	AGGAGCTCCT	ACAAGTTGTG	GAAGCCATGA	AGACACTGCT	TTTGAAGGAA	CGACAGGAAA	1800
	AGCTACAGCT	GGAGATGCAT	CTCCGAGATG	AAATTGTCAA	TGAGATGGTA	GAACAGATGC	1860
	AACAGCGGGA	ACAGTGGTGC	AGTGAACATT	TGGACACCCA	AAAGGAACAT	TTGGAGGAAA	1920
	TGTATGAAGA	AAAACTAAAT	ATCCTCAAGG	AGTCACTGAC	AAGTTTATAC	CAAGAAGAGA	1980
	TTCAAGGAGC	GGATGAAGAG	ATTGAAGAGC	TAGAAGCTCT	CTTGCAAGAA	GCCAGACAA	2040
60	AGTCAGTGGC	CCATCAGCAA	TCAGGCTCTG	AATTGGCCCT	ACGGCGGTCA	CAAAGGTTGG	2100
	CAGCTTCTGC	CTCCACCCAG	CAGCTTCAGG	AGGTTAAAGC	TAAATTACAG	CAGTGCAAG	2160
	CAGAGCTAAA	CTCTACCACT	GAAGAGTTGC	ATAAGTATCA	GAAATGTTA	GAACCAACAC	2220
	CCTCAGCCAA	GCCCTTCACC	ATTGATGTGG	ACAAGAAATT	AGAAGAGGGC	CAGAAGATA	2280
	TAAGGCTGTT	GCGGACAGAG	CTTCAGAAAC	TTGGTGAGTC	TCTCCAATCA	GCAGAGAGAG	2340
65	CTTGTTGCCA	CAGCACTGGG	GCAGGAAAC	TTCGTCAAGC	CTTGACCACT	TGTGATGACA	2400
	TCTTAATCAA	ACAGGACCAG	ACTCTGGCTG	AACTGCAGAA	CAACATGGTG	CTAGTGAAAC	2460
	TGGACCTTCG	GAAGAAGGCA	GCAATGATTG	CTGAGCAGTA	TCATACTGTG	TTGAAACTCC	2520
	AAGGCGAGGT	TTCTGCCAAA	AAGCGCCTTG	GTACCAACCA	GGAAATCAG	CAACCAAAAC	2580
	AACAACCAAC	AGGGAAGAAA	CCATTCCCTC	GAAATTTACT	TCCCGAACA	CCAACCTGCC	2640
70	AAAGCTCAAC	AGACTGCAGC	CCTTATGCCC	GGATCCTACG	CTCACGGCGT	TCCCTTTTAC	2700
	TCAAATCTGG	GCCTTTTGGC	AAAAAGTACT	AAGGCTGTGG	GGAAAGAGAA	GAGCAGTCAT	2760
	GGCCCTGAGG	TGGGTGACCT	ACTCTCCTGA	AGAAATAGGT	CTCTTTTATG	CTTTACCAT	2820
	TATCAGGAAT	TATATCCAGG	ATGCAATACT	CAGACACTAG	CTTTTCTCTC	ACTTTGTAT	2880
	TATAACCACC	TATGTAATCT	CATGTTGTTG	TTTTTTTTTA	TTTACTTATA	TGATTTCTAT	2940
75	GCACACAAA	ACAGTTATAT	TAAAGATATT	ATTGTTTACA	TTTTTTTATG	AATTCCAAAT	3000
	GTAGCAAAAT	CATTAACAAA	AATTATAAAA	GGGACAGAAA	AA		

Seq ID NO: 26 Protein sequence:  
Protein Accession #: Eos sequence

	1	11	21	31	41	51	
80	MSQGILSPPA	GLLSDDVVV	SPMFESTAAD	LGSVVRKNLL	SDCSVSTSL	EDKQVPSSE	60
	SMEKVKVYLR	VRPLLPSELE	RQEDQGCVR	ENVETLVLLQ	PKDSFALKSN	ERGIGQATHR	120
85	FTFSQIFGPE	VQAGSFNLT	VKEMVKDVLK	GQNWLIYTYG	VINSKTHITI	QGTIKDGGIL	180
	PRSLALIFNS	LQQQLHPTPD	LKPLLSNEVI	WLDKQIRQIE	EMKKLSLLNG	GLQEEELSTS	240
	LKRSVYIESR	IGTSTSFDSG	IAGLSSISQC	TSSSQLDETS	HRWAQPDAP	LPVPANIRFS	300



IWISFFEIYN ELLYDLLEPP SQQRKRQTLR LCEDQNGNPY VKDLNWIHVQ DAEEAWKLLK 360  
 VGRKNQSFAS THLNQNSRRS HSIFSIIRILH LQEGEDIVPK ISELSLCDLA GSERCKDQKS 420  
 GERLKEAGNI NTSLHTLGRG IAA LRQNNQN RSKQNLVPRF DSKLTRVFPQ FFTGRGRSCM 480  
 IVNVNPCAST YDETLHVAKF SAIASQVTCA CPTYATGIPI PALVHQGT

Seq ID NO: 27 DNA sequence  
 Nucleic Acid Accession #: Eos sequence  
 Coding sequence: 13-1424

1 11 21 31 41 51  
 TAGAAGTTTA CAATGAAGTT TCTTCTAATA CTGCTCCTGC AGGCCACTGC TTCTGGAGCT 60  
 CTTCCTCCCTGA ACAGCTCTAC AAGCCTGGAA AAAAATAATG TGCTATTGGG TGAAAGATAC 120  
 TTAGAAAAAT TTTATGGCCT TGAGATAAAC AAACCTCCAG TGACAAAAAT GAAATATAGT 180  
 GGAACCTTAA TGAAGGAAAA AATCCAAGAA ATGCAGCACT TCTTGGGTCT GAAAGTGACC 240  
 GGGCAACTGG ACACATCTAC CCTGGAGATG ATGCACGCAC CTCGATGTGG AGTCCCCGAT 300  
 GTCCATCATT TCAGGGAAT GCCAGGGGG CCCGTATGGA GGAAACATTA TATCACCTAC 360  
 AGAATCAATA ATTACACACC TGACATGAAC CGTGAGGATG TTGACTACGC AATCCGAAA 420  
 GCTTTCCAAG TATGAGTAA TGTTACCCCT TGAAATTCA GCAAGATTAA CACAGGCATG 480  
 GCTGACATT TGGTGGTTT TGCCCGTGGA GCTCATGGAG ACTTCCATGC TTTTGATGGC 540  
 AAAGGTGGA TCCTAGCCCA TGCTTTTGGA CCTGGATCTG GCATTGGAGG GGATGCACAT 600  
 TTCGATGAGG ACGAATTCTG GACTACACAT TCAGGAGGCA CAAACTTGTT CCTCACTGCT 660  
 GTTCACGAGA TTGGCCATT CTTAGGTCTT GGCCATTCTA GTGATCCAAA GGCCGTAATG 720  
 TTCCCACTT ACAAATATGT TGACATCAAC ACATTTCGCC TCTCTGCTGA TGACATACGT 780  
 GGCATTCACT CCCTGTATGG AGACCCAAAA GAGAACCAAC GCTTGCCAAA TCCTGACAAT 840  
 TCAGAACCCAG CTCTCTGTGA CCCCATTG AGTTTTGATG CTGTCACTAC CGTGGGAAAT 900  
 AAGATCTTTT TCTTCAAAGA CAGGTTCTTC TGGCTGAAGG TTTCTGAGAG ACCAAAGACC 960  
 AGTGTGAATT TAATTCTTC CTTATGGCCA ACCTTGCCAT CTGGCATTGA AGCTGCTTAT 1020  
 GAAATTGAAG CCAGAAATCA AGTTTTCTT TTTAAGATG ACAAATACTG GTTAATTAGC 1080  
 AATTTAAGAC CAGAGCCAAA TTATCCCAAG AGCATACATT CTTTGGTTT TCCTAACTTT 1140  
 GTGAAAAAAA TTGATGCAGC TGTTTTTAAC CCACGTTTT ATAGGACCTA CTTCTTTGTA 1200  
 GATAACCACT ATTGGAGTGA TGATGAAAGG AGACAGATGA TGGACCCCTGG TTATCCCAAA 1260  
 CTGATTACCA AGAATTCCA AGGAATCGGG CCTAAAATG ATGCAGTCTT CTACTCTAAA 1320  
 AACAAATACT ACTATTTCTT CCAAGGATCT AACCAATTG AATATGACTT CCTACTCCAA 1380  
 CGTATCACCA AAACACTGAA AAGCAATAGC TGGTTTGGTT GTTGAAAAATG GTGTAAATTA 1440  
 TGGTTTTTGT TAGTTCACTT CAGCTTAATA AGTATTTAT GCATATTTGC TATGTCCTCA 1500  
 GTGTACCATT ACTTAGAGAT ATGTATCATA AAAATAAAAT CTGTAAACCA TAGGTAATGA 1560  
 TTATATAAAA TACATAATAT TTTTCAATTT TGAAACTCT AATTGTCCAT TCTTGCTTGA 1620  
 CTCTACTATT AAGTTTGAAT ATAGTTACCT TCAAAGCAAG ATAATTTCTAT TTGAAGCATG 1680  
 CTCTGTAAGT TGCTTCCTA CATCCTTGGA CTGAGAAAT ATACTTACTT CTGGCATAAC 1740  
 TAAATTAAG TATATATATT TTGGCTCAAA TAAATTG

Seq ID NO: 28 Protein sequence:  
 Protein Accession #: Eos sequence

1 11 21 31 41 51  
 MKFLILLLLQ ATASGALPLN SSTSLKNNV LFGERYLEKF YGLEINKLPV TKMKYSGNLM 60  
 KEKIQEMQHF LGLKVTGQLD TSTLEMMHAP RCGVPDVHVF REMPGGPVWR KHYITYRINN 120  
 YTPDMNREDV DYAIRKAFQV WSNVTPLKFS KINTGMADIL VVFARGAHGD FHAFDGKGGI 180  
 LAHAFPGPSG IGGDAHFDDE EFWTTHSGGT NLFLTAVHEI GHSGLGLHSS DPKAVMPPTY 240  
 KYVDINTFRL SADDIRGIQS LYGDPKENQR LNPNDNSEPA LCDPNLSFDA VTTVGNKIFF 300  
 FKDRFPWLKV SERPKTSVNL ISSLWPTLPS GIEAAYEIEA RNQVFLFKDD KYWLISNLRP 360  
 EPNYPKSIHS FGFPNFVKKI DAAVFNPRFY RTYFFVDNQY WRYDERRQMM DPGYPKLITK 420  
 NFQGGTGPKE AVFYSKNKY YFFQGSNQFE YDFLLQRTK TLKSNSWFGC

Seq ID NO: 29 DNA sequence  
 Nucleic Acid Accession #: NM\_006115.1  
 Coding sequence: 236..1765

1 11 21 31 41 51  
 GCTTCAGGGT ACAGCTCCCC CGCAGCCAGA AGCCGGGCCT GCAGCCCCTC AGCACCCTC 60  
 CGGGACACCC CACCCGCTTC CCAGGCGTGA CCTGTCAACA GCAACTTCGC GGTGTGGTGA 120  
 ACTCTCTGAG GAAAAACCAT TTTGATTATT ACTCTCAGAC GTGCGTGGCA ACAAGTACT 180  
 GAGACCTAGA AATCCAAGCG TTGGAGGTCC TGAGGCCAGC CTAAGTCGCT TCAAAATGGA 240  
 ACGAAGGCGT TTGTGGGGTT CCATTACAG CCGATACATC AGCATGAGTG TGTGGACAAG 300  
 CCCACGGAGA CTTGTGGAGC TGGCAGGGCA GAGCCTGCTG AAGGATGAGG CCCTGGCCAT 360  
 TGCCGCCCTG GAGTTGCTGC CCAGGAGCT CTCCCGCCA CTCTCATGG CAGCCTTTGA 420  
 CGGGAGACAC AGCCAGACCC TGAAGGCAAT GGTGCAGGCC TGGCCCTTCA CCTGCCTCCC 480  
 TCTGGGAGTG CTGATGAAGG GACAACATCT TCACCTGGAG ACCTTCAAAG CTGTGCTTGA 540  
 TGGACTTGAT GTGCTCCTTG CCCAGGAGGT TCGCCCGAG AGGTGGAAC TTCAAGTGCT 600  
 GGATTACCG AAGAACTCT ATCAGGACTT CTGACTGTA TGGTCTGGAA ACAGGGCCAG 660  
 TCTGTACTCA TTCCAGAGC CAGAAGCAGC TCAGCCCATG ACAAGAAGC GAAAAGTAGA 720  
 TGGTTTGAGC ACAGAGGCG AGCAGCCCTT CATTCAGTA GAGGTGAGG TAGACCTGTT 780  
 CCTCAAGGAA GGTGCTGTG ATGAATTGTT CTCCTACCTC ATTGAGAAAG TGAAGCGAAA 840  
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 TATCAAGATG ATCCTGAAAA TGGTGCAGCT GGACTCTATT GAAGATTGG AAGTGAATTG 960  
 TACCTGGAAG CTACCCACTT TGGCGAAATT TTCTCCTTAC CTGGGCCAGA TGATTAACT 1020  
 GCGTAGACTC CTCTCTCCC ACATCCATGC ATCTTCTTAC ATTTCCCGCG AGAAGGAAGA 1080  
 GCAGTATATC GCCCAGTTCA CCTCTCAGTT CCTCAGTCTG CAGTGCCTGC AGGCTCTCTA 1140  
 TGTGGACTCT TTATTTTTCT TTAGAGGCCG CCTGGATCAG TTGCTCAGG ACCTGATGAA 1200  
 CCCCTTGGAA ACCCTCTCAA TAACTAACTG CCGGCTTTCG GAAGGGGATG TGATGCATCT 1260  
 GTCCACAGAT CCCAGCGTCA GTCAGCTAAG TGTCTGAGT CTAAGTGGGG TCATGCTGAC 1320  
 CGATGTAAGT CCCAGCCCC TCCAAGCTCT GCTGGAGAGA GCCTCTGCCA CCCTCCAGGA 1380  
 CCTGGTCTTT GATGAGTGTG GGATCACGGA TGATCAGCTC CTTGCCCTCC TGCCTTCCCT 1440  
 GAGCCACTGC TCCCAGCTTA CAACCTTAAG CTCTACGGG AATTCATCT CCATATCTGC 1500



CTTGCAGAGT CTCCTGCAGC ACCTCATCGG GCTGAGCAAT CTGACCCACG TGCTGTATCC 1560  
 TGTCCCCCTG GAGAGTTATG AGGACATCCA TGGTACCCTC CACCTGGAGA GGCTTGCCTA 1620  
 TCTGCATGCC AGGCTCAGGG AGTTGCTGTG TGAGTTGGGG CGGCCACGA TGGTCTGGCT 1680  
 TAGTGCCAAC CCTGTCTCTC ACTGTGGGGA CAGAACCTTC TATGACCCGG AGCCCATCCT 1740  
 5 GTGCCCTGT TTCATGCCTA ACTAGCTGGG TGCACATATC AAATGCTTCA TTCTGCATAC 1800  
 TTGGACACTA AAGCCAGGAT GTGCATGCAT CTTGAAGCAA CAAAGCAGCC ACAGTTTCAG 1860  
 ACAAAATGTC AGTGTGAGTG AGGAAAACAT GTTCAGTGAG GAAAAAACAT TCAGACAAAT 1920  
 GTTCAGTGAG GAAAAAAGG GGAAGTTGGG GATAGGCAGA TGTGTACTTG AGGAGTTAAT 1980  
 10 GTGATCTTTG GGGAGATACA TCTTATAGAG TTAGAAATAG AATCTGAATT TCTAAAGGGA 2040  
 GATTCTGGCT TGGGAAGTAC ATGTAGGAGT TAATCCCTGT GTAGACTGTT GTAAAGAAAC 2100  
 TGTGAAAAAT AAAGAGAAGC AATGTGAAGC AAAAAAAAAA AAAAAAAA

Seq ID NO: 30 Protein sequence:  
 Protein Accession #: NP\_006106.1

1 11 21 31 41 51  
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 GCTTCAGGGT ACAGCTCCCC CGCAGCCAGA AGCCGGGCTT GCAGCGCCTC AGCACCGCTC 60  
 CGGGACACCC CACCCGCTTC CCAGGCGTGA CCTGTCAACA GCAACTTCGC GGTGTGGTGA 120  
 20 ACTCTCTGAG GAAAAACCAT TTTGATTATT ACTCTCAGAC GTGCGTGGCA ACAAGTGAAT 180  
 GAGACCTAGA AATCCAAGCG TTGGAGGTCC TGAGGCCAGC CTAAGTCGCT TCAAAATGGA 240  
 ACCGAAGCGT GTGTGGGGTT CCATTTCAGAG CCGATACATC AGCATGAGTG TGTGGACAAG 300  
 CCCACGGAGA CTTGTGGAGG TGGCAGGGCA GAGCCTGCTG AAGGATGAGG CCCTGGCCAT 360  
 25 TGCCGCCCTG GAGTTGCTGC CCAGGGAGCT CTTCCCGCCA CTCTTCATGG CAGCCTTTGA 420  
 CGGGAGACAC AGCCAGACCC TGAAGGCAAT GGTGCAGGCC TGGCCCTTCA CTTGCCTCCC 480  
 TCTGGGAGTG CTGATGAAGG GACAACATCT TCACCTGGAG ACCTTCAAAG CTGTGCTTGA 540  
 TGGACTTGAT GTGCTCCTTG CCCAGGAGGT TCGCCCCAGG AGGTGGAAAC TTCAAGTGCT 600  
 GGATTTACGG AAGAACTCTC ATCAGGACTT CTGGACTGTA TGGTCTGGAA ACAGGGCCAG 660  
 30 TCTGTACTCA TTTCCAGAGC CAGAAGCAGC TCAGCCCATG ACAGAAGAGC GAAAAAGTAGA 720  
 TGGTTTGAGC ACAGAGGCGAG AGCAGCCCTT CATTCAGTA GAGGTGCTCG TAGACCTGTT 780  
 CCTCAAGGAA GGTGCCTGTG ATGAATTGTT CTCCTACCTC ATTGAGAAAG TGAAGCGAAA 840  
 GAAAAATGTA CTACGCTGTG GCTGTAAGAA GCTGAAGATT TTTGCAATGC CCATGCAGGA 900  
 TATCAAGATG ATCCTGAAAA TGGTGCAGCT GGACTCTATT GAAGATTGGA AAGTGACTTG 960  
 35 TACCTGGAAG CTACCCACCT TGGGGAATTT TTCTCCTTAC CTGGGCCAGA TGATTAATCT 1020  
 GCCTAGACTC CTCCTCTCCC ACATCCATGC ATCTTCCTAC ATTTCCCGG AGAAGGAAGA 1080  
 GCAGTATATC GCCCAGTTCA CCTCTCAGTT CCTCAGTCTG CAGTGCCTGC AGGCTCTCTA 1140  
 TGTGGACTCT TTAATTTTCC TTAGAGGCCG CTTGGATCAG TTGCTCAGGC ACGTGATGAA 1200  
 40 CCCCTTGGAA ACCCTCTCAA TAACCTAAGT CCGGCTTTCC GAAGGGGATG TGATGCATCT 1260  
 GTCCACAGAGT CCCAGCGCTA GTCAAGCTAAG TGTCTGAGT CTAAGTGGGG TCATGCTGAC 1320  
 CGATGTAAGT CCGAGAGCCC TCCAAGCTCT GCTGGAGAGA GCCTCTGCCA CCCTCCAGGA 1380  
 CCTGGTCTTT GATGAGTGTG GGATCACGGA TGATCAGCTC CTTGCCCTCC TGCTTCCCT 1440  
 GAGCCACTGC TCCCAGCTTA CAACCTTAAG CTTCTACGGG AATTCCATCT CCATATCTGC 1500  
 45 TCTGCAGAGT CCTCTGCAGC ACCTCATCGG GCTGAGCAAT CTGACCCACG TGTGTATCTC 1560  
 TGTCCCCCTG GAGAGTTATG AGGACATCCA TGGTACCCTC CACCTGGAGA GGCTTGCCTA 1620  
 TCTGCATGCC AGGCTCAGGG AGTTGCTGTG TGAGTTGGGG CGGCCACGA TGGTCTGGCT 1680  
 TAGTGCCAAC CCTGTCTCTC ACTGTGGGGA CAGAACCTTC TATGACCCGG AGCCCATCCT 1740  
 GTGCCCTGT TTCATGCCTA ACTAGCTGGG TGCACATATC AAATGCTTCA TTCTGCATAC 1800  
 50 TTGGACACTA AAGCCAGGAT GTGCATGCAT CTTGAAGCAA CAAAGCAGCC ACAGTTTCAG 1860  
 ACAAAATGTC AGTGTGAGTG AGGAAAACAT GTTCAGTGAG GAAAAAACAT TCAGACAAAT 1920  
 GTTCAGTGAG GAAAAAAGG GGAAGTTGGG GATAGGCAGA TGTGTACTTG AGGAGTTAAT 1980  
 GTGATCTTTG GGGAGATACA TCTTATAGAG TTAGAAATAG AATCTGAATT TCTAAAGGGA 2040  
 GATTCTGGCT TGGGAAGTAC ATGTAGGAGT TAATCCCTGT GTAGACTGTT GTAAAGAAAC 2100  
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Seq ID NO: 31 DNA sequence  
 Nucleic Acid Accession #: Eos sequence  
 Coding sequence: 64-2754

1 11 21 31 41 51  
 | | | | | |  
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 CCGATGCGCG CCGCTGGGCC CCGGCGCTCC GTGCGCGGAG CCGTCTGCCT GCATCTGCTG 120  
 65 CTGACCTCTG TGATCTTCAG TCGTGATGGT GAAGCCTGCA AAAAGGTGAT ACTTAATGTA 180  
 CCTTCTAAAC TAGAGGCAGA CAAATAAATT GGCAGAGTTA ATTTGGAAGA GTGCTTCAGG 240  
 TCTGCAGACC TCATCCGGTC AAGTGATCCT GATTTCAAG TTTCAATGA TGGGTCAAGT 300  
 TACACAGCCA GGGCTGTGTC GCTGTCTGAT AAGAAAAGAT CATTACCATT ATGGCTTTCT 360  
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 GAATCTGATG CAGCACAGAA CTATACCTGC TTCTACTCAA TAAGTGGACG TGGAGTTGAT 600  
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 CCTGTGGATC GTGAAGAAATA TGATGTTTTT GATTTGATTG CTTATGCGTC AACTGCAGAT 720  
 75 GGATATTTCAG CAGATCTGCG CCTCCCACTA CCCATCAGGG TAGAGGATGA AAATGACAAC 780  
 CACCTGTGTT TCAAGAGAGC AATTTATAAT TTTGAAAGTT TGGAAAGTAG TAGACCTGGT 840  
 ACTACAGTGG GGTGTGTTTG TGCCACAGAC AGAGATGAAC CGGACACAAT GCATACCGCG 900  
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 80 TCATTGTATA TGAAGATACA AGACATGGAT GGCCAGTTTT TTGGATTGAT AGGCACATCA 1080  
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 GTTCATGTGA GGGATCTGGA TGAGGGGCTT GAATGCACTC CTGCAGCCCA ATATGTGCGG 1500  
 ATTAAGAAAA ACTTAGCAGT GGGGTCAAAG ATCAACGCTT ATAGGCATA TGACCCCGAA 1560



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	CCCAAAAATG	AGTTGTATAA	TATTACAGTC	CTGGCAATAG	ACAAAAGATG	TAGATCATGT	1740
5	ACTGGAACAC	TTGCTGTGAA	CATTGAAGAT	GTAATGATA	ATCCACCAGA	AATACTTCAA	1800
	GAATATGTAG	TCATTTGCAA	ACCAAAAATG	GGGTATACCG	ACATTTTAGC	TGTTGATCCT	1860
	GATGAACCTG	TCCATGGAGC	TCCATTTTAT	TTGAGTTTGC	CCAATACTTC	TCCAGAAATC	1920
	AGTAGACTGT	GGAGCCTCAC	CAAAGTTAAT	GATACAGCTG	CCCGTCTTTC	ATATCAGAAA	1980
	AATGCTGGAT	TTCAAGATA	TACCATTCTT	ATTACTGTAA	AAGACAGGGC	CGGCCAAGCT	2040
10	GCAACAAAAT	TATTGAGAGT	TAATCTGTGT	GAATGTACTC	ATCCAACCTCA	GTGTCGTGCG	2100
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	ACCCTGGAGT	CTGCGAGGGG	AGGACACACG	GAGGTGGACA	ACTGCAGATA	CACCTTACTCG	2520
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	GAAGACCGCA	TGCCATCCCA	AGATTATGTC	CTCACTTATA	ACTATGAGGG	AAGAGGATCT	2640
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	TTCAATTTC	ACATGTATGT	ATATGATGAT	TTTTTTCTCA	ATTTTGAATT	ATGCTACTCA	2880
	CCATTTTATA	TTTTTAAAGC	CAGTTGTGTC	TTATCTTTTC	CAAAAAGTGA	AAAAATGTTAA	2940
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30	ACCAAATTCA	TTTGACTTTG	GAGGCAAAAT	GTGTTGAAGT	GCCCTATGAA	GTAGCAATTT	3300
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	ATTATAACTG	AGTCTATGAG	GAAATAGTTC	CTGTCCAATT	TGTGTAATTT	GTTTAAAAAT	3540
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	GCACCCCTGGG	GAGATTGATT	GTCCTTAAAC	CTAAGCCCCA	CAAACTTGAC	ACCTGATCAG	3960
	GTCTGGGAGC	TACAAAAATTT	CATTTTCTCT	CTCACTGCCC	TTCTCTGAG	TGGCATTTGGC	4020
	CTGAATCAAG	GAAAGCCAGG	CCTTGTGGGC	CCCCTTCTTT	CGGCTTTCTG	CTAAAGCAAC	4080
	ACCTCCAGCA	GAGATTCCTT	TAAGTGACTC	CAGGTTTTC	ACCATCCTTC	AGCGTGAATT	4140
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	CTTTTTCCTA	GGCTTGGCAC	TGCCCTTTTC	TTTCTCAGGC	CAATGGCAAC	TGCCATTGTA	4440
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	AAGGAGACAG	AGCTGACTGC	ATGATGAGTC	TGAAGGCATT	TGCAGGATGA	GCCTGAACTG	4560
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	GCTCCGATCT	CTGCTCACTG	AAAGCTCCGC	CTCCCGGTTT	CATGCCATTG	TCCTGCCTCA	4860
	GCCTCCTGAG	TAGCTGGGAC	TACAGGCGCC	CACCACCACG	CCCGGCTAAT	TTTTTTGTATT	4920
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	ATCCGCGCTG	CTCGGCCCTC	CAAAGTGCTG	GGATTACAGG	CATGACCCAC	CGCTCCCGGC	5040
60	CTTGTTTTCC	GTTTAAAGTC	GTCTTCTTTT	AATGTAATCA	TTTTGAACAT	GTGTGAAAGT	5100
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	ACTGTGTTTT	GCTCACTCCC	TCACCTACCG	ATCAAAACCT	GCTACCTCCC	CAAGACTTTA	5340
65	CTAGTGCCGA	TAAACTTTCT	CAAAGAGCAA	CCAGTATCAC	TTCCCTGTTT	ATAAAACTTC	5400
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	CATATGTAGT	ATTATTATTT	CCTTATATGT	GTAAGGTGAA	ATTTATGGTA	TTTGAGTGTG	5580
	CAAGAAAATA	TATTTTTTAA	GCTTTTATTT	TTCCCCAGT	GAATGATTTA	GAATTTTTTA	5640
70	TGTAAATATA	CAGATGTTTT	TTTCTTACTT	TTATAAGGAA	GCAGCTGTCT	AAAAATGCAGT	5700
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	TGCTTTTAAA	GAAACTTTGG	TGCTTAAAT	AAGCAAAAAT	TGGATGCATA	AAGTAATATT	5820
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	ATTAAAGATA	TTTCAAGGTG	GTTTATAATTG	CAGAGTATTC	CATGAATAGT	ACACTGACAC	6180
	AGGGGTTTTA	CTTTGAGGAC	CAGTGTAGTC	AAGGGAAAAC	ATGAGTTAAA	AAGAAAAGCA	6240
80	GGCAATATTG	CAGTCTTGAT	TCTGCCACTT	ACAGGATAGA	TAATGCCCTGA	ACCTTAAATGA	6300
	CAAGATGATC	CAACCATAAA	GGTGCTCTGT	GCTTCACAGT	GAATCTTTTC	CCCTATGCAGG	6360
	AGTGTGCTCC	CCTACAAACG	TTAAGACTGA	TCATTTCAAA	AATCTATTAG	CTATATCAAA	6420
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	CATTATTTTT	GATATTGTCT	TCAAGATGTT	TCATTGGATT	TTTGTTTGTA	ATAGTAAAT	6540
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	TTCTGTGTGA	CCTTTGAAAG	GCTACTTATT	TCCTCTCTTA	GCTTTCTCAT	TAAATCAAT	6720
	GAACAATGCC	AGCCTCATGG	GGTTGTTGAA	TGATTAAATT	AGTTAATATA	CCTAAAGTAC	6780



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5

Seq ID NO: 32 Protein sequence:  
 Protein Accession #: NP\_001932.1

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KTRHTRETVL	RRAKRRWAPI	PCSMQENSLG	PFPLFLQOVE	SDAAQNYTVF	YSISGRGVDK	180
EPLNLFYIER	DTGNLFCTRP	VDREEDVDFD	LIAYASTADG	YSADLPLPLP	IRVEDENDNH	240
PVFTAIYNF	EVLESSRPGT	TVGVVCATDR	DEPDTMHTRL	KYSILQQTFR	SPGLFSVHPS	300
TGVITTVSHY	LDREIVVDKYS	LIMKVDMDG	QFFGLIGTST	CIITVTDSDN	NAPTFRQNAV	360
EAFVEENAFN	VEILRIPIED	KDLINTANWR	VNFTILKGNE	NGHFKISTDK	ETNEGVLSV	420
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KENLAVGSKI	NGYKAYDPEN	RNGNGLRYKK	LHDPKGWITI	DEISGSIITS	KILDREVETP	540
KNELYNITVL	AIDKDDRSCT	GTLAVNIEDV	NDNPPEILQE	YVVICPKMG	YTDILAVDPD	600
EPVHGAPFYF	SLPNTSPSIS	RLWSLTKVND	TAARLSYQKN	AGFQEYTIPI	TVKDRAGQAA	660
TKLLRVNLCE	CTHTPTQCRAT	SRSTGVILGK	WAILAILLGI	ALLFSVLLTL	VCGVFGATKG	720
KRFPEDLAQ	NLIISNTPEAP	GDDRVCSANG	FMTQTTNNSS	QGFCTMGSG	MKNGGQETIE	780
MMKGGNQTL	SCRAGHHHT	LDSCRGGHTE	VDNCRYTYSE	WHSFTQPRLG	EKLHRCNQNE	840
DRMPSQDVL	TYNVEGRGSP	AGSVGCCSEK	QEEDGLDFLN	NLEPKFITLA	EACTKR	

25

Seq ID NO: 33 DNA sequence  
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 Coding sequence: 64-2583

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 TCAATCTTGA TATGCTCAAC CAAAGACAG TCGAGAAGCC AGGGGGAGAA AGAAGCTCAG 5220  
 GCACAAAATA TTGCTCTGAG AATGGAATTC TCTGTAAGCC TAGTTGCTGA AATTTCTGTC 5280  
 35 TGTAACAGCA AGCCAGTTT ATCTAACGGC TACTGAAACA CCCACTGTGT TTTGCTCACT 5340  
 CCCACTCACC GATCAAAACC TGCTACCTCC CCAAGACTTT ACTAGTGCCG ATAAACTTTT 5400  
 TCAAGAGACA ACCAGTATCA CTTCCCTGTT TATAAAACCT CTAACCATCT CTTTGTTCCT 5460  
 TGAACATGCT GAAAACCAAC TGGTCTGCAT GTATGCCGA ATTTGTAATT CTTTCTCTC 5520  
 AAATGAAAT TTAATTTTAG GGATTCATT CTATATTTTC ACATATGTAG TATTATTATT 5580  
 40 TCCTTATATG TGTAAAGTGA AATTTATGGT ATTTGAGTGT GCAAGAAAAT ATATTTTAA 5640  
 AGCTTTCATT TTTCCCCAG TGAATGATTT AGAATTTTTT ATGTAAATAT ACAGAAATGT 5700  
 TTTTCTTACT TTTATAAGGA AGCAGCTGTC TAAATGCAG TGGGGTTTGT TTTGCAATGT 5760  
 TTTAAACAGA GTTTTAGTAT TGCTATTAAA AGAAGTTACT TTGCTTTTAA AGAAACTTGG 5820  
 CTGCTTAAAA TAAGCAAAAA TTGGATGCAT AAAGTAATAT TTACAGATGT GGGGAGATGT 5880  
 45 AATAAAACAA TATTAACCTG GCTGCTTAAA ATAAGCAAAA ATTGGATGCA TAAAGTAATA 5940  
 TTTACAGATG TGGGAGATG TAATAAACA ATATTAACCT GGTTCCTGT TTTTGTGTA 6000  
 TTTAGAGATT AAATAATTCT AAGATGATCA CTTTGCAAAA TTAGCTTAT GGCCTGGCATG 6060  
 GAAATAGAAA TACTCAATTA TGTCTTTGTT GTATTAAATG GGAATATTTT GGACAATGTT 6120  
 TCATATCAAA ATTTGTCACA TCATTAAATAT ATATTGTAAT GTTGGGAAGA GATCACTATT 6180  
 50 TTGAAGCACA GCTTTACAGA TGAGTATCTA TGATACATAT GTATAATAAA TTTTGTATCGG 6240  
 GTATTAAAAA TATTAGAAGG TGGTTATAAT TGCAGAGTAT TCCATGAATA GTACACTGAC 6300  
 ACAGGGGTTT TACTTTGAGG ACCAGTGTAG TCAAGGGAAA ACATGAGTTA AAAAGAAAAA 6360  
 CAGGCAATAT TGCACTCTTG ATCTGCCAC TTAAGGATA GATAATGCCT GAACCTTAAAT 6420  
 GACAAAGATG TGCACACATA AAGGTGCTCT GTGCTTACA GTGAATCTTT TCCCATGCA 6480  
 55 GGAGTGTGCT CCCCTACAAA CGTTAAGACT GATCATTTCA AAAATCTATT AGCTATATCA 6540  
 AAAGCCTTAC ATTTTAAATAT AGGTTGAACC AAAATTTCAA TTCCAGTAAC TTCTATTGTA 6600  
 ACCATTATTT TTTGCTATGT CTTCAAGAA GTTCATTGGA TTTTGTGTTG TAATAGTAAA 6660  
 ATACCGGATA CATTTACAGT GTCCTTCAGT ATTTGATTGG TTGAATATTG GGTCTAATG 6720  
 GTTGAGAAGC ATGGACACTA GAGCCAGAAT GCTTGGATAT GAATCCTGGA TCTGTCACTT 6780  
 60 ACTTCTGTGT GACCTTTGAA AGGCTACTTA TTTCTCTCT TAGCTTTCTC ATTAATAATCA 6840  
 ATGAACAATG CCAGCCTCAT GGGGTTGTTG AATGATTAAT TTAGTTAATA TACCTAAAGT 6900  
 ACATAGAACA CTGCTGCAC ATAGTAAAAG AATTATAAGT GTGAGGTAGT TGGTAAAAAT 6960  
 ATGTAGTTGG ATATACTACC GAACAATATC TAATCTCTTT TTAGGGAAAT AAAGTTTGTG 7020  
 CATATATATA ATCCCGAACC ATG

Seq ID NO: 34 Protein sequence:  
 Protein Accession #: NP\_077741.1

1 11 21 31 41 51  
 | | | | |  
 70 MAAAGPRRSV RGAVCLHLLL TLVIFSRDGE ACKKVILNVP SKLEADKIIG RVNLEECFRS 60  
 ADLIRSSDPD FRVLNDGSVY TARAVASDK KRSFTINLSD KRKQTQKEVT VLEHQKKVS 120  
 KTRHRTRETVL RRAKRRWAPI PCSMQENSLG PFPLFLQQVE SDAAQNYTVF YSISGRGVDK 180  
 EPLNLFYIER DTGNLFCTRP VDREYDVFD LIAYASTADG YSADLPLPLP IRVEDENDNH 240  
 75 PVFTEAIYNF EVLESSRPGT TVGVVCAADR DEPDTHMTRL KYSILQTPR SPGLFSVHPS 300  
 TGVITTVSHY LDREVVDKYS LIMKVQMDG QFFGLIGTST CIITVTDSND NAPTFRQNAV 360  
 EAFVEENAFN VEILRIPIED KDLINTANWR VNFILKGNE NGHFKISTDK ETNEGVLSSV 420  
 KPLNYEENRQ VNLEIGWNE PFARDIPRV TALNRALVTV HVRDLDEGPE CTPAAQVRI 480  
 KENLAVGSKI NGYKAYDPEN RNNGRLRYKK LHDPKGWITI DEISGSIITS KILDREVETP 540  
 80 KNELYNITVL AIDKDDRSCT GTLAVNIEDV NDNPPFELQE YVICKPKMG YTDILAVDPD 600  
 BPVHGAPFYF SLPNTSPFIS RLWSLTQVND TAARLSYQKN AGFQYETIPI TVKDRAGQAA 660  
 TKLRLVNLCE CTHPTQCRAT SRSTGVILGK WAILAILLGI ALLFSVLLTL VCGVFGATKG 720  
 KRFPEDLAQQ NLIISNTEAP GDDRVCSSANG FMTQTNNSS QGFCGTMGSG MKNGGQETIE 780  
 MMKGNGQTLN SCRGAGHHT LDCRGGHTE VDNCRYTYSE WHSFTQPRLG EESIRGHTG

Seq ID NO: 35 DNA sequence  
 Nucleic Acid Accession #: Eos sequence  
 Coding sequence: 146-1273.



	1	11	21	31	41	51	
5	GGGAGTGGGC	GTGGCGGTGC	TGCCCAGGTG	AGCCACCGCT	GCTTCTGCCC	AGACACGGTC	60
	GCCTCCACAT	CCAGGTCTTT	GTGCTCCTCG	CTTGCTGTGT	CCTTTTCCAC	GCATTTTCCA	120
	GGATAACTGT	GACTCCAGGC	CCGCAATGGA	TGCCCTGCAA	CTAGCAAATT	CGGCTTTTGC	180
	CGTTGATCTG	TTCAAACAAC	TATGTGAAAA	GGAGCCACTG	GGCAATGTCC	TCTTCTCTCC	240
	AATCTGTCTC	TCCACCTCTC	TGTCACTTGC	TCAAGTGGGT	GCTAAAGGTG	ACACTGCAAA	300
10	TGAAATTGGA	CAGGTTCTTC	ATTTTGAAAA	TGTCAAAGAT	ATACCCCTTG	GATTTCAAAC	360
	AGTAACATCG	GATGTAACA	AACTTAGTTC	CTTTTACTCA	CTGAAACTAA	TCAAGCGGCT	420
	CTACGTAGAC	AAATCTCTGA	ATCTTCTAC	AGAGTTCATC	AGCTCTACGA	AGAGACCCTA	480
	TGCAAAGGAA	TTGAAACTG	TTGACTTCAA	AGATAAATG	GAAAGAACGA	AAGGTCAGAT	540
	CAACAACCTCA	ATTAAGGATC	TCACAGATGG	CCACTTTGAG	AACATTTTAG	CTGACAAACAG	600
15	TGTGAACGAC	CAGACCAAAA	TCCTTGTGGT	TAATGCTGCC	TACTTTGTGT	GCAAGTGGAT	660
	GAAGAAATTT	CCTGAATCAG	AAACAAAAGA	ATGTCCTTTC	AGACTCAACA	AGACAGACAC	720
	CAAACCCAGT	CAGATGATGA	ACATGGAGGC	CACGTTCTGT	ATGGGAAACA	TTGACAGTAT	780
	CAATTGTAAG	ATCATAGAGC	TTCTTTTCA	AAATAAGCAT	CTCAGCATGT	TCATCCTACT	840
	ACCCAAGGAT	GTGGAGGATG	AGTCCACAGG	CTTGGAGAAG	ATTGAAAAAC	AACTCAACTC	900
20	AGAGTCACTG	TCACAGTGGG	CTAATCCCAG	CACCATGGCC	AATGCCAAGG	TCAAACCTCT	960
	CATTCCAAAA	TTTAAGGTGG	AAAAGATGAT	TGATCCCAAG	GCTTGTCTGG	AAAATCTAGG	1020
	GCTGAAACAT	ATCTTCACTG	AAGACACATC	TGATTTCTCT	GGAATGTCTG	AGACCAAGGG	1080
	AGTGGCCCTA	TCAAATGTGA	TCCACAAAGT	GTGCTTAGAA	ATAACTGAAG	ATGCTGGGGA	1140
	TTCCATAGAG	GTGGCAGAGG	CACGGATCCT	GCAGCACAA	GATGAATTGA	ATGCTGACCA	1200
25	TTCCCTTTATT	TACATCATCA	GGCACAAACA	AACTCGAAAC	ATCATTTTCT	TTGGCAAATT	1260
	CTGTTCTCCT	TAAGTGGCAT	AGCCCATGTT	AAGTCTCTCC	TGACTTTTCT	GTGGATGCCG	1320
	ATTTCTGTAA	ACTCTGCATC	CAGAGATTCA	TTTTCTAGAT	ACAATAAATT	GCTAATGTTG	1380
	CTGGATCAGG	AAGCCGCCAG	TACTGTCTAT	ATGTAGCCTT	CACACAGATA	GACCTTTTTT	1440
	TTTTTCCAAT	TCTATCTTTT	GTTCCTTTT	TTCCCATAG	ACAATGACAT	ACGCTTTTAA	1500
30	TGAAAGGAA	TCACGTTAGA	GGAAAAATAT	TTATTCATTA	TTTGTCAAAT	TGTCGGGGT	1560
	AGTTGGCAGA	AATACAGTCT	TCCACAAAGA	AAATTCCTAT	AAGGAAGATT	TGGAAGCTCT	1620
	TCTTCCCAGC	ACTATGCTTT	CCTTCTTTGG	GATAGAGAAT	GTTCCAGACA	TTCTCGCTTC	1680
	CCTGAAAGAC	TGAAGAAAGT	GTAGTGCATG	GGACCCACGA	AACTGCCCTG	GCTCCAGTGA	1740
	AACTTGGGCA	CATGCTCAGG	CTACTATAGG	TCCAGAAATC	CTTATGTTAA	GCCCTGGCAG	1800
35	GCAGGTGTTT	ATTAATAATC	TGAATTTTGG	GGATTTTCAA	AAGATAATAT	TTTACATACA	1860
	CTGTATGTTA	TAGAACTTCA	TGGATCAGAT	CTGGGGCAGC	AACCTATAAA	TCAACACCTT	1920
	AATATGCTGC	AACAAAATGT	AGAATATTCA	GACAAAATGG	ATACATAAAG	ACTAAGTAGC	1980
	CCATAAGGGG	TCAAAATTTG	CTGCCAAATG	CGTATGCCAC	CAACTTACAA	AAACACTTCG	2040
	TTCCGACAGC	TTTTCAGATT	GTGGAATGTT	GGATAAGGAA	TTATAGACCT	CTAGTAGCTG	2100
40	AAATGCAAGA	CCCCAAGAGG	AAGTTCAGAT	CTTAATATAA	ATTCACCTTC	ATTTTGTGATA	2160
	GCTGTCCCAT	CTGCTCATGT	GGTTGGCACT	AGACTGGTGG	CAGGGGCTTC	TAGCTGACTC	2220
	GCACAGGGAT	TCTCACAAAT	GCCGATATCA	GAATTTGTGT	TGAAGGAACT	TGTCTCTTCA	2280
	TCTAATATGA	TAGCGGGAAA	AGGAGAGGAA	ACTACTGCCT	TTAGAAAAAT	TAAGTAAAGT	2340
	GATTAAAGTG	CTCACGTTAC	CTTGACACAT	AGTTTTTCAG	TCTATGGGTT	TAGTTACTTT	2400
45	AGATTGGCAG	CATGTAACCT	ATATTAAATG	TAATTTGTAA	AGTTGGGTGG	ATAAGCTATC	2460
	CCTGTTGCCG	GTTTCATGGAT	TACTTCTCTA	TAAAAAATAT	ATATTACCA	AAAAATTTTG	2520
	TGACATTCTC	TCTCCATCT	CTTCTTGAC	ATGCATTGTA	AATAGGTTCT	TCTTGTCTCG	2580
	AGATTCAATA	TTGAATTCT	CCTATGCTAT	TGACAATAAA	ATATTATTGA	ACTACC	

Seq ID NO: 36 Protein sequence:  
Protein Accession #: NP\_002630.1

	1	11	21	31	41	51	
55	MDALQLANSA	FAVDLFKQLC	EKEPLGNVLF	SPICLSTSL	LAQVGAKGDT	ANEIGQVLHF	60
	ENVKDIPFGF	QTVTSDVNKL	SSFYSLKLIK	RLYVDKSLNL	STEFISSTKR	PYAKELETVD	120
	FKDKLEETKG	QINNSIKDLT	DGHFENILAD	NSVNDQTKIL	VVNAAYFVGK	WMKKFPSEST	180
	KECPFRLNKT	DTKPVQMMNM	EATFCMGNID	SINCKIIELP	FQNKHLSMFI	LLPKDVEDES	240
	TGLEKIEKQL	NSESLSQWTN	PSTMANAKVK	LSIPKFKVEK	MIDPKACLEN	LGLKHIFSED	300
60	TSDFSGMSET	KGVALSNVIH	KVCLEITEDG	GDSEVPGAR	ILQHKDELNA	DHPFIYIIRH	360
	NKTRNIIFFG	KFCSP					

Seq ID NO: 37 DNA sequence  
Nucleic Acid Accession #: NM\_0168583  
Coding sequence: 72-842

	1	11	21	31	41	51	
70	GGAGTGGGGG	AGAGAGAGGA	GACCAGGACA	GCTGCTGAGA	CCTCTAAGAA	GTCCAGATAC	60
	TAAGAGCAAA	GATGTTTCAA	ACTGGGGGCC	TCATTGTCTT	CTACGGGCTG	TTAGCCCAAG	120
	CCATGGCCCA	GTTTGGAGGC	CTGCCCGTGC	CCCTGGACCA	GACCTGCCCC	TTGAATGTGA	180
	ATCCAGCCCT	GCCCTTGAGT	CCCACAGGTC	TTGCAGGAAG	CTTGACAAAT	GCCCTCAGCA	240
	ATGGCCTGCT	GTCGTGGGGC	CTGTTGGGCA	TTCTGGAAAA	CCTTCCGCTC	CTGGACATCC	300
75	TGAAGCCTGG	AGGAGGTACT	TCTGGTGGCC	TCCTTGGGGG	ACTGCTTGGG	AAAGTGACGT	360
	CAGTGATTCC	TGGCCTGAAC	AACATCATTG	ACATAAAGGT	CACCTGACCC	CAGCTGCTGG	420
	AACTTGGCCT	TGTGCAGAGG	CCTGATGGCC	ACCGTCTCTA	TGTCAACATC	CCTCTCGGCA	480
	TAAAGCTCCA	AGTGAATACG	CCCCTGGTCG	GTGCAAGTCT	GTTGAGGCTG	GCTGTGAAGC	540
	TGGACATCAC	TGCAGAAATC	TTAGCTGTGA	GAGATAAGCA	GGAGAGGATC	CACCTGGTCC	600
	TTGGTGACCT	CACCCATTCC	CCTGGAAGCC	TGCAAAATTC	TCTGCTTGAT	GGACTTGGCC	660
80	CCCTCCCAT	TCAAGGCTCT	CTGGACAGCC	TCACAGGGAT	CTTGAATAAA	GTCCTGCGCTG	720
	AGTTGGTTCA	GGGCAACGTG	TGCCCTCTGG	TCAATGAGGT	TCTCAGAGGC	TTGGACATCA	780
	CCCTGGTGCA	TGACATTGTT	AACATGCTGA	TCCACGSACT	ACAGTTTGTG	ATCAAGGTCT	840
	AAGCCTTCCA	GGAAGGGGCT	GGCCTCTGCT	GAGCTGCTTC	CCAGTGCTCA	CAGATGGCTG	900
	GCCCATGTGC	TGGAAGATGA	CACAGTTGCC	TTCTCTCCGA	GGAACCTGCC	CCCTCTCTCT	960
85	TCCACCCAGG	CGTGTGTAAC	ATCCCATGTG	CCTCACCTAA	TAAATGCGCT	CTTCTTCTGC	1020
	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA				



Seq ID NO: 38 Protein sequence:  
Protein Accession #: NP\_057667

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5      1      11      21      31      41      51
      |      |      |      |      |      |
      MFQTGGGLIVF YGLLAQTMQAQ FGGLEFVPLDQ TLPLNVNPNAL PLSPTGLAGS LTNALSNGLL 60
      SGGLLGILEN LPLLDILKPG GGTSGGLLGG LLGKVTSVIP GLNNIIDIKV TDPQLLELGL 120
      VQSPDGHRLY VTIPLGKILQ VNTPLVGASL LRLAVKLDIT AEILAVRDKQ ERIHLVLGDC 180
10     THSPGSLQIS LLDGLGLPLPI QGLLDSLTGI LNKVLPELVQ GNVCPVNEV LRGLDITLVH 240
      DIVNMLIHGL QFVIVK

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Seq ID NO: 39 DNA sequence  
Nucleic Acid Accession #: NM\_004363.1  
Coding sequence: 115-2223

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15     1      11      21      31      41      51
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      CTCAGGGCAG AGGGAGGAAG GACAGCAGAC CAGACAGTCA CAGCAGCCTT GACAAAACGT 60
      TCCTGGAAGT CAAGCTCTTC TCCACAGAGG AGGACAGAGC AGACAGCAGA GACCATGGAG 120
      TCTCCCTCGG CCCCTCCCCA CAGATGGTGC ATCCCTGGC AGAGGCTCCT GCTCACAGCC 180
      TCACCTCTAA CCTTCTGGAA CCCGCCACCC ACTGCCAAGC TCACTATTGA ATCCACGCCG 240
      TTCAATGTCG CAGAGGGGAA GGAGGTGCTT CTACTTGTC ACAAATCTGCC CCAGCATCTT 300
      TTTGGCTACA GCTGGTACAA AGGTGAAAGA GTGGATGGCA ACCGTCAAAT TATAGGATAT 360
25     GTAATAGGAA CTCAACAAGC TACCCAGGG CCCGCATACA GTGGTCGAGA GATAATATAC 420
      CCCAATGCAT CCCTGCTGAT CCAGAATATC ATCCAGAATG ACACAGGATT CTACACCCTA 480
      CACCTCATATA AGTCAGATCT TGTGAATGAA GAAGCAACTG GCCAGTTCCG GGTATACCCG 540
      GAGCTGCCCA AGCCCTCCAT CTCCAGCAAC AACTCCAAAC CCGTGGAGGA CAAGGATGCT 600
      GTGGCCTTCA CCTGTGAACC TGAGACTCAG GACGCAACCT ACCTGTGGTG GGTAAACAAT 660
30     CAGAGCCTCC CGGTGAGTCC CAGGCTGCAG CTGTCCAATG GCAACAGGAC CCTCACTCTA 720
      TTCAATGTCA CAAGAAATGA CACAGCAAGC TACAAATGTG AAACCCAGAA CCCAGTGAGT 780
      GCCAGGCCGA GTGATTCAGT CATCCTGAAT GTCCTCTATG GCCCGGATGC CCCCAACATT 840
      TCCCTCTAA ACACATCTTA CAGATCAGGG GAAATCTGA ACCTCTCCTG CCACGCAGCC 900
      TCTAACCCAC CTGCACAGTA CTCTTGGTTT GTCAATGGGA CTTTCCAGCA ATCCACCCAA 960
35     GAGCTCTTTA TCCCAACAT CACTGTGAAT AATAGTGGAT CCTATACGTG CCAAGCCCAT 1020
      AACTCAGACA CTGGCCTCAA TAGACCACA GTCCAGCAGA TCACAGTCTA TGCAGAGCCA 1080
      CCCAAACCTT TCATCACCAG CAACAACCTC AACCCGTGG AGGATGAGGA TGCTGTAGCC 1140
      TTAACCTGTG AACCTGAGAT TCAGAAACACA ACCTACCTGT GGTGGGTAAA TAATCAGAGC 1200
      CTCCCGGTCA GTCCCAAGCT GCAGCTGTCC AATGACAAAC GGACCCCTAC TCTACTCAGT 1260
40     GTCACAAGGA ATGATGTAGG ACCCTATGAG TGTGGAATCC AGAACGAATT AAGTGTGAC 1320
      CACAGCGACC CAGTCATCCT GAATGTCCTC TATGGCCAG ACGACCCAC CATTTCCCCC 1380
      TCATACACCT ATTACCGTTC AGGGGTGAAC CTCAGCCTCT CCTGCCATGC AGCCTCTAAC 1440
      CCACCTGCAC AGTATTCTTG GCTGATTGAT GGGAAACATC AGCAACACAC ACAAGAGCTC 1500
      TTTATCTCCA ACATCACTGA GAAGAACAGC GGACTCTATA CCTGCCAGGC CAATAACTCA 1560
45     GCCAGTGGCC ACAGCAGGAC TACAGTCAAG ACAATCACAG TCTCTGCGGA GCTGCCCAAG 1620
      CCCTCCATCT CCAGCAACAA CTCCAAACCC GTGGAGGACA AGGATGCTGT GGCCTTCACC 1680
      TGTGAACCTG AGGCTCAGAA CACAACCTAC CTGTGGTGGG TAAATGGTCA GAGCCTCCCA 1740
      GTCAGTCCCA GGTGTCAGCT GTCCAATGGC AACAGGACCC TCACTCTATT CAATGTACAC 1800
50     AGAAATGACG CAAGAGCCTA TGTATGTGGA ATCCAGAACT CAGTGAGTGC AAACCGCAGT 1860
      GACCCAGTCA CCCTGGATGT CCTCTATGGG CCGGACACCC CCATCATTTT CCCCCAGAC 1920
      TCGTCTTACC TTTCCGGGAG GAACCTCAAC CTCTCTGCCC ACTCGGCCCTC TAACCCATCC 1980
      CCGCAGTATT CTGGGCGTAT CAATGGGATA CCGCAGCAAC ACACACAAGT TCTCTTTATC 2040
      GCCAAATACA CGCCAAATAA TAACGGGACC TATGCCTGTT TTGTCTCTAA CTTGGCTACT 2100
55     GGCCGCAATA ATTCCATAGT CAAGAGCATC ACAGTCTCTG CATCTGGAAC TTCTCCTGGT 2160
      CTCTCAGCTG GGGCCACTGT CGGCATCATG ATTGGAGTGC TGGTTGGGGT TGCTCTGATA 2220
      TAGCAGCCCT GGTGTAGTTT CTTCAATTTA GGAAGACTGA CAGTTGTTTT GCTTCTTCTT 2280
      TAAAGCATTT GCAACAGCTA CAGTCTAAAA TTGCTTCTTT ACCAAGGATA TTTACAGAAA 2340
      AGACTCTGAC CAGAGATCGA GACCATCCTA GCCAATATCG TGAAACCCCA TCTCTACTAA 2400
60     AAAATACAAA ATGAGCTGGG CTTGGTGGCG GCACCTGTGA GTCCCAAGTTA CTCGGGAGGC 2460
      TGAGGCAGGA GAATCGCTTG AACCCGGGAG GTGGAGATTG CAGTGAGCCC AGATCGCACC 2520
      ACTGCACCTC AGTCTGGCAA CAGACAAAGA CTCATCTCA AAAAGAAAAG AAAAGAAGAC 2580
      TCTGACCTGT ACTCTGAAT ACAAGTTTCT GATACCACCTG CACTGTCTGA GAATTTCCAA 2640
      AACTTTAATG AACTAACTGA CAGCTTCTAT AAATGTGTCA CCAAGATCAA GCAGAGAAAA 2700
      TAATTAATTT CATGGGACTA AATGAACTAA TGAGGATTGC TGATTCTTTA AATGTCTTGT 2760
65     TTCCAGATT TCAGGAAACT TTTTCTCTTT TAAGCTATCC ACTCTACAG CAATTTGATA 2820
      AAATATACTT TTGTGAACAA AAATTGAGAC ATTTACATTT TCTCCCTATG TGGTCGCTCC 2880
      AGACTTGGGA AACTATTTCAT GAATATTATG ATTGTATGGT AATATAGTTA TTGCACAAAGT 2940
      TCAATAAAAA TCTGCTCTTT GTATAACAGA AAAA

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Seq ID NO: 40 Protein sequence:  
Protein Accession #: NP\_004354.1

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70     1      11      21      31      41      51
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      MESPSAPPHR WCIWQRLLL TASLLTFWNP PTTAKLTIES TPFNVAEGKE VLLLHVHNLPO 60
      HLFEGYSWKYK ERVDGNRQII GYVIGTQAT PGPAYSGREI IYPNASLLIQ NIIQNDTGFY 120
      TLHVIKSLDV NEEATGQFRV YPELPKPSIS SNNKPFVEDK DAVAFTCEPE TQDATYLVWV 180
      NNQSLFVSPR LQLSNGNRTL TLFNVTRNDT ASYKCBETQNF VSARRSDSVI LNVLYGPDAP 240
      TISPLNTSYR SGENLNLSCH AASNPPAQYS WFNVTGTFQQS TQELFIPNIT VNNSGSYTCQ 300
      AHNSTGLNR TTVTITIVYA EPPKPFITSN NSNPVEDEDA VALTCEPEIQ NTTYLWVWNN 360
      QSLFVSPRLQ LSNDRNLTLL LSVTRNDVGP YECGIONELS VDHSDPVILN VLYGPDPTI 420
      SPSYTYRPG VNLSSLCHAA SNPPAQYSWL IDGNIQHTQ ELFISNITEK NSGLYTCQAN 480
      NSASGHSRTT VKTITVSAEL PKPSISSNNS KPVEDKDAVA FTCEPEAQNT TYLWVWNGQS 540
      LPVSPRLQLS NGNRTLTLFN VTRNDARAYV CGIQNSVSAN RSDPVTLVDL YGPDPTIISP 600
85     PDSSYLSGAN LNLSCSASGN PSPQYSWRIN GIPQOHTQVL FIAKITPNNN GTYACFVSNL 660
      ATGRNNSIVK SITVSASGTS PGLSAGATVG IMIGVLVGVA LI

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Seq ID NO: 41 DNA sequence  
Nucleic Acid Accession #: NM\_006952.1  
Coding sequence: 11-793

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1      11      21      31      41      51
|      |      |      |      |      |
AATCCCGACA ATGGCGAAAG ACAACTCAAC TGTTCTGTGC TTCCAGGGCC TGCTGATTTT 60
TGGAAATGTG ATTATTGGTT GTTTCGGCAT TGCCCTGACT GCGAGATGCA TCTTCTTTGT 120
ATCTGACCAA CACAGCCTCT ACCCACTGCT TGAAGCCACC GACAACGATG ACATCTATGG 180
GGCTGCCTGG ATCGGCATAT TTGTGGGCAT CTGCCTCTTC TGCCTGTCTG TTCTAGGCAT 240
TGTAGGCATC ATGAAGTCCA GCAGGAAAAT TCTTCTGGCG TATTTTCATC TGATGTTTAT 300
AGTATATGCC TTTGAAGTGG CATCTTGAT CACAGCAGCA ACACAACGAG ACTTTTTCAC 360
ACCCAACCTC TTCTGAAGC AGATGCTAGA GAGGTACCAA AACACAGGCC CTCCAAACAA 420
TGATGACCAG TGGAAAAACA ATGGAGTCAC CAAAACCTGG GACAGGCTCA TGCTCCAGGA 480
CAATTGCTGT GCGCTAAATG GTCCATCAGA CTGGCAAAAA TACACATCTG CCTTCCGGAC 540
TGAGAATAAT GATGCTGACT ATCCCTGGCC TCGTCAATGC TGTGTTATGA ACAATCTTAA 600
AGAACCCTCT AACCTGGAGG CTGTGAAACT AGGCGTGCCT GGTTTTATAT ACAATCAGGG 660
CTGCTATGAA CTGATCTCTG GTCCAATGAA CCGACACGCC TGGGGGGTTG CCTGGTTTGG 720
ATTTGCCATT CTCTGCTGGA CTTTTTGGGT TCTCTGGGT ACCATGTTCT ACTGGAGCAG 780
AATTGAATAT TAAGAA

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Seq ID NO: 42 Protein sequence:  
Protein Accession #: NP\_008883.1

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1      11      21      31      41      51
|      |      |      |      |      |
MAKDNSTVRC FQGLLIFGNV IIGCCGIALT AECIFFVSDQ HSLYPLLEAT DNDDIYGAAW 60
IGIFVIGICLF CLSVLGI VGI MKSSRKILLA YFILMFIVYA FEVASCITAA TQRDFFTPNL 120
FLKQMLERYQ NNSPPNDDQ WKNNGVTKTW DRLMLQDNCC GVNGPSDWQK YTSAFRTENN 180
DADYFWPRQC CVMNNLKEPL NLEACKLGVP GFYHNQGCYE LISGPMNRHA WGVAVFGFAI 240
LCWTFWVLLG TMFYWSRIEY

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Seq ID NO: 43 DNA sequence  
Nucleic Acid Accession #: Eos sequence  
Coding sequence: 83-2605

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1      11      21      31      41      51
|      |      |      |      |      |
GCCCGACAGA TCTGCGCGTA TCCTGGAGCC GGCCCAAGTTG TGAAGTAGGA GAGCTTTGGG 60
ACCTCTGTCC CAAGCAAGAG AGATGAATGG AGAGTATAGA GGCAGAGGAT TTGGACGAGG 120
AAGATTTCAA AGCTTGGAAA GGGGAAGAGG TGGTGGGAAC TTCTCAGGAA AATGGAGAGA 180
AAGAGAACAC AGACCTGATC TGAGTAAAC CACAGGAAAA CGTACTTCTG AACAAACCCC 240
ACAGTTTTTG CTTTCAACAA AGACCCACA GTCAATGCAG TCAACATGG ATCGATTCA 300
ACCATATAAA GGCTGGAAGC TTTATTTCTC TGAAGTTTAC AGCGATAGCT CTCCTTTGAT 360
TGAGAAGATT CAAGCATTTG AAAAATTTT CACAAGGCAT ATTGATTGT ATGACAAGGA 420
TGAAATAGAA AGAAGGGGAA GTATTTTGGT AGATTTTAAA GAACTGACAG AAGGTGGTGA 480
AGTAACTAAC TTGATACCAG ATATAGCAAC TGAACATAAG GATGCACCTG AGAAAACTT 540
GGCTTGCAATG GGTTTGGCAA TACATCAGGT GTTAACTAAG GACCTTGAAA GGCATGCAGC 600
TGAGTTACAA GCCCAGGAAG GATTGTCTAA TGATGGAGAA ACAATGGTAA ATGTGCCACA 660
TATTTCATGCA AGGGTGTACA ACTATGAGCC TTTGACACAG CTCAGAATG TCAGAGCAAA 720
TTACTATGGA AAATACATTG CTCCTAAGAGG GACAGTGGTT CGTGTGAGTA ATATAAAGCC 780
TCTTTGCACC AAGATGGCTT TTCTTTGTGC TGCATGTGGA GAAATTCAGA GCTTTCCTCT 840
TCCAGATGGA AAATACAGTC TTCCACAAA GTGTCTCTGT CCTGTGTGTC GAGGCAGGTC 900
ATTTACTGCT CTCGCGAGCT CTCCTCTCAC AGTTACGATG GACTGGCAGT CAATCAAAAT 960
CCAGGAATTG ATGCTGTATG ATCAGAGAGA AGCAGGTCGG ATTCACGAA CAATAGAAATG 1020
TGAGCTTGTT CATGATCTTG TGGATAGCTG TGTCCCGGGA GACACAGTGA CTATTACTTG 1080
AATTGTCAAA GTCTCAAAAT CGGAAGAAGG TTCTCGAAAT AAGAATGACA AGTGTATGTT 1140
CCTTTTGTAT ATTGAAGCAA ATTTATTAG TAATAGCAAA GGACAGAAAA CAAAGAGTTC 1200
TGAGGATGGG TGTAAGCATG GAATGTTGAT GGAGTTCTCA CTTAAAGACC TTTATGCCAT 1260
CCAAGAGATT CAAGCTGAAG AAAACCTGTT TAAACTCATT GTCAACTCGC TTTGCCCTGT 1320
CATTTTGGT CATGAACCTG TTAAGCAGG TTTGGCATTG GCACCTCTTG GAGGAAGCCA 1380
GAAATACGCA GATGACAAAA ACAGAATTCC AATTGCGGGA GACCCCAACA TCCTTGTGTT 1440
TGGAGATCCA GGCCTAGGAA AAAGTCAAA GCTACAGGCA GCGTGCAATG TTGCCCAACG 1500
TGGCGTGTAT GTTTGTGGTA ACACCACGAC CACCTCTGGT CTGACGGTAA CTCTTTCAAA 1560
AGATAGTTCC TCTGGAGATT TTGCTTTGGA AGCTGGTGCC CTGGTACTTG GTGATCAAGG 1620
TATTTGTGGA ATCATGTAAT TTGATAAGAT GGGGAATCAA CATCAAGCCT TGTGGAAGC 1680
CATGGAGCAG CAAAGTATTA GTCTTGCTAA GGCTGGTGTG GTTTGTAGCC TTCCTGCAAG 1740
AACTTCCATT ATTGCTGCTG CAAATCCAGT TGGAGGACAT TACAATAAAG CCAAAACAGT 1800
TTCTGAGAA TTAATAATGG GGAGTGCACT ACTATCCAGA TTTGATTGG TCTTTATCCT 1860
GTTAGATACT CCAATGAGC ATCATGATCA CTTACTCTCT GAACATGTGA TTGCAATAAG 1920
AGCTGGAAG CAGAGAACCA TTAGCAGTGC CACAGTAGCT CGTATGAATA GTCAAGATTC 1980
AAATACTTCC GTACTTGAAG TAGTTTCTGA GAAGCCATTA TCAGAAAGAC TAAAGTGGT 2040
TCTTGGAGAA ACAATAGATC CCATTCCCCA CCAGCTATTG AGAAAGTACA TTGGCTATGC 2100
TCGGCAGTAT GTGTACCCAA GGCTATCCAC AGAAGCTGCT CGAGTTCTTC AAGATTTTTA 2160
CCTTGAGCTC CGGAACAGA GCCAGAGGTT AAATAGCTCA CCAATCACTA CCAGGCAGCT 2220
GGAATCTTTG ATTCGTCTGA CAGAGGCACG AGCAAGGTTG GAATTGAGAG AGGAAGCAAC 2280
CAAGAAGAGC GCTGAGGATA TAGTGAAAT TATGAAATAT AGCATGCTAG GAACCTACTC 2340
TGATGAATTT GGGAACTTAG ATTTGAGCG ATCCAGCAT GGTCTGGAA TTGACCAACAG 2400
GTCAACAGCG AAAAGATTTA TTTCTGCTCT CAACAACGTT GCTGAAAGAA CTTATAATAA 2460
TATATTTCAA TTTTCATCAAC TTCGGCAGAT TGCCAAAGAA CTAACATTC AGGTTGCTGA 2520
TTTTGAAAT TTTATTGGAT CACTAAATGA CCAGGTTTAC CTCTTGAAAA AAGGCCCAAA 2580
AGTTTACCAG CTTCAAACTA TGTAAAAGGA CTTACCAAG TTAGGGCTC CTGGGTTTAT 2640
TGCAATTAAC ACCATCTCTA GTGAAGATAT GCGTGCACGC ACAGACAGAC AGACACACAC 2700
ACACACACAC ACACACACAC ACACACACAC ACACACAGTC AAATACTGTT CTCTGAAAAA 2760
TGATGTCCCA AAAGTATTAT AATAGGAAAA AAGCATTAAA TATAATAAAC TAATTTAAGA 2820

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AGTGATAAAG TCTCCAGATG CAGTAGCTCA CACTGTAATC ACAGTGACTC AGGAGGCTGA 2880
GGTGAGAGGA TTCCTTGAGG CCAGGGTTCG AGACCAACCT TGGGCAACAT AGCAAGACCC 2940
CATTCTTTAA AAAAAAAAAA AAAAAATTA AACTTAGCTG GGTATGGTGG CACATGCCTA 3000
TAGTCTCAGC TACTTGTGAG GCTGAGGCAG GAGGATTCTT TGAGCCAGG AGTTTGAGGT 3060
5 TACAGTGAGC CACAATCACA CCAATCACTG CACTCCAGCC TGGGCAATAA AGTAACTCTT 3120
GACTCAAAAA AATAAAAAAA ATTGTAGTGG TAGCCATGTG TTAATTGTGA AATAAATTCT 3180
CCAAAGGGCT AAAAGTAAAT TACTTATAAA TTTTATTAG TTGTATTTT GACCTGCCTT 3240
TTATATGTAT GAATATTTC AATGTTTGCA TATCAGATGT AGGCATACAG ACAATAACAT 3300
AAACCAATGA ATATATTACA TATTCTGTGT TCCAATAAAA CTTTATTAT GGACACTAAA 3360
10 ATTTGAATTT CATAAAATTT TCCCATGTCA AGAATACAAA ATACTTGAGT TTTGTTTTTA 3420
GCTATTTAAT AATAGGTCTC ATTTATTCCA CAGGCTGTAG TTTGTAGTCT TGCTTGAAAC 3480
AATAGAAACA GACTGATTAA GCAGGAGAAG TTTTTTGAAA GAATTTTGT TGGCTCACGG 3540
AATTATTAGA AGGCAGGTGA ACCAGGAGGG TAAGCTTCCA GCAGCAATTT GTAAAAACAT 3600
15 GCCTTAGAAT TGGACTAAGG AAGAAGCTGC TGACACTCCA CTGCCACACA GGGCACTGGA 3660
AGAAAGTGCT GCTGCCTCCC TGCCCCACTT TGGCCACTTC TGACAGCAGGA ATAGGTAGAA 3720
GAATGCCCCC ACCCGCACCG GAACAGCAAC AAAAGGATTC TGCAATGAGT GCCTCCCTAA 3780
ATTGCTGAAT TCAAAAAAGA AGTTGCATAC AAAGACATCT GATTGAAAAA GGGTATGTTA 3840
TATGCCCCCT TCATAGGCTG CTAGGGAGTT TTCTTGTTT TACTTTCAGG TGGTGGGATC 3900
20 AATAAGACCA GAATTTCTCA TATGTTGTGA GAGGATTCAA ATGTTACAGG GTTGCCAGCC 3960
AAACTATCAA TCATGTATAA ATCCAACAAA CACTTTGTAA CATACAAGAA CTCAGGAAAT 4020
GTGAACCAAT GTTGGAGAAT CTAATAAAT ACGGCTTCCC GCAACGAAAG ATGAATGGAA 4080
AATGTAAATA AAAAGAACTG GCAGTGTATA TCAGATGTTT AACTATAGGA CCAGAACTAA 4140
GATGTGGAGA CTATTGCCAT AGACCACAAT GTAAATTTT AAGTGAGGAA GGAATAATCA 4200
25 GGAATCAAAA GGGGCCAGGT GCAGTGGCTC ACATCTATAA TCCAGAGCT TTGGGAGTTC 4260
GAGGCAGGAG GATCACTTGA AGCCAGTTT GAGACCAGCC TATGCAACAC ATTGAGACCC 4320
TATCTCTACA AAAAATAGAT TAGCTGGGCA CGGTGGTGCA TGCCTATTGT CCTACCTACT 4380
GTGGAGGCTG AAGTAGGAAA TCACCTGAGC CCGAGAGTTT GAGGTTACAG TGAGCTATGA 4440
TTATACCACT GCATCCAGC CTGGGCAAGA GAGCAAGACC TTGTCTCTT

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Seq ID NO: 44 Protein sequence:  
Protein Accession #: CAB55276.2

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1      11      21      31      41      51
|      |      |      |      |      |
35 MNGEYRGRGF GRGRFQSWKR GRGGGNFSGK WREREHRPDL SKTTGKRTSE QTPQFLLSTK 60
TPQSMQSTLD RFIPYKWKWL YFSEVYSDSS PLIEKIQAFE KFFTRHIDLY DKDEIERKGS 120
ILVDFKELTE GGEVINLIPD IATELRDAPE KTLACMLAI HQVLTKDLER HAAELQAEQEG 180
LSNDGETMVN VPHIHARVYN YEPLTQLKNV RANYYGKYIA LRGTVVVRVSN IKPLCTKMAF 240
LCAACGEIQS FPLPDGKYSL PTKCPVPVCR GRSFTALRSS PLVTMDWQS IKIQELMSDD 300
40 QREAGRIPRT IECBLVHDLV DSCVPGDVT ITGIVKVSNA BEGSRNKNDK CMFLLYIEAN 360
SISNSKGQKT KSSBDGCKHG MLMEFSLKDL YAIQEIQABE NLFKLIVNSL CPVIFGHELV 420
KAGLALALFG GSQKYADDKN RPIRGDPHI LVVGDPLGLK SQMLQAAACNV APRGVYVCGN 480
TTTTSGLTVT LSKDSSSDGF ALEAGALVLG DQICGIDEF DKMGNHQAL LEAMEQQSIS 540
LAKAGVVCSL PARTSIIIAA NPVGGHYNKA KTVSENLMKG SALLSRFDLV FILDTPNEH 600
45 HDHLLSEHVI AIRAGKQRTI SSATVARMNS QDSNTSVLEV VSEKPLSERL KVPGETIDP 660
IPHQLLRKYI GYARQYVYPR LSTEARVLQ DFYLELRKQS QRLNSSPITT RQLESILRLT 720
BARARLELRE EATKEDADI VEIMKYSMLG TYSDEFNLND FERSQHSGSM SNRSTAKRFI 780
SALNNVAERT YNNIFQFHQL RQIAKELNIQ VADFENFIGS LNDQGYLLKK GPKVYQLQTM

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Seq ID NO: 45 DNA sequence  
Nucleic Acid Accession #: NM\_005416.1  
Coding sequence: 149..658

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1      11      21      31      41      51
|      |      |      |      |      |
55 ACCAGATCCC AGAGGCTGAA CACCTCGACC TTCTCTGCAC AGCAGATGAT CCCTGAGCAG 60
CTGAAGACCA GAAAGGCCAC TAAGACTTTC TGCTTAATTC AGGAGCTTAG AGGATTCTTC 120
AAAGAGTGTG TCCACGATCC TTTGAAGCAT GAGTTCCTAC CAGCAGAAGC AGACCTTTAC 180
60 CCCACCACTC CAGCTTCAAC AGCAGCAGGT GAAACAACCC AGCCAGCCTC CACCTCAGGA 240
AATATTGTGT CACACAACCA AGGAGCCATG CCACTCAAAG GTTCCACAAC CTGGAAACAC 300
AAAGATTCCA GAGCCAGGCT GTACCAAGGT CCCTGAGCCA GGCTGTACCA AGGTCCCTGA 360
GCCAGGCTGT ACCAAGGTCC CTGAGCCAGG TTGTACCAAG GTCCCTGAGC CAGGCTGTAC 420
CAAGGTCCCT GAGCCAGGTT GTACCAAGGT CCCTGAGCCA GGCTACACCA AGGTCCCTGA 480
65 ACCAGGCAGC ATCAGGTCC CTGACCAAGG CTTATCAAG TTTCTGAGC CAGGTGCCAT 540
CAAAGTTCTT GAGCAAGGAT ACACCAAAGT TCCTGTGCCA GGCTACACAA AGCTACCAGA 600
GCCATGTCTT TCAACGGTCA CTCCAGGCCC AGCTCAGCAG AAGACCAAGC AGAAGTAATT 660
TGGTGCACAG ACAAGCCCTT GAGAAGCCAA CCACCAGATG CTGGACACCC TCTTCCCATC 720
70 TGTCTCTGTG TCTTAATTGT CTGTAGACCT TGTAATCAGC ACATTGTAC CCACAGCCAT 780
AGTCTCTCTC TTATTGTAT CCTAAAAATA CGTACTATAA AGCTTTTGT CACACACACT 840
CTGAAGAATC CTGTAAGCCC CTGAATTAAG CAGAAAGTCT TCATGGCTTT TCTGGTCTTC 900
GGCTGCTCAG GGTTCATCTG AAGATTCGAA TGAAAAGAAA TGCATGTTTC CTGCTCTTCC 960
CTCATTAAT TGCTTTTAAT TCCA

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Seq ID NO: 46 Protein sequence:  
Protein Accession #: NP\_005407.1

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1      11      21      31      41      51
|      |      |      |      |      |
80 MSSFYQKQTF TPPQLQQQQ VKQPSQPPFQ EIFVPTTKEP CHSKVPQPGN TKIPEPGCTK 60
VPEPGCTKVP EPGCTKVPFV GCTKVPFPGC TKVPEPGCTK VPEPGYTKVP EPGSIKVPDQ 120
GFIFKPEPGA IKVPEQGYTK VPPVGYTKLP EPCPSTVTPG PAQKQTKQK

```

Seq ID NO: 47 DNA sequence  
Nucleic Acid Accession #: Eos sequence



1	11	21	31	41	51	
GCGTCGTGTG	CAGGCGTCCC	CGGGCTGTGG	ATAATTAGAC	ACGTTCTTCC	CTCATTGCCC	60
AAGGTCGTGT	AGAATTCGCC	CTAGAGCTGT	ATCATGTATT	TTCTTTCAAA	TTAACTTTGC	120
TTGCAATTAA	GCTTAGGGAA	CCAGCAACAA	AAGCAAACTT	GGCCCGAGGT	CGTTCACCGC	180
GAAAATGGAT	TAGAGAAACT	TCTTCCCCGA	TTTAAGGGGA	AAGATTCCTG	CGGCCAGCGC	240
TTTGGGGAAA	GTGCCCGGAG	CGCAGAGGGC	ACGACAGGGG	AGCAGGAAGC	TGCTCACGGT	300
AGTCGGCGTT	GGCGCGACGC	GTGGCCTTCC	TCATCTGGGC	GATGTGGGCT	CCTAGAAGAG	360
TAAGGATAAC	ATCCTGGAAA	TGACTTCTGT	ACGGTTTGAG	CCCAACTGCA	CACTCATGAC	420
TTGGAGCTGC	CCTGTGGAGT	TACAGTTTAC	CAAAACACATT	CATGAACATA	ATCTCATTTA	480
CTAAAAACTT	TGTGAGAAAT	TTCTTTTACT	AAAAATTTT	CTTATTACAA	A	

Seq ID NO: 48 DNA sequence:

Nucleic Acid Accession #: CAT cluster

1	11	21	31	41	51	
TTCCAAATTT	TTTTTTTTGT	AATAAGAAAA	AATTTTAGTA	AAAGAAAATT	CTCACAAAGT	60
TTTTAGTAAA	TGAGATTATG	TTCATGAATG	TGTTTGGTAA	ACTGTAACTC	CACAGGGCAG	120
CTCCAAGTCA	TGAGTGTGCA	GTTGGGCTCA	AACCGTACAG	AAGTCATTTC	CAGGATGTTA	180
TCCTTACTCT	TCTCGGAGCC	CACATCGCCC	AGATGAGGAA	GGCCACCGCT	GCCGCCAACG	240
CCGACTACCG	TGAGCAGCTT	CCTGCTCCCC	TGTCGTCGCC	TCTGCGGTCG	GGGCACTTTC	300
CCCAAGCGC	TGGCGCAGG	AATCTTTCCC	CTTAAATCGG	GGAAGAAAGT	TCTCTAATCC	360
ATTTTCGCGG	TGAACGACCT	CGGGCCAAGT	TTGCTTTTGT	TGCTGGTTCC	CTAAGCTTAA	420
TTGCAAGCAA	AGTTAATTTG	AAAGAAAATA	CATGATACAG	CTCTAGGGCG	AATTCTAACG	480
AGCCTTGGGC	AATGAGGGAA	GAACGTGTCT	AGTTATCCAC	AGCCCGGGGA	CGCCTGCACA	540
CGACGCT						

Seq ID NO: 49 DNA sequence

Nucleic Acid Accession #: CAT cluster

1	11	21	31	41	51	
TCTTTCTTCT	GCTGCTCGTT	TGTCCTCTCT	GTGCTCTTCT	TCTTTCTTTC	CCTCGCGGCT	60
CCTGCGGACC	TCTGTGTGCT	CTTCTCTGAT	GGCGGGGGGC	GGGAGAAGCT	GACCGGTGAG	120
ACCGTAGACC	GCAAAACCAT	GGGTGTACAC	AGCCGGTCGC	CGGCTTTTTT	GGGAGAACCC	180
GACACATGCA	GACCAGTTTT	CCTGGAACNG	CATGACCATG	TTATTACTAT	GGGCCGCCTC	240
CCCAACCAAA	GTGTTTAAAA	CTTTTATAGG	CACCCCCAAA	ATTTTTTTTT	TTTTTTTTTT	300
TTCAATTTAA	AAACTCTAAT	ATTTATATTA	AATACAAAGA	TACCCAAACC	CTTTATGCTT	360
CTTTCTCTGA	TCTGTGTCTT	TTTTCTTTGA	CAGCATCTCC	ATTTTTTTTC	TGCTGCTTCA	420
TCGCTGTAGC	CATGGGAATC	CGTTTTCATTA	TTATGGTAGC	AATATGGAGT	GCTGTATTCC	480
TAAAGAAACT	GACACAGGAG	AATCACTTGA	ACTTGGGAGG	CAGAGTTTGC	AGTGAGCCGA	540
GATTGAACCA	GTGCACTCCA	GCCTTGGCAG	CGGAGCAAGA	TTCTGTACCA	GTTCTGAAG	600
TGCTGTATC	GTCCTGCAGC	CCCATCTCTG	GTTCCATTGC	GCTGCCAGGC	AGGGTGTGG	660
GACGTGGGGA	GAGCTGGTCT	ATATATCCGG	GTGAAGCTCA	GCTGTGGCAC	ACCTTGGATG	720
CCGGGTCTCT	CCTGCCCCCG	GGGACCTAGT	ATTTTGGCCA	CGAGTGTACA	CCAAACAAAG	780
GAGACAGCAT	CATTATGAG	CCTGAGCAT	CCACCTACT	GCTGTATCCA	GTTTCCATTG	840
ACTG						

Seq ID NO: 50 DNA sequence

Nucleic Acid Accession #: L05187

Coding sequence: 1991..2260

1	11	21	31	41	51	
CTGCAGGGAG	GCAGGTAGAA	AAGGCTTTTG	GGTTTTCAGG	TGGGGGGCAG	TCTAGCCTGA	60
TCAGAAAGGA	GGAAAAGGCC	AGGGCAGATG	TCTGGGTGGA	GTGAAGGGAA	AAAGTGATCC	120
CAGAGAAGAG	ATTAGCCCTT	GAAAGTCCCT	GAAGTAGGAG	AAGGGTAAAG	GTGTGGTTGG	180
TGAAGGAAG	CAGTTTTTCC	CAGATTAGCA	ACCACTCAGG	GGGAGGAAGG	TGAGAGTGGG	240
AGAGTCATAA	GTAATATTAT	CTGAATGTGT	GTAAGTTAAT	GGAATTGGGA	AAAAGATGGG	300
GGAAATGGAT	GGAAGGTCTT	GGACTCTGAG	ACAAGGGGTC	TATAATCAGT	CCATTTCATT	360
ATTTCTAGCT	TCCACCTTCA	CCAAGGCAGA	CAAGGAGGGC	CCACCTCAGC	TCCTCTGCTC	420
CCCCTCCCTT	TCCCACCTAT	TCATGTGTGC	AAGAGTGCCC	TGTCCCACAG	AACACGGGGA	480
ACAACCATCT	CAATGACAAG	GACAGCAGGT	GGCAAGGCTC	AACAGGACTC	AGATGTCCCC	540
CCAGGGTTAA	CTCATGAAAC	CCTCCATGAA	GCCTGCTGCT	CACCCCTCCC	TCAAGGCAAG	600
CCCTGCACCT	GGGTCTGAGG	ATGAGGGTGG	CAGTGAAAAT	TAGGCCAGTG	ACATCATTTT	660
CAGCCAGCTA	GTGCCAAAAA	ATATCAGGTG	GTGTTTCATCA	AATAAGCCGA	GCCAAACGGT	720
GATGAGGATG	GTAAGTGTGA	TCATGTGTGA	CAGGTGAGGA	ATGAAAACAG	AGTGCCCGAG	780
AGCTTCTATT	TCCTTGAGGC	AGGGCTCATT	CATCTTATAA	AAGCCAGCTG	GCCATTGCCT	840
TCACACCAAA	CCCAAGGGAC	CACACAGCCC	ATTCTGTCTC	GTATACCAGG	TAAGTCTCTG	900
ATTGCAACAA	ACTGGCAATT	CTAGTGTACT	TTTTCAATTAT	TAGAAATTAG	CTAAAGGCAA	960
ATATGTGTAA	GCAGGTAAAT	CCAGGGTTTC	AATGGGAGAT	AGAGAATAGT	GGAATATCTT	1020
TATTTTAAGT	TAAATTACAG	TCTGGATTTG	AAAGGACCTT	AGAGATGGTT	AGGGCTCCCC	1080
CCTCAGTAGA	TAGTCATTGA	ACTGGGAGTC	CTGGAGAAGA	TTGTTCAAAAT	GCCCATGGGA	1140
AGTTCATAGC	AGAACTAGAA	CTCAGGCCAG	AGCACTCTCA	GTAACACTGC	AATTTCCCCC	1200
TGACAAGATA	TTTATAGAAA	TTTTAATTTA	TTAGATGGAT	CTCTACTGAG	CATTTATTCC	1260
ATTTAAGGCA	GTATGCTAGG	CACTTTGGAC	AAATCAATGC	CCTAACGTAC	TTACTTAACA	1320
AACATAAAAC	CTAGCAGGAA	GGTAATACAT	ATATATAAAT	AAATGAAATG	CAAAAGTAGAT	1380
AGTAATTGGC	ATGACGGAGA	TGGGCAGAGA	AGGGCTGTGC	ACTTTTGGGA	GACTTGCTCA	1440
AGGAGACCTC	TAGGGTGTCA	AGTGTGTGA	GCTATGATGG	AGGGGTATT	GGACAAGCAG	1500
AGATGGGAAG	AAAAGCATTT	GGAAGGGACT	GTGTAAGCAC	AGACCAGAAG	CAAAACCATA	1560
GAGGCTTAGA	TGAATATAAA	GCCATCCTAT	AAGTCACAGG	CTTTCTACAT	GGAAGTAGGA	1620
GAGGAAAGTG	GTCTGATGCC	ATTTTCCAAA	AGACCTAATA	TGCGGACCTC	ATGTCCTCTC	1680
GAAGCCAGCT	TTAGTAGTCC	ATTTTCCAG	AACAGATATA	AGGTGCCTTG	GGTAGGAAGG	1740
GAGCCAAGAA	GAGAACTCCA	ATAAATGGA	GCAGAAGAAA	TTGCCTTTTA	GCTCCTCCTC	1800
TTCAAGGGC	CTGAAATTA	TCCAAGCTTA	TTTCATTTTT	AAATGTAATG	GGGAGCTTAA	1860



GGGAGATGAA AGGCTTTCTC TTCTAAAGGG TCCTGAAATA AAATCTGTTT GGCATTGAAT 1920  
 TTGTATCCAT CTTTCTTTAA TTGAATCACT GTGTCAGCTT TCTGTCTCTA GAAAAAACA 1980  
 CATTGGAAGC ATGAATTTCT AGCAGCAGAA GCAGCCTTGC ACCCCACCCC CTCAGCCTCA 2040  
 GCAGCAGCAG GTGAACAAC CTTGCCAGCC TCCACCCAG GAACCATGCA TCCCCAAAAC 2100  
 CAAGGAGCCC TGCCAACCCA AGGTGCCTGA GCCCTGCCAC CCCAAAGTGC CTGAGCCCTG 2160  
 CCAGCCCAAG ATTCCAGAGC CCTGCCAGCC CAAGGTGCCT GAGCCCTGCC CTTCAACGGT 2220  
 CACTCCAGCA CCAGCCAGC AGAAGACCAA GCAGAAGTAA TGTGGTCCAC AGCCATGCCC 2280  
 TTGAGGAGCT GGCACTGGA TACTGAACAC CCTACTCCAT TCTGCTTATG AATCCCATTT 2340  
 GCCTATTGAC CCTGCAGTTA GCATGCTGTC ACCCTGAATC ATAATCGCTC CTTTGCACCT 2400  
 CTAAGAAAGAT GTCCCTTACC CTCATTCTGG AGGCTCCTGA GCCTCTGCGT AAGGCTGAAC 2460  
 GTCTCACTGA CTGAGCTAGT CTTCTTGTG CTCGGGTGCA TTTGAGGATG GATTTGCGGA 2520  
 AGGTCAAGTG ACCATCCCTA G

Seq ID NO: 51 Protein sequence:  
 Protein Accession #: AAC26838

1 11 21 31 41 51  
 MNSQQQKQPC TPPPQPOQQQ VKQPCQPPQ EPCIPKTKEP CQPKVPEPCH PKVPEPCQPK 60  
 IPEPCQPKVP EPCPSTVTPA PAQQTQKQK

Seq ID NO: 52 DNA sequence  
 Nucleic Acid Accession #: NM\_002638.1  
 Coding sequence: 120-473

1 11 21 31 41 51  
 CAATACAGCT AAGGAATTAT CCCTTGTAAG TACCACAGAC CCGCCCTGGA GCCAGGCCAA 60  
 GCTGGACTGC ATAAAGATTG GTATGGCCTT AGCTCTTAGC CAAACACCTT CCTGACACCA 120  
 TGAGGGCCAG CAGCTTCTTG ATCGTGGTGG TGTTCCTCAT CGCTGGGACG CTGTTTCTAG 180  
 AGGCAGCTGT CACGGGAGTT CCGTTAAAG GTCAGACAC TGTCAAAGGC CGTGTTCAT 240  
 TCAATGGACA AGATCCCCTT AAAGGACAAG TTTCAAGTAA AGGTCAAGAT AAAGTCAAAG 300  
 CGCAAGAGCC AGTCAAAGGT CCAGTCTCCA CTAAGCCTGG CTCCTGCCCC ATTATCTTGA 360  
 TCCGGTGGCG CATGTTGAAT CCCCCTAAC GCTGCTTGAA AGATACTGAC TGCCAGGAA 420  
 TCAAGAAAGT CTGTGAAGGC TCTTGCGGGA TGGCCTGTTT CGTTCCCCAG TGAAGGGAGC 480  
 CGGTCTTTCG TGCACCTGTG CCGTCCCCAG AGCTACAGGC CCCATCTGGT CCTAAGTCCC 540  
 TGCTGCCCTT CCGCTTCCCA CACTGTCCAT TCTTCTCTCC ATTACAGGATG CCCACGGCTG 600  
 GAGCTGCCTC TCTCATCCAC TTTCAATAA A

Seq ID NO: 53 Protein sequence:  
 Protein Accession #: NP\_002629.1

1 11 21 31 41 51  
 MRASSFLIVV VFLIAGTLVL EAAVTGVPVK GQDITVGRVP FNGQDPVKQ VSVKGQDKVK 60  
 AQEPVKGPVS TKPGSCPIIL IRCAMLNPPN RCLKDITDCPG IKKCEGSCG MACFVPQ

Seq ID NO: 54 DNA sequence  
 Nucleic Acid Accession #: NM\_019618  
 Coding sequence: 75-584

1 11 21 31 41 51  
 GGCACGAGCC ACGATTCACT CCCCTGGACT GTAGATAAAG ACCCTTTCTT GCCAGGTGCT 60  
 GAGACAACCA CACTATGAGA GGCACCTCAG GAGACGCTGA TGGTGGAGGA AGGGCCGTCT 120  
 ATCAATCAAT GTGTAAACCT ATTACTGGGA CTATTAATGA TTTGAATCAG CAAGTGTGGA 180  
 CCCTTCAGGG TCAGAACCTT GTGGCAGTTC CACGAAGTGA CAGTGTGACC CCAAGTCACTG 240  
 TTGCTGTTAT CACATGCAAG TATCCAGAGG CTCTTGAGCA AGGCAGAGGG GATCCCATTT 300  
 ATTTGGGAAT CCAGAATCCA GAAATGTGTT TGTATTGTGA GAAGGTGGA GAACAGCCCA 360  
 CATTGCAGCT AAAAGAGCAG AAGATCATGG ATCTGTATGG CCAACCCGAG CCCGTGAAAC 420  
 CCTTCCTTTT CTACCGTGCC AAGACTGGTA GGACCTCCAC CCTTGAGTCT GTGGCCTTCC 480  
 CGGACTGTTT CATTCCTTCC TCCAAGAGAG ACCAGCCCAT CATTCGTACT TCAGAACTTG 540  
 GGAAGTCATA CAACACTGCC TTTGAATTAA ATATAAATGA CTGAACTCAG CCTAGAGGTG 600  
 GCAGCTGGT CTTTGTCTTA AAGTTTCTGG TTCCCAATGT GTTTCTGTCT ACATTTTCTT 660  
 AGTGTCAATT TCACGCTGGT GCTGAGACAG GGGCAAGGCT GCTGTTATCA TCTCATTTTA 720  
 TAATGAAGAA GAAGCAATTA CTTCATAGCA ACTGAAGAAC AGGATGTGGC CTCAGAAGCA 780  
 GGAGAGCTGG GTGTATTAAG GCTGTCTTCT CAAGCTGGTG CTGTGTAGGC CACAAGGCAT 840  
 CTGCATGAGT GACTTTAAGA CTCAAAGACC AAACACTGAG CTTTCTTCTA GGGGTGGGTA 900  
 TGAAGATGCT TCAGAGCTCA TGCGCGTTAC CCACGATGGC ATGACTAGCA CAGAGCTGAT 960  
 CTCTGTTTCT GTTTTGTCTT ATTCCTCTT GGGATGATAT CATCCAGTCT TTATATGTTG 1020  
 CCAATATACC TCATTGTGTG TAATAGAACC TTCTTAGCAT TAAGACCTTG TAAACAAAAA 1080  
 TAATTCTTGT GTTAAGTTAA ATCATTTTGT TCCTAATTGT AATGTGTAAT CTTAAAGTTA 1140  
 AATAAACTTT GTGTATTAT ATAATAAAAA AAAAAAAAA AAA

Seq ID NO: 55 Protein sequence:  
 Protein Accession #: NP\_062564

1 11 21 31 41 51  
 MRGTPGDADG GGRAVYQSMC KPITGTINDL NQQVWTLQGG NLVAVPRSDS VTPVTVAVIT 60  
 CKYPEALEQG RGDPIYLGIO NPEMCLYCEK VGEQPTLQLK EQKIMDLYGQ PEPVKPFLFY 120  
 RAKTGRSTSL ESVAFPDWFI ASSKRDQPII LTSELGKSYN TAFELNIND

Seq ID NO: 56 DNA sequence  
 Nucleic Acid Accession #: NM\_003125  
 Coding sequence: 65-334



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1      11      21      31      41      51
|      |      |      |      |      |
5 AGCAGTTCTA AGGGACCATA CAGAGTATTC CTCTCTTCAC ACCAGGACCA GCCACTGTTG 60
  CAGCATGAGT TCCAGCAGC AGAAGCAGCC CTGCATCCCA CCCCTCAGC TTCAGCAGCA 120
  GCAGGTGAAA GAGCCTTGCC AGCCTCCACC TCAGGAACCA TGCATCCCCA AAACCAAGGA 180
  GCCTTGCCAC CCCAAGGTGC CTGAGCCCTG CACCCCAAAA GTGCCCTGAGC CCTGCCAGCC 240
  CAAGCTTCCA GAGCCATGCC ACCCAAGGT GCCTGAGCCC TGCCCTTCAA TAGTCACTCC 300
  AGCACCAGCC CAGCAGAAGA CCAAGCAGAA GTAATGTGGT CCACAGCCAT GCCCTTGAGG 360
  AGCCGGCCAC CAGATGCTGA ATCCCTATC CCATTCTGTG TATGAGTCCC ATTTGCCTTG 420
  CAATTAGCAT TCTGTCTCCC CCAAAAAAGA ATGTGCTATG AAGCTTTCTT TCCTACACAC 480
  TCTGAGTCTC TGAATGAAGC TGAAGTCTT AGTACCAGAG CTAGTTTTC A GCTGCTCAGA 540
  ATTCATCTGA AGAGAGACTT AAGATGAAAG CAAATGATTG AGCTCCCTTA TACCCCATTT 600
  AAATCACTT TCAATTTCA

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Seq ID NO: 57 Protein sequence:  
Protein Accession #: NP\_003116

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1      11      21      31      41      51
|      |      |      |      |      |
20 MSSQQQKQPC IPPFQLQQQQ VKQPCQPPFQ EPCIPKTKEP CHPKVPEPCH PKVPEPCQPK 60
  LPEPCHPKVP EPCFSIVTPA PAQKTKQK

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Seq ID NO: 58 DNA sequence  
Nucleic Acid Accession #: NM\_001793.2  
Coding sequence: 71-2560

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1      11      21      31      41      51
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30 AAAGGGGCAA GAGCTGAGCG GAACACCGGC CCGCCGTCGC GGCAGCTGCT TCACCCCTCT 60
  CTCTGCAGCC ATGGGGCTCC CTCGTGAGCC TCTCGCGTCT CTCCTCCTTC TCCAGGTTTG 120
  CTGGCTGCAG TGGCGCGCCT CCGAGCCGTG CCGGGCGGTC TTCAGGAGG CTGAAGTGAC 180
  CTTGGAGGCG GAGAGCGCGG AGCAGGAGCC CGGCCAGGCG CTGGGGAAAG TATTTCATGGG 240
  CTGCCCTGGG CAAGAGCCAG CTCGTGTTAG CACTGATAAT GATGACTTCA CTGTGCGGAA 300
  TGGCGAGACA GTCCAGGAAA GAAGGTCACT GAAGGAAAGG AATCCATTGA AGATCTTCCC 360
  ATCCAAACGT ATCTTACGAA GACACAAGAG AGATTGGGTG GTTGCTCCAA TATCTGTCCC 420
  TGAATAATGGC AAGGGTCCCT TCCCCAGAG ACTGAATCAG CTCAACTCTA ATAAAGATAG 480
  AGACACCAAG ATTTTCTACA GCATCACGGG GCCGGGGGCA GACAGCCCCC CTGAGGGTGT 540
  CTTGCTGTGA GAGAAGGAGA CAGGCTGGTT GTTGTGAAT AAGCCACTGG ACCGGGAGGA 600
  GATTGCCAAG TATGAGCTCT TTGGCCAGCG TGTGTCAGAG AATGGTGCCT CAGTGGAGGA 660
  CCCCATGAAC ATCTCCATCA TCGTGACCGA CCAGAATGAC CACAAGCCCA AGTTTACCCA 720
  GGACACCTTC CGAGGGAGTG TCTTAGAGGG AGTCTTACCA GGTACTTCTG TGTATGCAGG 780
  GACAGCCACG GATGAGGATG ATGCCATCTA CACCTACAAT GGGGTGGTTG CTTACTCCAT 840
  CCATAGCCAA GAACCAAGAG ACCCACACGA CCTCATGTTT ACCATTACCC GGAGCACAGG 900
  CACCATCAGC GTCATCTCCA GTGGCCTGGA CCGGGAAAAA GTCCCTGAGT ACACACTGAC 960
  CATCCAGGCC ACAGACATGG ATGGGGACGG CTCACCAACC ACCGCACTGG CAGTAGTGGA 1020
  GATCCTTGAT GCCAATGACA ATGCTCCCAT GTTTGACCCC CAGAAGTACG AGGCCCATGT 1080
  GCCTGAGAAT GCAGTGGGCC ATGAGGTGCA GAGGCTGACG GTCAGTGATC TGGACGCCCC 1140
  CAACCTACCA CACTTACCTT CCACCTACCT TATCATGGGC GGTGACGACG GGGACCATTT 1200
  TACCATCACC ACCCACCTCT AGAGCAACCA GGGCATCCTG ACAACCAGGA AGGGTTTGGA 1260
  TTTTGAGGCC AAAAACCCAG ACACCTGTGA CGTTGAAGTG ACCAACGAGG CCCCTTTTGT 1320
  GCTGAAGCTC CCAACCTCCA CAGCCACCAT AGTGGTCCAC GTGGAGGATG TGAATGAGGC 1380
  ACCTGTGTTT GTCCCCACCT CCAAGTTCGT TGAGGTCCAG GAGGGCATCC CCACTGGGGA 1440
  GCCTGTGTGT GTCTACATCG CAGAAGACCC TGACAAGGAG AATCAAAAGA TCAGCTACCG 1500
  CATCTGAGA GACCCAGCAG GGTGGCTAGC CATGGACCCA GACAGTGGGC AGGTACACAGC 1560
  TGTGGGCACC CTCGACCGTG AGGATGAGCA GTTTGTGAGG AACAACATCT ATGAAGTCAT 1620
  GGTCTTGGCC ATGACCAATG GAAGCCCTCC CACCACTGGC ACGGGAACCC TTCTGTAAAC 1680
  ACTGATTGAT GTCATATGAC ATGGCCAGT CCCTGAGCCC CGTCAGATCA CCATCTGCAA 1740
  CCAAGGCCCT GTGCGCCAGG TGCTGAACAT CACGGACAAG GACCTGTCTC CCCACACCTC 1800
  CCCTTTCAG GCCAGCTCA CAGATGACTC AGACATCTAC TGGACGCGAG AGGTCAACGA 1860
  GGAAGGTGAC ACAGTGTGCT TGTCCCTGAA GAAGTTCCTG AAGCAGGATA CATATGACGT 1920
  GCACCTTTCT CTGTCTGACC ATGGCAACAA AGAGCAGCTG ACGGTGATCA GGGCCACTGT 1980
  GTGCGACTGC CATGCCATG TCGAAACCTG CCCTGGACCC TGGAAAGGAG GTTTCATCCT 2040
  CCCTGTGCTG GGGGCTGTCC TGGCTCTGCT GTTCTCTCTG CTGGTGTCTG TTTTGTGGT 2100
  GAGAAAGAAG CGGAAGATCA AGGAGCCCTT CCTACTCCCA GAAGATGACA CCCGTGACAA 2160
  CGCTCTTAC TATGGCGAAG AGGGGGGTGG CGAAGAGGAC CAGGACTATG ACATCACCCA 2220
  GCTCCACCGA GGTCTGGAGG CCAGGCCGGA GGTGTTCTC CGCAATGACG TGGCACCAAC 2280
  CATCATCCCG ACACCCATGT ACCGTCTCG GCCAGCCAAC CCAGATGAAA TCGGCAACTT 2340
  TATAATTGAG AACCTGAAGG CGGCTAACAC AGACCCCA GCGCCGCCCT ACACACCTT 2400
  CTTGGTGTTC GACTATGAGG GCAGCGGCTC CGACGCGCG TCCCTGAGCT CCTCACCTC 2460
  CTCGCCCTCC GACCAAGACC AAGATTACGA TTATCTGAAC GAGTGGGGCA GCCGCTTCAA 2520
  GAAGCTGGCA GACATGTACG GTGGCGGGGA GGACGACTAG GCGGCCTGCC TGCAGGGCTG 2580
  GGGACCAAAC GTACAGGCCAC AGAGCATCTC CAAGGGGTCT CAGTTCCTCC TTCACTGAG 2640
  GACTTCGAGC CTTGTGAGGA AGTGGCCGTA GCAACTTGGC GGAGACAGGC TATGAGTCTG 2700
  ACGTTAGAGT GGTGTCTTCC TTAGCCTTTC AGGATGGAGG AATGTGGGCA GTTTGACTTC 2760
  AGCACTGAAA ACCTCTCCAC CTGGGCCAGG GTTGCCTCAG AGGCCAAGTT TCCAGAAGCC 2820
  TCTTACCTGC CGTAAAAATG TCAACCTGT GTCTTGGGCC TGGGCCTGCT GTGACTGACC 2880
  TACAGTGAGC TTCTCTCTG GAAATGGAACC TTCTTAGGCC TCCTGGTGCA ACTTAATTTT 2940
  TTTTATTAAT GCTATCTTCA AAACGTTAGA GAAAGTCTT CAAAGTGCA GCCCAGAGCT 3000
  GCTGGGCCCA CTGGCCGTCC TGCATTTCTG GTTTCAGAC CCCAATGCCT CCCATTCGGA 3060
  TGGATCTCTG CGTTTATATA CTGAGTGTGC CTTATTTT TATTTTCCCT 3120
  GTTGCCTTGC TATAGATGAA GGGTGAGGAC AATCGTGAT ATGTACTAGA ACTTTTTTAT 3180
  TAAAGAACT TTTCCAGAAA AAAAA

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Seq ID NO: 59 Protein sequence:



Protein Accession #: NP\_001784.2

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QEPALFSTDN	DDFTVRNGET	VQERRSLKER	NPLKIFPSKR	ILRRHKRDWV	VAPISVPENG	120
KGPPFQRLNQ	LKSNKDRDTK	IFYSITGPGA	DSPPEGVFAV	EKETGWLLLN	KPLDREEIAK	180
YELFGHAYSE	NGASVEDPMN	ISIIIVTDQND	HKPKFTQDTF	RGSVLEGVLP	GTSMQVTAT	240
DEDDAIYTYN	GVVAYSIIHSQ	BPKDPHDLMF	TIHRSTGTIS	VISSGLDREK	VPEYTLTIQA	300
TDMGDGGSTT	TAVAVVEILD	ANDNAPMFDP	QKYEAHVPEN	AVGHEVQRLT	VTDLDAPNSP	360
AWRATYLMG	GDDGDHFTIT	THPESNQIL	TRKGLDFEA	KNQHTLYVEV	TNEAPFVLKL	420
PTSTATIVVH	VEDVNEAPVF	VPPSKVVEVQ	EGIPTGEPVC	VYTAEDPDKE	NQKISYRILR	480
DPAGWLAMP	DSGQVTAVGT	LDREDEQFVR	NNIYEVMLA	MDNGSPPTG	TGTLTLTLID	540
VNDHGPVPEP	RQITICNQSP	VRQVLNITDK	DLSPHTSPFQ	AQLTDDSDIY	WTAEVNBEED	600
TVVLSLKKFL	KQDPTDVHLS	LSDHGNKEQL	TVIRATVCDC	HGHVETCPGP	WKGGFILPVL	660
GAVLALLEFL	LVLLLLVRKK	RKIKEPLLLP	EDDTRDNVYF	YGEEGGGEED	QDYDITQLHR	720
GLEARPEVVL	RNDVAPTIIIP	TPMYRPRPAN	PDEIGNFIIE	NLKAANTDPT	APPYDTLLVF	780
DYEGSGSDAA	SLSLTSSAS	DQDQDYDYLN	EWGSRFKKLA	DMYGGGEDD		

Seq ID NO: 60 DNA sequence  
 Nucleic Acid Accession #: Eos sequence  
 Coding sequence: 162-428

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AGCACCTCGG	AAGCTGAGGC	AGCTGGTACT	TGACAGAGAG	GATGGCGCTG	TCGACCATAG	180
TCTCCAGAG	GAAGCGAAGG	CTCCCGTGG	CTTTCTAAG	CGAGTCTTCA		240
AGCGAAAGAA	GCCTCAACTT	CGTCTGGAGA	AAAGTGGTGA	CTTATTGGTC	CATCTGAAC	300
GTTTACTGTT	TGTTTCATCGA	TTAGCAGAAG	AGTCCAGGAC	AAACGCTTGT	GCGAGTAAAT	360
GTAGAGTCAT	TAAACAAGGAG	CATGTACTGG	CCGCAGCAAA	GGTAATTCTA	AAGAAGAGCA	420
GAGGTTAGAA	GTCAAAGAAC	ATATTCTTGA	AAGTTATGAT	GCATTCTTTT	GGGTGGTAAC	480
AGATCATAAA	GACATTTTTT	ACACATCAGT	TAATATGGGA	TTATTAAATA	TTGG	

Seq ID NO: 61 Protein sequence:  
 Protein Accession #: Eos sequence

1	11	21	31	41	51	
MALSTIVSQR	KQIKRKAPRG	FLKRVFKRKK	PQLRLEKSGD	LLVHLNCLLF	VHRLAEESRT	60
NACASKCRVI	NKEHVLAAAK	VILKKSRRG				

Seq ID NO: 62 DNA sequence  
 Nucleic Acid Accession #: NM\_000094.2  
 Coding sequence: 99-8933

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GGGCTGGAGG	GGCGCTGGGC	TCGGACCTGC	CAAGGCCACC	GCAGGGGGGA	GCAAGGGACA	60
GAGGCGGGGG	TCCTAGCTGA	CGGCTTTTAC	TGCCTAGGAT	GACGCTGCGG	CTTCTGGTGG	120
CCGCGCTCTG	CGCCGGGATC	CTGGCAGAGG	CGCCCCGAGT	GCGAGCCGAG	CACAGGGAGA	180
GAGTGACCTG	CACGCGCCTT	TACGCCGCTG	ACATTGTGTT	CTTACTGGAT	GGCTCCTCAT	240
CCATTGGCCG	CAGCAATTTC	CGCGAGGTCC	GCAGCTTTCT	CGAAGGGCTG	GTGCTGCCTT	300
TCTCTGGAGC	AGCCAGTGCA	CAGGTGTGTC	GCTTTGCCAC	AGTGCAGTAC	AGCGATGACC	360
CACGACAGAG	GTTTCGGCTG	GATGCACCTG	GCTCTGGGGG	TGATGTGATC	CGCGCCATCC	420
GTGAGCTTAG	CTACAAGGGG	GGCAACACTC	GCACAGGGGC	TGCAATTCTC	CATGTGGCTG	480
ACCATGCTCT	CCTGCCCGAC	CTGGCCCGAC	CTGGTGTCCC	CAAGGTCTGC	ATCCTGATCA	540
CAGACGGGAA	GTCCCGAGAC	CTGGTGGACA	CAGCTGCCCA	AAGGCTGAAG	GGGCAGGGGG	600
TCAAGCTATT	TGCTGTGGGG	ATCAAGAAATG	CTGACCCCTGA	GGAGCTGAAG	CGAGTTGCCT	660
CACAGCCAAAC	CTCCGACTTC	TTCTTCTTCG	TCAATGACTT	CAGCATCTTG	AGGACACTAC	720
TGCCCTCTGT	TTCCCGGAGA	GTGTGCACGA	CTGCTGGTGG	CGTGCCCTGTG	ACCCGACCTC	780
CGGATGACTC	GACCTCTGCT	CCACGAGACC	TGGTGCTGTC	TGAGCCAGC	AGCCAATCCT	840
TGAGAGTACA	GTGGACAGCG	GCCAGTGGCC	CTGTGACTGG	CTACAAGGTC	CAGTACACTC	900
CTCTGACGGG	GCTGGGACAG	CCACTGCCGA	GTGAGCGGCA	GGAGGTGAAC	GTCCACAGCTG	960
GTGAGACCAG	TGTGCGGCTG	CGGGGTCTCC	GGCCACTGAC	CGAGTACCAA	GTGACTGTGA	1020
TTGCCCTCTA	CGCCAACAGC	ATCGGGGAGG	CTGTGAGCGG	GACAGCTCGG	ACCACTGCCC	1080
TAGAAGGGCC	GGAACTGACC	ATCCAGAATA	CCACAGCCCA	CAGCCTCCTG	GTGGCCTGGC	1140
GGAGTGTGCC	AGGTGCCACT	GGCTACCGTG	TGACATGGCG	GGTCTCTCAGT	GGTGGGCCCA	1200
CACAGCAGCA	GGAGCTGGGC	CCTGGGCAGG	GTTCAAGTGT	GCTGCGTGAC	TTGGAGCCTG	1260
GCACGGACTA	TGAGGTGACC	GTGAGCACCC	TATTGTGGCG	CAGTGTGGGG	CCCGCCACTT	1320
CCCTGATGGC	TCGCACTGAC	GCTTCTGTGT	AGCAGACCC	GCGCCCGGTC	ATCCTGGGCC	1380
CCACATCCAT	CCTCTTTTCC	TGGAACCTGG	TGCCTGAGGC	CCGTGGCTAC	CGGTTGGAAT	1440
GGCGGCGTGA	GACTGGCTTG	GAGCCACCGC	AGAAGGTGGT	ACTGCCCTCT	GATGTGACCC	1500
GCTACCAATT	GGATGGGCTG	CAGCCGGGCA	CTGAGTACCG	CCTCACACTC	TACACTCTGC	1560
TGGAGGGCCA	CGAGGTGGCC	ACCCCTGCAA	CCGTGGTTCC	CACTGGACCA	GAGCTGCCTG	1620
TGAGCCCTGT	AACAGACCTG	CAAGCCACCG	AGCTGCCCGG	GCAGCGGGTG	CGAGTGTCTT	1680
GGAGCCAGT	CCCTGGTGCC	ACCCAGTACC	GCATCATTTG	GCGCAGCACC	CAGGGGGTTG	1740
AGCGGACCTT	GGTGCTTCTT	GGGAGTCAGA	CAGCATTCGA	CTTGGATGAC	GTTTCAGGCTG	1800
GGCTTAGCTA	CAGTGTGGCG	GTGTCTGCTC	GAGTGGGTCC	CCGTGAGGGC	AGTGCCAGTG	1860
TCCTCACTGT	CGCGCGGAG	CGGAAACTC	CACCTGTCTG	TCCAGGGCTG	CGGTTGTGG	1920
TGTCAATGTC	AACGCGAGTG	AGGGTGGCCT	GGGGACCCGT	CCCTGGAGCC	AGTGGATTTC	1980
GGATTAGCTG	GAGCACAGGC	AGTGGTCCGG	AGTCCAGCCA	GACACTGCCC	CCAGACTCTA	2040
CTGCCACAGA	CATCACAGGG	CTGCAGCCTG	GAACCACTA	CCAGGTGGCT	GTGTCGGTAC	2100
TGCGAGGAG	AGAGGAGGCG	CCTGCTGCAG	TCATCGTGGC	TCGAACGGAC	CCACTGGGCG	2160
CAGTGAGGAC	GGTCCATGTG	ACTCAGGCCA	GCAGCTCATC	TGTCAACATT	ACCTGGACCA	2220
GGGTTCTCTG	CGCCACAGGA	TACAGGGTTT	CCTGGCACTC	AGCCACGGC	CCAGAGAAAT	2280



	CCCAGTTGGT	TTCFGGGGAG	GCCACGGTGG	CTGAGCTGGA	TGGACTGGAG	CCAGATACTG	2340
	AGTATACGGT	GCATGTGAGG	GCCCATGTGG	CTGGCGTGGA	TGGGCCCCCT	GCCTCTGTGG	2400
	TTGTGAGGAC	TGCCCTTGAG	CCTGTGGGTC	GTGTGTGAG	GCTGCAGATC	CTCAATGCTT	2460
5	CCAGCGAGCT	TCTACGGATC	ACCTGGGTAG	GGGTCACTGG	AGCCACAGCT	TACAGACTGG	2520
	CCTGGGGCCG	GAGTGAAGGC	GGCCCCATGA	GGCACCAGAT	ACTCCCAGGA	AACACAGACT	2580
	CTGCAGAGAT	CCGGGGTCTC	GAAGGTGGAG	TCAGCTACTC	AGTGCGAGTG	ACTGCACTTG	2640
	TCGGGGACCG	CGAGGGACAC	CCTGTCTCCA	TTGTGTGTAC	TACGCCGCTT	GAGGCTCCGC	2700
	CAGCCCTGGG	GACCGCTTAC	GTGTGTGAGC	GCGGGGAGCA	CTCGCTGAGG	CTGCGCTGGG	2760
10	AGCCGGTGCC	CAGAGCGCAG	GGCTTCCTTC	TGCACTGGCA	ACCTGAGGGT	GGCCAGGAAC	2820
	AGTCCCGGGT	CCTGGGGCCC	GAGCTCAGCA	GCTATCACCT	GGACGGGCTG	GAGCCAGCGA	2880
	CACAGTACCG	CGTGAGGCTG	AGTGTCTTAG	GGCCGGCTGG	AGAAGGGGCC	TCTGCAGAGG	2940
	TGACTGCGCG	CAGTGAAGTC	CCTCGTGTTC	CAAGCATTGA	ACTACGTGTG	GTGGACACCT	3000
	CGATCGACTC	GGTGACTTTG	GCCTGGACTC	CAGTGTCCAG	GGCATCCAGC	TACATCCTAT	3060
15	CCTGGCGGCC	ACTCAGAGGC	CCTGGCCAGG	AAGTGCCTGG	GTCCCGCGAG	ACACTTCCAG	3120
	GGATCTCAAG	CTCCAGCGGG	GTGACAGGGC	TAGAGCCTGG	CGTCTCTTAC	ATCTTCTCCC	3180
	TGACGCGTGT	CCTGGATGGT	GTGCGGGGTC	CTGAGGCATC	TGTACACAGC	ACGCCAGTGT	3240
	GCCCCCGTGG	CCTGGCGGAT	GTGGTGTTC	TACCACATGC	CACCTCAAGAC	AATGCTCACC	3300
	GTGCGGAGGC	TACGAGGAGG	GTCTTGGAGC	GTCTGGTGT	GGCACTTGGG	CCTCTTGGGC	3360
20	CACAGGCACT	TCAGGTTGGC	CTGCTGTCTT	ACAGTCATCG	GCCCTCCCCA	CTGTTCCAC	3420
	TGAATGGCTC	CCATGACCTT	GGCATTATCT	TGCAAAAGGAT	CCGTGACATG	CCCTACATGG	3480
	ACCCAAGTGG	GAAACACCTT	GGCACAGCCG	TGCTCACAGC	TCACAGATAC	ATGTTGGCAG	3540
	CAGATGCTCC	TGGGCGCCGC	CAGCACGTAC	CAGGGGTGAT	GGTTCTGCTA	GTGGATGAAC	3600
	CCTTGAGAGG	TGACATATTT	AGCCCCATCC	GTGAGGCCCA	GGCTTCTGGG	CTTAATGTGG	3660
25	TGATGTTGGG	AATGCTGCTG	GCAGGCCAG	AGCAGCTGCG	TCGCTTGGCG	CCGGGTATGG	3720
	ACTCTGTCCA	GACCTTCTTC	GCCGTGGATG	ATGGGCCAAG	CCTGGACCAG	GCAGTCAGTG	3780
	GTCTGGCCAC	AGCCCTGTGT	CAGGCATCCT	TCCTACTTCA	GCCCCGGCCA	GAGCCCTGCC	3840
	CAGTGTATTG	TCCAAAGGGC	CAGAGGGGGG	AACCTGGAGA	GATGGGCGTG	AGAGGACAAG	3900
	TTGGGCTTCC	TGGCGACCTT	GGCCTTCCCG	GCAGGACCGG	TGCTCCCGGC	CCCCAGGGGC	3960
30	CCCCTGGAAG	TGCCACTGCC	AAGGGCGAGA	GGGGCTTCCC	TGGAGCAGAT	GGGCGTCCAG	4020
	GCAGCCCTGG	CCGCGCCGGG	AATCCTGGGA	CCCCTGGAGC	CCCTGGCCTA	AAGGGCTCTC	4080
	CAGGGTTGCC	TGGCCCTCGT	GGGGACCCGG	GAGAGCGAGG	ACCTCGAGGC	CCAAAGGGGG	4140
	AGCCGGGGGC	TCCCGGACAA	GTCTCGGAG	GTGAAGGACC	TGGGCTTCTT	GGGCGGAAAG	4200
	GGGACCCCTG	ACCATCGGGC	CCCCCTGGAC	CTCGTGGACC	ACTGGGGGAC	CCAGGACCCC	4260
35	GTGGCCCCCC	AGGGCTTCTT	GGAACAGCCA	TGAAGGGTGA	CAAAGGCGAT	CGTGGGGAGC	4320
	GGGGTCCCCC	TGGACCCAGT	GAAGGTGGCA	TTGCTCCTGG	GGAGCTTGGG	CTGCCGGGTC	4380
	TTCCCGGAAG	CCCTGGAGCC	CAAGGCCCCG	TTGGCCCCCC	TGGAAAGAAA	GGAGAAAAG	4440
	GTGACTCTGA	GGATGGAGCT	CCAGGCCTCC	CAGGACAACC	TGGGTCTCCG	GGTGAGCAGG	4500
	GCCCCAGGGG	ACCTCCTGGA	GCTATTGGCC	CCAAAGGTGA	CCGGGGCTTT	CCAGGGCCCC	4560
40	TGGGTGAGGC	TGGAGAGAAG	GGCGAACCTG	GACCCCCAGG	CCCAGCGGGA	TCCCGGGGGC	4620
	TGCCAGGGGT	TGCTGGAGCT	CCTGGAGCCA	AGGGTCTGTA	AGGGCCACCA	GGACCCACTG	4680
	GCCGCCAAGG	AGAGAAGGGG	GAGCCTGGTC	GCCCTGGGGA	CCCTGCAGTG	GTGGGACCTG	4740
	CTGTTGTCTG	ACCCAAAGGA	GAAAAGGGAG	ATGTGGGGCC	CGCTGGGCCC	AGAGGAGCTA	4800
45	CCGGAGTCCA	AGGGGAACCG	GGCCCAACCG	GCTTGGTTCT	TCCTGGAGAC	CCTGGCCCCA	4860
	AGGGAGACCC	TGGAGACCGG	GGTCCCATTT	GCCTTACTGG	CAGAGCAGGA	CCCCCAGGTG	4920
	ACTCAGGGCC	TCTTGGAGAG	AAGGGAGACC	CTGGGCGGCC	TGGCCCCCCA	GGACCTGTGT	4980
	GCCCCCGAGG	ACGAGATGGT	GAAGTTGGAG	AGAAAGGTGA	CGAGGGTCTT	CCGGGTGACC	5040
	CGGGTTTGCC	TGGAAAAGCA	GGCGAGCGTG	GCCTTCGGGG	GGCACCTGGA	GTTCGGGGGC	5100
50	CTGTGGGTGA	AAAGGGAGAT	CAGGGAGATC	CTGGAGAGGA	TGGACGAAAT	GGCAGCCCTG	5160
	GATCATCTGG	ACCCAAGGGT	GACCGTGGGG	AGCCGGGTCC	CCCAGGACCC	CCGGGACGGC	5220
	TGGTAGACAC	AGGACCTGGA	GCCAGAGAGA	AGGGAGAGCC	TGGGGACCGC	GGACAAGAGG	5280
	GTCTCTGAGG	GCCCAAGGGT	GATCCTGGCC	TCCCTGGAGC	CCCTGGGGAA	AGGGGCATTG	5340
	AAGGGTTTCG	GGGACCCCCA	GGCCACACAG	GGGACCCAGG	TGTCCGAGGC	CCAGCAGGAG	5400
55	AAAAGGGTGA	CCGGGGTCCC	CCTGGGCTGG	ATGGCCGGAG	CGGACTGGAT	GGGAAACGAG	5460
	GAGCCGCTGG	GCCCTCTGGG	CCGAATGGTG	CTGCAGGCAA	AGCTGGGGAC	CCAGGGAGAG	5520
	ACGGGCTTCC	AGGCTCTCGT	GGAGAACAAG	GCCTCCCTGG	CCCCCTCTGGT	CCCCCTGGAT	5580
	TACCCGGAAA	GCCAGGAGAG	GATGGGAAAC	CTGGCCTGAA	TGGAAAAAAC	GGAGAACCTG	5640
	GGGACCCCTG	AGAAGACCGG	AGGAAGGGAG	AGAAAGGAGA	TTCAGGCGCC	TCTGGGAGAG	5700
60	AAGGTCTGTA	TGGCCCCAAG	GGTGAGCGTG	GAGCTCCTGG	TATCCTTGGG	CCCCAGGGGC	5760
	CTCCAGGCCCT	CCAGGGGCCA	GTGGGCCCTC	CTGGCCAGGG	TTTTCTCTGGT	GTCCCAAGGAG	5820
	GCACGGGGCC	CAAGGGTGAC	CGTGGGGAGA	CTGGATCCAA	AGGGGAGCAG	GGCCTCCCTG	5880
	GAGAGCGTGG	CCTGGGAGAG	GAGCCTGGAA	GTGTGCCGAA	TGTGGATCGG	TTGCTGGAAA	5940
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65	GTAGCTTCTT	GCCTGTGCCC	GAACGGCGTC	GAGGCCCCAA	GGGGGACTCA	GGCGAACAGG	6060
	GCCCCCAGG	CAAGGAGGGC	CCCATCGGCT	TTCCTGGAGA	ACGCGGGCTG	AAGGGCGACC	6120
	GTGGAGACCC	TGGCCCTCAG	GGGCCACCTG	GTCTGGCCCT	TGGGGAGAGG	GGCCCCCCCG	6180
	GGCCTTCCGG	CCTTGCCGGG	GAGCCTGGAA	AGCCTGGTAT	TCCCGGGCTC	CCAGGCAGGG	6240
	CTGGGGGTGT	GGGAGAGGCA	GGAAGGCCAG	GAGAGAGGGG	AGAACGGGGA	GAGAAAGGAG	6300
	AACGTGGAGA	ACAGGGCAGA	GATGGCCCTC	CTGGACTCCC	TGGAACCCCT	GGGCCCCCGG	6360
70	GACCCCTTGG	CCCCAAGGTT	TCTGTGGATG	AGCCAGGTCC	TGGACTCTCT	GGAGAACAGG	6420
	GACCCCTTGG	ACTCAAGGGT	GCTAAGGGGG	AGCCGGGCGA	CAATGGTGAC	CAAGGTCCCA	6480
	AAGGAGACAG	GGGTGTGCCA	GGCATCAAGG	GAGACCGGGG	AGAGCCTGGA	CCGAGGGGTC	6540
	AGGAAGGGCAA	CCCGGCTCTA	CCAGGAGAGC	GTGGTATGGC	TGGGCTGAA	GGGAAGCCGG	6600
	GTCTGCAGGG	TCCAAGAGGC	CCCCCTGGCC	CAGTGGGTGG	TCTGAGAGAC	CCTGGACCAC	6660
75	CTGGTGCCCC	GGGTCTTGCT	GGCCTTGACG	GACCCCAAGG	ACCTTCTGGC	CTGAAGGGGG	6720
	AGCCTGGAGA	GACAGGACCT	CCAGGACGGG	GCCTGACTGG	ACCTACTGGA	GCTGTGGGAC	6780
	TTCCTGGACC	CCCCGGCCCT	TCAGGCCTTG	TGGGTCCACA	GGGGTCTCCA	GGTTTGCCCTG	6840
	GACAAAGTGG	GGAGACAGGC	AAGCCGGGAG	CCCCAGGTGG	AGATGGTGCC	AGTGGAAAAG	6900
	ATGGAGACAG	AGGGAGCCCT	GGTGTGCCAG	GGTCACACAG	TCTGCCTGGC	CCTGTGCGAC	6960
80	CTAAAGGAGA	ACCTGGCCCC	ACGGGGGGCC	CTGGACAGGC	TGTGGTGGG	GTCCTGGGAG	7020
	CAAAAGGAGA	GAAGGGAGCC	CCTGGAGGCC	TTGCTGGAGA	CCTGGTGGGT	GAGCCGGGAG	7080
	CCAAAGGTGA	CCGAGGACTG	CCAGGGCCGC	GAGGCGAGAA	GGGTGAAGCT	GGCCGTGCAG	7140
	GGGAGCCCGG	AGACCCTGGG	GAAGATGGTC	AGAAAGGGGC	TCCAGGACCC	AAAGGTTTCA	7200
	AGGGTGACCC	AGGAGTCGGG	GTCCCGGGCT	CCCCTGGGCC	TCCTGGCCCT	CCAGGTGTGA	7260
85	AGGGAGACTT	GGGCTCCCTT	GGCCTGCCCG	GTGCTCCTGG	TGTTGTTGGG	TTCCCGGGTC	7320
	AGACAGGCCC	TCGAGGAGAG	ATGGGTGAGC	CAGGCCCTAG	TGGAGAGCGG	GGTCTGGGAG	7380
	GCCCCCAGG	GAGAGAAGGA	ATCCACAGAC	CCCTGGGGCC	ACCTGGACCA	CCGGGGTCAG	7440
	TGGGACACCC	TGGGGCTTCT	GGACTCAAAG	GAGACAAGGG	AGACCCTGGA	GTAGGGCTGC	7500



	CTGGGCCCCG	AGGCGAGCGT	GGGGAGCCAG	GCATCCGGGG	TGAAGATGGC	CGCCCCGGCC	7560
	AGGAGGGACC	CCGAGGACTC	ACGGGGCCCC	CTGGCAGCAG	GGGAGAGCGT	GGGGAGAAGG	7620
	GTGATGTTGG	GAGTGCAGGA	CTAAGGGTG	ACAAGGGAGA	CTCAGCTGTG	ATCCTGGGGC	7680
5	CTCCAGGCC	ACGGGGTGCC	AAGGGGGACA	TGGGTGAACG	AGGGCCTCGG	GGCTTGGATG	7740
	GTGACAAAGG	ACCTCGGGGA	GACAAATGGG	ACCCTGGTGA	CAAGGGCAGC	AAGGGAGAGC	7800
	CTGGTGACAA	GGGCTCAGCC	GGGTGCCCAG	GACTGCGTGG	ACTCCTGGGA	CCCCAGGGTC	7860
	AACCTGGTGC	AGCAGGGATC	CCTGGTGACC	CGGGATCCCC	AGGAAAGGAT	GGAGTGCCTG	7920
	GTATCCGAGG	AGAAAAAGGA	GATGTTGGCT	TCATGGGTCC	CCGGGGCCTC	AAGGGTGAAC	7980
10	GGGGAGTGAA	GGGAGCCTGT	GGCCTTGATG	GAGAGAAAGG	AGACAAGGGA	GAAGCTGGTC	8040
	CCCCAGGCCG	CCCCGGGCTG	GCAGGACACA	AAGGAGAGAT	GGGGGAGCCT	GGTGTGCCGG	8100
	GCCAGTCGGG	GGCCCTGGC	AAGGAGGGCC	TGATCGGTCC	CAAGGGTGAC	CGAGGCTTTG	8160
	ACGGGCAGCC	AGGCCCAAG	GGTGACCAGG	GCGAGAAAGG	GGAGCGGGGA	ACCCAGGAA	8220
	TGGGGGGCTT	CCCAGGCCCC	AGTGGAATG	ATGGCTCTGC	TGGTCCCCCA	GGGCCACCTG	8280
15	GCAGTGTGG	TCCAGAGGC	CCCAGAGGAC	TTCAGGGCCA	GAAGGGTGA	CGAGGTCCCC	8340
	CCGGAGAGAG	AGTGGTGGGG	GCTCCTGGGG	TCCCTGGAGC	TCCTGGCGAG	AGAGGGGAGC	8400
	AGGGCGCGCC	AGGGCCTGCC	GGTCCCTGAG	GCGAGAAAGG	AGAAGCTGCA	CTGACGGAGG	8460
	ATGACATCCG	GGGCTTTGTG	CGCCAAGAGA	TGAGTCAGCA	CTGTGCCTGC	CAGGGCCAGT	8520
	TCATCGCATC	TGGATCAGCA	CCCCCTCCCTA	GTTATGCTGC	AGACACTGCC	GGCTCCCAGC	8580
20	TCCATGCTGT	GCCTGTGCTC	CGCGTCTCTC	ATGCAGAGGA	GGAAGAGCGG	GTACCCCTTG	8640
	AGGATGATGA	TGACTCTGAA	TACTCCGAGT	ATTCTGTGGA	GGAGTACCAG	GACCTGGAAG	8700
	CTCCTTGGGA	TAATGATGAT	CCCTGTTCCC	TGCCACTGGA	TGAGGGCTCC	TGCACTGCCT	8760
	ACACCCTGGC	CTGGTACCAT	CGGGCTGTGA	CAGGCAGCAC	AGAGGCTGT	CACCTTTTGT	8820
	TCTATGGTGG	CTGTGGAGGG	AATGCCAACC	GTTTTGGGAC	CCGTGAGGCC	TGCGAGCGCC	8880
25	GCTGCCACCC	CCGGGTGCTC	CAGAGCCAGG	GGACAGGTAC	TGCCCAGGAC	TGAGGCCAGC	8940
	ATAATGAGCT	GAGATTACAG	ATCCCTCGGA	GGAGTCCGGG	TCTCAGCAGA	ACCCCACTGT	9000
	CCCTCCCTTT	GGTGCTAGAG	GCTTGTGTGC	ACGTGAGCGT	GCGAGTGAC	GTCCGTATT	9060
	TCAGTGACTT	GGTCCCGTGG	GTCAGCCCTT	CCCCCTGTG	GACAAACCC	CATTGTGGCT	9120
	CCTGCCACCC	TGGCAGATGA	CTCACTGTGG	GGGGGTGGCT	GTGGGCAGTG	AGCGGATGTG	9180
30	ACTGGCGTCT	GACCCGCCCC	TTGACCCAAG	CCTGTGATGA	CATGGTGTG	ATTCTGGGGG	9240
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Seq ID NO: 63 Protein sequence:  
Protein Accession #: NP\_000085.1

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	EELKRVASQP	TSDFFFVND	FSILRTLPL	VSRRCCTTAG	GVPVTRPDD	STSAPRDLVL	240
	SEPSQSRLV	QWTAASGPVT	GKVKQYTPLT	GLGQPLPSER	QEVNVPAGET	SVRLRGLRPL	300
	TEYQVTVIAL	YANSIGEAVS	GTARTTALEG	PELTIONNTA	HSLLVAVRSV	FGATGYRVWT	360
	RVLSGGPTQQ	QELSGPQGSV	LLRLDEPGTD	YEVTVSTLFG	RSVGPATSLM	ARTDASVEQT	420
45	LRPVILGPTS	ILLWNLVPE	ARGYRLEWR	ETGLEPPQKV	VLPSPDVTRYQ	LDGLQPGTEY	480
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	VRSTQGVERT	LVLPGSQTA	DLDDVQAGLS	YTVRVSVARV	PREGSASVLT	VRREPETPLA	600
	VPGLRVVSD	ATRVRAVAG	VPASGFRIS	WSTGSGPSS	QTLPPDSTAT	DITGLQPGTT	660
	YQVAVSVLRG	REEGPAIV	ARTDPLGPVR	TVHVTQASS	SVTITWTRPV	GATGYRVSWH	720
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	RLQILNASSD	VLRTVWVGT	GATAYRLAWG	RSEGGPMRHQ	ILPQNTDSAE	IRGLEGGVSY	840
	SVRVTAIVGD	REGTFVSI	TTPPEAPPAL	GTLHVVRQGE	HSLRLRWEPV	PRAQGFLLHW	900
	QPEGQEQESR	VLGPELSSYH	LDGLEPATQY	RVRLSVLGP	GEGPSAEVTA	RTSEPRVPSI	960
	ELRVVDTSID	SVTLAWTPE	RASSYILSWR	PLRGPQGEVP	GSPQTLPGIS	SSQRTVLEP	1020
55	GVSYIFSLTP	VLDGVRGPEA	SVTQTPVCP	GLADVVLFLP	ATQDNAHRAE	ATRRVLERLV	1080
	LALGPLGPPA	VQVGLLSYSH	RPSPLFPLNG	SHDLGIIQ	IRDMFYMDPS	GNNLGTAVVT	1140
	AHRYMLAPDA	PGRQHVPV	MVLVDEPLR	GDIFSPIREA	QASGLNVVML	GMAGADPEQL	1200
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	PLGDPGRPG	PGLPGTAMK	DKGRGERG	PGPGGGIAP	GEPGLPLPG	SPGPGPVGP	1440
	PGKKEGKDS	EDGAPGLPG	PGSPGEQGR	GPPGAIGPKG	DRGFPGLGE	AGEKGERGPP	1500
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	APGERGIEGF	RGPPGPGQDP	GVRGPAGEK	DRGPPGLDGR	SGLDCKPGAA	GPGFNGAAG	1800
	KAGDPGRDGL	PGLRGEQGLP	GPGPPGGLPG	KPGEDGKPLG	NGKNGEPGDP	GEDGRKEGK	1860
	DSGASGREGR	DGPKGERGAP	GILGPQGP	LPGPVGP	GFPVPGGTG	PKGDRGETGS	1920
70	KGEQQLPGER	GLRGEPSV	NVDRLLTAG	IKASALREIV	ETWDESSGSF	LPVPERRRGP	1980
	KGDSGEQGP	GKEGPIGFP	ERGLKGRGD	PGPQGPPLA	LGERGPPGPS	GLAGEPGKPG	2040
	IPGLPGRAGG	VGEAGRGER	GERGEKGERG	EQGRDGPPL	PPTGPPGPP	GPKVSVDEPG	2100
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85	ADTAGSQLHA	VPVLRVSHAE	EEERVPPEDD	EYSEYSEYSV	EYQDPEAPW	DSDDPCSLPL	2880
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Nucleic Acid Accession #: NM\_006945  
Coding sequence: 1-219

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10     TGTCCACAGC CCTGCCACC TCAGCAGTGC CAGCAGAAAT ATCCTCCTGT GACACCTTCC 180
      CCACCTGCC AGCCAAAGTA TCCACCGAAG AGCAAGTAA

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Seq ID NO: 65 Protein sequence:  
Protein Accession #: NP\_008876

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      PPCQPKYPPK SK

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30     CGGGGCGGGG GCGCGGGGCC ACAGGCCCTT GCTCCGCGCG TCGTTTGAGC ACCGCGGGCG 240
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CTTCTGTGTA GCAGCTTTAA CCCACGTTTG TCTGTACGCT CCAGTCCCGA GACGGCTGAG 3780  
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 GCCAGAAGGT GGGTAGGATG ACCTGGGGTT TCAATTGACT TCTGTTCTTT GCTTTTAGTT 2940  
 TTGATAGTAA GGAAGACCTG CAGTGACCG TTTCTTCCAG GCTGAGGTAC CTGGATCTTG 3000  
 GGTTCCTTCA TGCAGGGACC CAGACAAAGT GATCTGCTTG CCAGAGTCTT TTTTGCCCT 3060  
 CCCTGCCACC TCCCGTGT TCCAAGTCAG CTTTCTGCA AGAAGAAATC CTGGTTAAAA 3120  
 AAGTCTTTTG TATTGGGTCA GGAGTTGAAT TTGGGGTGGG AGGATGGATG CAACTGAAGC 3180  
 AGAGTGTGGG TGCCAGATG TGCGCTATTA GATGTTTCTC TGATAATGTC CCAATCATA 3240  
 CCAGGGAGAC TGGCATTCAG GAGAACTCAG GTGGAGGCTT GAGAAGGCCG AAGGGCCCC 3300  
 TGACCTGCCT GCTTCTTCA GCTTGCCCTC CAGCTTTGCA AAGAGCCACC CTAGGCCCCA 3360  
 GCTGACCACA TGGGTGTGAG CCAGCTTGAG AACACTAACT ACTCAATAAA AGCGAAGGTG 3420  
 GACCNAAAAA AAAAAAAAAA AAAA



Seq ID NO: 69 Protein sequence:  
Protein Accession #: NP\_068772.1

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5      1      11      21      31      41      51
      |      |      |      |      |      |
      MKASPRRPLI LKRRRLPLPV QNAPSETSEE EPKRSPAQQE SNQAEASKEV AESNSCKFPA 60
      GIKIINHPTM PNTQVVAIPN NANHSIIITA LTAQKESGSG SGNPKFILIS CGGAPTQPPG 120
      LRPQTQTSYD AKRTEVTLET LGPKPAARDV NLRPPPGALC EQKRETCADG EAAGCTINNS 180
10     LSNIQWLKRM SSDGLGSRSI KQEMEEKENC HLEQRQVKVE EPSRPSASWQ NSVSRPPYS 240
      YMAMIQFAIN STERKRMTLK DIYTWIEDHF PYFKHIAKPG WKNSIRHNLS LHD MFVRETS 300
      ANGKVSFWTI HPSANRYLTL DQVFKPLDPG SPQLPEHLES QKRPNPPELR RNMTIKTELP 360
      LGARRKMKPL LPRVSSYLVP IQFPVNQSLV LQPSVKVPLP LAASLMSEEL ARHSKRVRIA 420
      PKVLLAEEGI APLSSAGPGK EEKLLFGEFG SPLLPVQTIK EEEIQPGEEM PHLARPIKVE 480
15     SPPLLEWESP APSKKESSH SWEDSSQSPT PRPKKSYSGL RSPTRCVSEM LVIQHRRERE 540
      RSRRRKQHL LPPCVDEPEL LFSEGPSTSR WAAELPPFAD SSDPASQLSY SQEVGGPFKT 600
      PIKETLPISS TPSKSVLPRT PESWRLTPPA KVGGLDFSPV QTSQGASDPL PDLGLMDLS 660
      TTPQLQSAFPL ESPQLLSSE PLDLISVPFG NSSPSDIDVP KPGSPPEQVS GLAANRSLTE 720
20     GLVLDTMNDS LSKILLDISF PGLDEDPLGP DNINWSQFIP ELQ

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Seq ID NO: 70 DNA sequence  
Nucleic Acid Accession #: BC006529.1  
Coding sequence: 178-2424

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25     1      11      21      31      41      51
      |      |      |      |      |      |
      GGCACGAGGG GGACCCGCGC GGTCCGGCGC GAGCCCCCGT CCGGGGCCCT GGCTCGGCCC 60
      CCAGGTTGGA GGAGCCCGGA GCCCGCCTTC GGAGCTACGG CCTAACGGCG CGCGCGACTG 120
30     CAGTCTGGAG GGTCCACACT TGTGATTCTC AATGGAGAGT GAAAACGCAG ATTCATAATG 180
      AAAACTAGCC CCGTCCGCC ACTGATTCTC AAAAGACGGA GGCTGCCCTT TCCTGTTCAA 240
      AATGCCCCAA GTGAAACATC AGAGGAGGAA CCTAAGAGAT CCCCTGCCCA ACAGGAGTCT 300
      AATCAAGCAG AGGCCTCCAA GGAAGTGGCA GAGTCCAAC TTTGCAAGTT TCCAGCTGGG 360
      ATCAAGATTA TTAACCAACC CACCATGCCC AACACGCAAG TAGTGGCCAT CCCCAACAAT 420
35     GCTAATATTC ACAGCATCAT CACAGCACTG ACTGCCAAGG GAAAAGAGAG TGGCAGTAGT 480
      GGGCCCAACA AATTCATCCT CATCAGCTGT GGGGGAGCCC CAACTCAGCC TCCAGGACTC 540
      CGGCCTCAAA CCCAACCAG CTATGATGCC AAAAGGACAG AAGTGACCCT GGAGACCTTG 600
      GGACCAAAAC CTGCAGCTAG GGATGTGAAT CTTCTAGAC CACCTGGAGC CCTTTGCGAG 660
      CAGAAACGGG AGACCTGTGC AGATGGTGAG GCAGCAGGCT GCACTATCAA CAATAGCCTA 720
40     TCCAACATCC AGTGGCTCG AAAGATGAGT TCTGATGGAC TGGGCTCCCG CAGCATCAAG 780
      CAAGAGATGG AGGAAAAGGA GAATTGTAC CTGGAGCAGC GACAGGTAA GGTGAGGAG 840
      CCTTCGAGAC CATCAGCGTC CTGGCAGAAC TCTGTGCTG AGCGGCCACC CTACTCTTAC 900
      ATGGCCATGA TACAATTCGC CATCAACAGC ACTGAGAGGA AGCGCATGAC TTTGAAAGAG 960
      ATCTATACGT GGATTGAGGA CCATTTCCCT TACTTTAAGC ACATTGCCAA GCCAGGCTGG 1020
45     AAGAACTCCA TCCGCCACAA CCTTTCCCTG CACGACATGT TTGTCCGGGA GACGCTGCCC 1080
      AATGGCAAGG TCTCCTCTG GACCATTAC CCCAGTGCCA ACCGCTACTT GACATTGGAC 1140
      CAGGTGTTTA AGCAGCAGAA ACGACCGAAT CCAGAGCTCC GCCGGAACAT GACCATCAA 1200
      ACCGAACCTC CCCTGGGCGC ACGGCGGAAG ATGAAGCCAC TGCTACCACG GGTGAGTCA 1260
50     TACCTGGTAC CTATCCAGTT CCCGGTGAAC CAGTCACTGG TGTTCAGGCC CTCGGTGAAG 1320
      GTGCCATTGC CCCTGGGCGC TTCCCTCATG AGCTCAGAGC TTGCCCGCCA TAGCAAGCGA 1380
      GTCCGCATTG CCCCAGAGT GCTGCTAGCT GAGGAGGGGA TAGCTCCTCT TTCTTCTGCA 1440
      GGACCCAGGA AAGAGGAGAA ACTCCTGTTT GGAGAAGGGT TTTCTCCTTT GCTTCCAGTT 1500
      CAGACTATCA AGGAGGAAGA AATCCAGCCT GGGGAGGAAA TGCCACACTT AGCGAGACCC 1560
55     ATCAAAGTGG AGAGCCCTCC CTTGGAAGAG TGGCCCTCCC CGGCCCATC TTTCAAAGAG 1620
      GAATCATCTC ACTCCTGGGA GGATTCTGTC CAATCTCCCA CCCCAAGACC CAAGAAGTCC 1680
      TACAGTGGGC TTAGGTCCTG AACCCTGGTGT GTCTCGGAAA TGCTTGATG TCAACACAGG 1740
      GAGAGGAGGG AGAGGAGCCG GTCTCGGAGG AAACAGCATC TACTGCCTCC CTGTGTGGAT 1800
      GAGCCGGAGC TGCTCTTCTC AGAGGGGGCC AGTACTTCCC GCTGGGCGCG AGAGCTCCCG 1860
      TTCCAGCAGC ACTCCTCTGA CCCTGCCTCC CAGCTCAGCT ACTCCCAGGA AGTGGGAGGA 1920
60     CCTTTAAGA CACCATTAAG GGAACCGCTG CCCATCTCCT CCACCCCGAG CAAATCTGTC 1980
      CTCCCCGAA CCCCTGAATC CTGGAGGCTC ACGCCCCAG CCAAAGTAGG GGGACTGGAT 2040
      TTCAGCCAG TACAACCCCT CCAGGGTGCC TCTGACCCTT TGCCTGACCC CCTGGGGCTG 2100
      ATGATCTCA GCACCACTCC CTGCAAAAGT GCTCCCCCCC TTGAATCACC GCAAAGGCTC 2160
      CTCAGTTCAG AACCTTAGA CCTCATCTCC GTCCCTTTG GCAACTCTTC TCCCTCAGAT 2220
65     ATAGACGTCC CCAAGCCAGG CTCCCGGAG CCACAGGTTT CTGGCCTTGC AGCCAATCGT 2280
      TCTCTGACAG AAGGCCTGGT CCTGGACACA ATGAATGACA GCCTCAGCAA GATCCTGCTG 2340
      GACATCAGCT TTCTGGGCTT GGACGAGGAC CCACTGGGCC CTGACAACAT CAACTGGTTC 2400
      CAGTTTATTC CTGAGCTACA GTAGAGCCCT GCCCTTGCCC CTGTGCTCAA GCTGTCCACC 2460
      ATCCCGGCA CTCGAAGGCT CAGTGCACCC CAAGCCTCTG AGTGAGGACA GCAGGCAGGG 2520
70     ACTGTTCTGC TCCTCATAGC TCCCTGCTGC CTGATTATGC AAAAGTAGCA GTCACACCCT 2580
      AGCCACTGCT GGGACCTTGT GTTCCCCAAG AGTATCTGAT TCCTCTGCTG TCCCTGCCAG 2640
      GAGCTGAAGG GTGGGAACAA CAAAGGCAAT GGTGAAAAGA GATTAGGAAC CCCCAGCCT 2700
      GTTTCCATTC TCTGCCAGC AGTCTCTTAC CTTCCCTGAT CTTTGAGGGG TGGTCCGTGT 2760
75     AAATAGTATA AATTCTCCAA ATTATCTCTT AATTATAAAT GTAAGCTTAT TTCCTTAGAT 2820
      CATTATCCAG AGACTGCCAG AAGGTGGGTA GGATGACCTG GGGTTTCAAT TGACTTCTGT 2880
      TCCTTGCTTT TAGTTTGGAT AGAAGGGAAG ACCTGCAGTG CACGTTTCT TCCAGGCTGA 2940
      GGTACCTGGA TCTTGGGTTT TTTACTGCAG GGACCCAGAC AAGTGGATCT GCTTGCCAGA 3000
      GTCCTTTTTC CCCCTCCCTG CCACCTCCCC GTGTTTCCAA GTCAGCTTTC CTGCAAGAAG 3060
      AAATCCTGGT TAAAAAAGT TTTTGTATTG GGTGAGGAGT TGAATTTGGG GTGGGAGGAT 3120
80     GGATGCAACT GAAGCAGAGT GTGGGTGCC AGATGTGCGC TATTAGATGT TTCTCTGATA 3180
      ATGTCCCAA TCATACCAGG GAGACTGGCA TTGACGAGAA CTCAGGTGGA GGCTTGAGAA 3240
      GGCCGAAAGG GCCCTGACC TGCCTGGCTT CCTTAGCTTG CCCCTCAGCT TTGCAAAGAG 3300
      CCACCTAGG CCCCAGCTGA CCGCATGGGT GTGAGCCAGC TTGAGAACAC TAAGTACTCA 3360
85     ATAAAGCGA AGGTGAAAAA AAAAAA

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Seq ID NO: 71 Protein sequence:  
Protein Accession #: AAH06529.1



	1	11	21	31	41	51	
5	MKTSFRRPLI	LKRRRLPLPV	QNAPSETSEE	EPKRSPAQQE	SNQAEASKEV	AESNSCKFFA	60
	GIIKIINHPTM	PNQTVVAIPN	NANHSIITA	LTAKEKESGS	SGPNKFILIS	CGGAPTQPPG	120
	LRPQTQTSYD	AKRTFVTTLET	LGPKPAARDV	NLPRPPGALC	EQKRETCADG	EAAGCTINNS	180
	LSNTQWLKRM	SSDGLGSRSI	KQEMEEKENC	HLEQRQVKVE	EPSRPSASWQ	NSVSERPPYS	240
	YMAIQFAIN	STERKRMTLK	DIYTWIEDHF	PYFKHIAKPG	WKNISIRHNS	LHDMFVRETS	300
10	ANGKVSFWTI	HPSANRYLT	DQVFKQKRP	NPELRRNMTI	KTEPLPLGARR	KMKPLLPVRS	360
	SYLVPIQFPV	NQSLVLQPSV	KVPLPLAASL	MSSELARHSK	RVRIAPKVLL	AEEGIAPLSS	420
	AGPGKEEKL	FGEGFSPLLP	VQTIKEEIQ	PGEEMPHLAR	PIKVESPLE	EWSPSPSPFK	480
	EESHSWEDS	SQSPTPRPK	SYSGLRSPTR	CVSEMLVIQH	RERRERSRSR	RKQHLLPPCV	540
	DEPELLFSEG	PSTSRWAEEL	PFPADSSDPA	SQLSYSQEVG	GPFKTPIKET	LPISSSTPSKS	600
15	VLPRTPESWR	LTPPAKVGG	DFSPVQTPQG	ASDPLPDPLG	LMDLSTTPLQ	SAPPLESPQR	660
	LLSSEPLDLI	SVPPGNSPSP	DIDVPKPGSP	EPQVSGLAAN	RSLTEGLVLD	TMNDSLSKIL	720
	LDISFPGLDE	DPLGPDNINW	SQFIPELQ				

20 Seq ID NO: 72 DNA sequence  
Nucleic Acid Accession #: U74612.1  
Coding sequence: 178-2583

	1	11	21	31	41	51	
25	GGCAGGAGGG	GGACCCGGCC	GGTCCGGCGC	GAGCCCCCGT	CCGGGGGCCCT	GGTCCGGCCC	60
	CCAGGTGTTGA	GGAGCCCGGA	GCCCGCCTTC	GGAGCTACGG	CCTAACGGCG	GCGCGGACTG	120
	CAGTCTGGAG	GGTCCACACT	TGTGATTCTC	AATGGAGAGT	GAAAACGCAG	ATTCATAATG	180
	AAAACAGGCC	CCCGTCGGCC	ACTGATTCTC	AAAAGACGGA	GGCTGCCCTC	TCCTGTTCAA	240
	AATGCCCCAA	GTGAACATC	AGAGGAGGAA	CCTAAGAGAT	CCCTGCCCA	ACAGGAGTCT	300
30	AATCAAGCAG	AGGCCTCCAA	GGAAGTGGCA	GAGTCCAAC	CTTGCAAGTT	TCCAGCTGGG	360
	ATCAAGATTA	TTAACACACC	CACCATGCC	AACACGCAAG	TAGTGGCCAT	CCCCAACAA	420
	GCTAATATTC	ACAGCATCAT	CACAGCACTG	ACTGCCAAGG	GAAAAGAGAG	TGGCAGTAGT	480
	GGGCCCAACA	AATTCATCCT	CATCAGCTGT	GGGGGAGCCC	CAACTCAGCC	TCCAGGACTC	540
	CGGCCTCAAA	CCCAAACCGA	CTATGATGCC	AAAAGGACAG	AAGTGACCCT	GGAGACCTTG	600
35	GGACCAAAAC	CTGCAGCTAG	GGATGTGAAT	CTTCCTAGAC	CACCTGGAGC	CCTTTGCGAG	660
	CAGAAACGGG	AGACTGTGTC	AGATGGTGAG	GCAGCAGGCT	GCACTATCAA	CAATAGCCTA	720
	TCCAACATCC	AGTGGCTTCG	AAAGATGAGT	TCTGATGGAC	TGGGCTCCCG	CAGCATCAAG	780
	CAAGAGATGG	AGGAAAAGGA	GAATTGTAC	CTGGAGCAGC	GACAGGTAA	GGTTGAGGAG	840
	CCTTCGAGAC	CATCAGCGTC	CTGGCAGAAC	TCTGTGCTG	AGCGGCCACC	CTACTCTTAC	900
40	ATGGCCATGA	TACAATTCCG	CATCAACAGC	ACTGAGAGGA	AGCGCATGAC	TTTGAAGAGC	960
	ATCTATACGT	GGATTGAGGA	CCACTTTCCC	TACTTTAAGC	ACATTGCCAA	GCCAGGCTGG	1020
	AAGAACTCCA	TCCGCCACAA	CCTTTCCCTG	CACGACATGT	TTGTCCGGGA	GACGTCTGCC	1080
	AATGGCAAGG	TCTCCTCTCG	GACCATTAC	CCCAGTGCCA	ACCGCTACTT	GACATTGGAC	1140
	CAGGTGTTTA	AGCCACTGGA	CCCAGGGTCT	CCACAATTGC	CCGAGCACTT	GGAATCACAG	1200
45	CAGAAACGAC	CGAATCCAGA	GCTCCGCGCG	AACATGACCA	TCAAAACCGA	ACTCCCCCTG	1260
	GGCGCACGGC	GGAAGATGAA	GCCACTGCTA	CCACGGGTCA	GCTCATACCT	GGTACCTATC	1320
	CAGTTCGCCG	TGAACCAATC	ACTGGTGTG	CAGCCCTCGG	TGAAGGTGCC	ATTGCCCTGT	1380
	GCGGCTTCCC	TCATGAGCTC	AGAGCTTGCC	CGCCATAGCA	AGCGAGTCCG	CATTGCCCTC	1440
	AAGGTTTTTG	GGGAACAGGT	GGTGTGTTGT	TACATGAGTA	AGTTCTTTAG	TGGCGATCTG	1500
50	CGAGATTTTG	GTACACCCAT	CACCACTTTG	TTTAATTTTA	TCTTCTTTTG	TTTATCAGTG	1560
	CTGCTAGCTG	AGGAGGGGAT	AGCTCCTCTT	TCTTCTGCAG	GACCAGGGAA	AGAGGAGAAA	1620
	CTCCTGTTTG	GAGAAGGGTT	TTCTCCTTTG	CTTCCAGTTC	AGACTATCAA	GGAGGAAGAA	1680
	ATCCAGCTCG	GAGAGGAAT	GCCACACTTA	GCGAGACCCA	TCAAAGTGGA	GAGCCCTCCC	1740
55	TTGGAAGAGT	GGCCCTCCCC	GGCCCATCT	TTCAAAGAGG	AATCATCTCA	CTCCTGGGAG	1800
	GATTCGTCCC	AATCTCCAC	CCCAGACCC	AAGAAGTCCT	ACAGTGGGCT	TAGGTCCCCA	1860
	ACCCGGTGTG	TCTCGGAAT	GCTTGTGATT	CAACACAGGG	AGAGGAGGGA	GAGGAGCCGG	1920
	TCTCGGAGGA	AACAGCATCT	ACTGCCTCCC	TGTGTGGATG	AGCCGGAGCT	GCTCTTCTCA	1980
	GAGGGGCCCA	GTACTTCCCG	CTGGGCCGCA	GAGTCTCCGT	TCCCAGCAGA	CTCCTCTGAC	2040
60	CCTGCCTCCC	AGCTPCAGCTA	CTCCCAGGAA	GTGGGAGGAC	CTTTTAAGAC	ACCCATTAAG	2100
	GAAACGCTGC	CAGTCTCCTC	CACCCCGAGC	AAATCTGTCC	TCCCCAGAAC	CCCTGAATCC	2160
	TGGAGGCTCA	CGACCCAGC	CAAAGTAGGG	GGACTGGATT	TCAGCCCACT	ACAAACCTCC	2220
	CAGGGTGCCT	CTGACCCCTT	GCCTGACCCC	CTGGGGCTGA	TGGATCTCAG	CACCACTCCC	2280
	TTGCAAGGTG	CTCCCCCTGT	TGAATCACCG	CAAAGGCTCC	TCAGTTTCTA	ACCCCTTAGAC	2340
65	CTCATCTCCG	TCCCCTTTGG	CAACTCTTCT	CCCTCAGATA	TAGACGTCCC	CAAGCCAGGC	2400
	TCCCCTGAGC	CACAGGTTTC	TGGCCTTGCA	GCCAATCGTT	CTCTGACAGA	AGGCCTGGTC	2460
	CTGGACACAA	TGAATGACAG	CCTCAGCAAG	ATCCTGCTGG	ACATCAGCTT	TCTTGGCCTG	2520
	GACGAGGACC	CAGTGGGCCC	TGACAACATC	AACTGGTCCC	AGTTTATTCC	TGAGCTACAG	2580
	TAGAGCCCTG	CCCTTGCCCC	TGTGCTCAAG	CTGTCCACCA	TCCCGGGCAC	TCCAAGGCTC	2640
70	AGTGACCCCC	AAGCCTCTGA	GTGAGGACAG	CAGGCAGGGA	CTGTTCTGCT	CCTCATAGCT	2700
	CCCTGCTGCC	TGATTATGCA	AAAGTAGCAG	TCACACCCTA	GCCACTGCTG	GGACCTTGTC	2760
	TTCCCCAAGA	GTATCTGATT	CCTCTGCTGT	CCCTGCCAGG	AGCTGAAGGG	TGGGAACAAC	2820
	AAAGGCAATG	GTGAAAAGAG	ATTAGGAACC	CCCCAGCCTG	TTTCCATTCT	CTGCCAGCA	2880
	GTCTCTTACC	TTCCCTGATC	TTTGCAAGGT	GGTCCGTGTA	AATAGTATAA	ATTCTCCAAA	2940
75	TTATCCTCTA	ATTATAAATG	TAAGCTTATT	TCCTTAGATC	ATTATCCAGA	GACTGCCAGA	3000
	AGGTGGGTAG	GATGACCTGG	GGTTTCAATT	GACTTCTGTT	CCTTGCTTTT	AGTTTTGATA	3060
	GAAGGGGAAG	CCTGCAGTGC	ACGGTTTCTT	CCAGGCTGAG	GTACCTGGAT	CTTGGGTTCT	3120
	TCACTGCAGG	GACCCAGCTG	AGTGGATCTG	CTTGCCAGAG	TCCTTTTGGC	CCCTCCCTGC	3180
	CACCTCCCCG	TGTTTCCAAG	TCAGCTTTCC	TGCAAGGAAG	AATCCTGGTT	AAAAAAGTCT	3240
	TTTGATTATG	GTCAGGAGTT	GAATTTGGGG	TGGGAGGATG	GATGCAACTG	AAGCAGAGTG	3300
80	TGGGTGCCCA	GATGTGCCCT	ATTAGATGTT	TCTCTGATAA	TGTCCTCAAT	CATACCAGGG	3360
	AGACTGGCAT	TGACGAGAAC	TCAGGTGGAG	GCTTGAGAAG	GCCGAAAGGG	CCCCTGACCT	3420
	GCCTGGCTTC	CTTAGCTTGC	CCCTCAGCTT	TGCAAGAGAC	CACCCTAGGC	CCCAGCTGAC	3480
	CGCATGGGTG	TGAGCCAGCT	TGAGAACACT	AACTACTCAA	TAAAGAGCGA	GGTGGACAAA	3540
85	AAAAAAAAAA	AAAAA					

Seq ID NO: 73 Protein sequence:  
Protein Accession #: AAC51128.1



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1      11      21      31      41      51
|      |      |      |      |      |
5  MKTSRRRLPI LKRRRLPLPV QNAPSETSEE EPKRSPAQQE SNQAEASKEV AESNSCKFPA 60
   GIKIINHPTM PNTQVVAIPN NANIHSIITA LTAKGKESGS SGPKNKFILIS CGGAPTQPPG 120
   LRPOQTQTSYD AKRTEVTLET LGPKPAARDV NLPRPPGALC EQKRETCADG EAAGCTINNS 180
   LSNIQWLKRM SSDLGLSSSI KQEMEEKENC HLEQRQVKVE EPSRPSASWQ NSVSERPPYS 240
   YMAMIQFAIN STERKRMTLK DIYTWIEDHF PYFKHIAKPG WKNSIRHNLs LHMDFVRETS 300
10  ANGKVSFWTI HPSANRYLTL DQVFKPLDPG SPQLPEHLES QQKRPNPBLR RNMTIKTELP 360
   LGARRKMKPL LPRVSSYLVP IQFPVNQSLV LQPSVKVPLP LAASLMSSSEL ARHSKRVRVA 420
   PKVFGQVVF GYMSKFFSGD LRDFGTPITS LFNFIPLCLS VLLAEEGIAP LSSAGPGKEE 480
   KLLFGEGFSP LLPVQTIKEE EIQPGGEEMPH LARPIKVESP PLEEWPSAP SFKESSHSHW 540
   EDSSQSPTPR PKKSYSGLRS PTRCVSEMLV IQHRERRERS RSRKQHLPL PCVDEPELLF 600
   SEGPPSTRWA AELPPPADSS DPASQLSYSQ EVGGPFKTP I KETLPISTP SKSVLPRTPE 660
15  SWRLTPPAKV GGLDFSPVQT SQGASDPLPD PLGLMDLSTT PLQSAAPPLES PQRLLSSEPL 720
   DLISVPFGNS SPSDIDVPKP GSPEPQVSGL AANRSLTEGL VLDTMNDSLs KILLDISFPG 780
   LDEDEPLGPDN INWSQFIPEL Q

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Seq ID NO: 74 DNA sequence  
Nucleic Acid Accession #: Eos sequence  
Coding sequence: 111-416

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1      11      21      31      41      51
|      |      |      |      |      |
25  GGGAAAGAGCC AGGCTGAGCC TTATAAAGGA CTGCTCTTTG TCCAAACACA CACATCTCAC 60
   TCATCCTTCT ACTCGTGACG CTTCCTCAGCT CTGGCTTTTT GAAAGCAAAG ATGAGCAACA 120
   CTAAGCTGA GAGGTCCATA ATAGGCATGA TCGACATGTT TCACAAATAC ACCAGACGTG 180
   ATGACAAGAT TGAGAAGCCA AGCCTGCTGA CGATGATGAA GGAGAACTTC CCCAACTTCC 240
   TTAGTGCCCTG TGACAAAAG GGCACAAATT ACCTCGCCGA TGTCTTTGAG AAAAAGGACA 300
30  AGAATGAGGA TAAGAAGATT GATTTTCTG AGTTTCTGTC CTTGCTGGGA GACATAGCCA 360
   CAGACTACCA CAAGCAGAGC CATGGAGCAG CGCCCTGTTC CGGGGGCAGC CAGTGACCCA 420
   GCCCCACCAA TGGGCCTCCA GAGACCCAG GAACAATAAA ATGTCCTTCTC CCACCAGA

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Seq ID NO: 75 Protein sequence:  
Protein Accession #: Eos sequence

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1      11      21      31      41      51
|      |      |      |      |      |
40  MSNTQAERSI IGMIDMFHYK TRDDKIEKP SLLTMMKENF PNFLSACDKK GTNYLADVFE 60
   KKDKNEDKKI DFSEFLSLLG DIAADYHKQS HGAAPCSGGS Q

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Seq ID NO: 76 DNA sequence  
Nucleic Acid Accession #: Eos sequence  
Coding sequence: 111-416

```

1      11      21      31      41      51
|      |      |      |      |      |
50  GGGAAAGAGCC AGGCTGAGCC TTATAAAGGA CTGCTCTTTG TCCAAACACA CACATCTCAC 60
   TCATCCTTCT ACTCGTGACA CTTCCTCAGTT CTGGCTTTTT GAAAGCAAAG ATGAGCAACA 120
   CTAAGCTGA GAGGTCCATA ATAGGCATGA TCGACATGTT TCACAAATAC ACCGGACGTG 180
   ATGGCAAGAT TGAGAAGCCA AGCCTGCTGA CGATGATGAA GGAGAACTTC CCCAATTTC 240
   TCAGTGCCCTG TGACAAAAG GGCATACATT ACCTCGCCAC TGTCTTTGAG AAAAAGGACA 300
55  AGAATGAGGA TAAGAAGATT GATTTTCTG AGTTTCTGTC CTTGCTGGGA GACATAGCCG 360
   CAGACTACCA CAAGCAGAGC CATGGAGCGG CGCCCTGTTC TGGGGGAAGC CAGTGATCCA 420
   GCCCCACCAA GGGGCCTCCA GAGACCCAG GAACAATAAG TGTCTCTTCC CACCAGA

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Seq ID NO: 77 Protein sequence:  
Protein Accession #: XP\_048124.1

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1      11      21      31      41      51
|      |      |      |      |      |
60  MSNTQAERSI IGMIDMFHYK TGRDGKIEKP SLLTMMKENF PNFLSACDKK GIHYLATVFE 60
   KKDKNEDKKI DFSEFLSLLG DIAADYHKQS HGAAPCSGGS Q

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Seq ID NO: 78 DNA sequence  
Nucleic Acid Accession #: Z73678.1  
Coding sequence: 253-2433

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1      11      21      31      41      51
|      |      |      |      |      |
75  GGGGTGGTGC AGGGCAGGGG TGGTATATCC TGTCTGACGG AGGGCGGGCC TCGCCAGTGC 60
   CAGAGAGGGA CGAACCAGGG TGAAGCGGCC AGGAGCAGCT GCAGGGAGCC CTCACGCGGA 120
   CCTCGCACTC TATGGCCGTA GGGAGCCGCT GAGAGCGAGA AGAGCACGCT CCTGCCCGCC 180
   CGCTGCACCG CACCTCGCCT CGCCTCTCTG CTCTCCTAGG CCCCAGCCGC GCGCCACCCG 240
   CCTCCCGACA CCATGAACCA CTCGCCCTC AAGACCGCCT TGGCGTACGA ATGCTTCCAG 300
   GACCAGGACA ACTCCACGTT GGCTTTGCGG TCGGACCAAA AGATGAAAC AGGCACGTCT 360
   GGCAGGCAGC GCGTGACGAG GCAGGTGATG ATGACCGTCA AGCGGCAGAA GTCCAAGTCT 420
   TCCAGTCTCT CCACCTGAG CCACCTCCAAT CGAGGTTCCA TGTATGATGG CTTGGCTGAC 480
   AATTCAACT ATGGGACCAC CAGCAGGAGC AGCTACTACT CCAAGTTCCA GGCAGGGAAT 540
   GGCTCATGGG GATATCCGAT CTACAATGGA ACCCTCAAGC GGGAGCCTGA CAACAGGCGC 600
   TTCAGTCTCT ACAGCCAGAT GGAGAACTGG AGCCGGCACT ACCCCCGGGC CAGCTGTAAC 660
   ACCACCGGGC CAGGCAGGCA CATCTGCTTC ATGCAGAAAA TCAAGGCAG CCGCAGTGAG 720
85  CCCGACCTCT ACTGTGACCC ACGGGGCACC CTGCGCAAGG GCACGCTGGG CAGCAAGGGC 780
   CAGAAGACCA CCCAGAACC GCTACAGCTTT TACAGCACCT GCAGTGGTCA GAAGGCCATA 840
   AAGAAGTGCC CTGTGCGCCC GCCCTCTTGT GCCTCCAAGC AGGACCTGT GTATATCCCG 900

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	CCCATCTCCT	GCAACAAGGA	CCTGTCTCTT	GGCCACTCTA	GGGCCAGCTC	CAAGATCTGC	960
	AGTGAGGACA	TCGAGTGCAG	TGGGCTGACC	ATCCCAAGG	CTGTGCAGTA	CCTGAGCTCC	1020
	CAGGATGAGA	AGTACCAAGG	CATTGGGGCC	TATTACATCC	AGCATACCTG	CTTCCAGGAT	1080
5	GAATCTGCCA	AGCAACAGGT	CTATCAGCTG	GGAGGCATCT	GCAAGCTGGT	GGACCTCCTC	1140
	CGCAGCCCCA	ACCAGAACGT	CCAGCAGGCC	GCSCGAGGGG	CCCTGCGCAA	CCTGGTGTTC	1200
	AGGAGCACC	CCACAAGCT	GGAGACCCGG	AGGCAGAATG	GGATCCGCGA	GGCAGTCAGC	1260
	CTCCTGAGGA	GAACCCGGAA	CGCCGAGATC	CAGAAGCAGC	TGACTGGGCT	GCTCTGGAAC	1320
	CTGTCTTCCA	CTGACGAGCT	GAAGGAGGAA	CTCATTTGCC	ACGCCCTGCC	TGTTCTGGCC	1380
10	GACCCGCTCA	TCATTCCCTT	CTCTGGCTGG	TGCGATGGCA	ATAGCAACAT	GTCCCGGGAA	1440
	GTGGTGGACC	CTGAGGTCTT	CTTCAATGCC	ACAGGCTGCT	TGAGGAACCT	GAGCTCGGCC	1500
	GATGCAGGCC	GCCAGACCAT	GCCTAACTAC	TCAGGGCTCA	TTGATTCCCT	CATGGCCTAT	1560
	GTCCAGAACT	GTGTAGCGGC	CAGCCGCTGT	GACGACAAGT	CTGTGGAAAA	CTGCATGTGT	1620
	GTTCTGCACA	ACCTCTCTTA	CCGCTGGGAC	GCCGAGGTGC	CCACCCGCTA	CCGCCAGCTG	1680
15	GAGTATAACG	CCCGCAACGC	CTACACCGAG	AAGTCTCTCA	CTGGCTGCTT	CAGCAACAAG	1740
	AGCGACAAGA	TGATGAACAA	CAACTATGAC	TGCCCCCTGC	CTGAGGAAGA	GACCAACCCC	1800
	AAGGGCAGCG	GCTGGTTTGA	CCATTACAGT	GCCATCCGCA	CCTACCTGAA	CCTCATGGGC	1860
	AAGAGCAAGA	AAGATGCTAC	CCTGGAGGCC	TGTGTCTGGT	CCCTGCAGAA	CCTGACAGCC	1920
	AGCAAGGGGC	TGATGTCCAG	TGGCATGAGC	CAGTTGATTT	GGCTGAAGGA	AAAGGGCCTG	1980
20	CCACAAATTG	CCCGCCTCCT	GCAATCTGGC	AACCTCTGAT	TGGTCCGCTC	CGGAGCCTCC	2040
	CTCCTGAGCA	ACATGTCCCG	CCACCCTCTG	CTGCACAGAG	TGATGGGGAA	CCAGGTGTTC	2100
	CCGGAGGTGA	CCAGGCTCCT	CACCAGCCAC	ACTGGCAATA	CCAGCAACTC	CGAAGACATC	2160
	TTGTCTCGG	CCTGCTACAC	TGTGAGGAAC	CTGATGGCCT	CGCAGCCACA	ACTGGCCAAG	2220
	CAGTACTTCT	CCAGCAGCAT	GCTCAACAAC	ATCATCAACC	TGTGCCGAAG	CAGTGCCTCA	2280
	CCCAAGGGCG	CAGAGCTTGC	CCGGCTTCTC	CTGTCTGACA	TGTGGTCCAG	CAAGGAACCTG	2340
25	CAGGGTGTCC	TCAGACAGCA	AGGTTTCGAT	AGGAACATGC	TGGGAACCTT	AGCTGGGGCC	2400
	AACAGCCTCA	GGAACTTCAC	CTCCCGATTG	TAAGAAGAGA	CTGTCCAAGC	AAGTTAGGCT	2460
	TGCAGGAAGA	TATGACCAGC	CTGAGAAGCC	CTCAGGCCTC	GCTGGATGGG	GTTTCTCTGC	2520
	CATCCTGTGC	AGTATTTGGG	AAAGTTTACA	AGAAACTGAG	AAGAAACCTA	AAAACCTGTG	2580
30	ATAGTGGAAA	GATTTTITAGA	TTTTTTTITG	CCTTGGGGAA	ACTGGCAGGC	AATGGGGGTT	2640
	AGGGAGGTTG	GGCGGGGGGG	GGCTTCTTTG	AGTTAAAGGG	GCTTATATGT	GATGTCAATA	2700
	TTTCTTCTCT	TGAGAAATGG	TATATATATG	TGTCTAATGT	AAGTGTGTGC	ATGCATGTGC	2760
	GGGTGCATGT	GTTGTGTGTG	GAGTGTCTTA	AAGCATAACC	ACAAACTGCA	AAAAGCTAGG	2820
	TAAGCTATTT	TGTTGCAGCT	CATAAGGTGG	TGAAAAGGAC	TCTCTGTGT	TTCTTACTCA	2880
35	TAGGCAAGGA	CAACATGTGC	TTTTTGGTGA	GCTGCTCATA	ATTCCTGAAA	TGTGTGGTGC	2940
	CAGGGCAAGG	GGGCCATCAC	TGCAGTCAGG	CCCTCAGAGG	AGTCTGTGAG	GCTTCTTACC	3000
	AGTGTCTTCC	AAGGGTGAG	GAGTAACTGG	GGCTGGGCCA	GCCTCCCCCC	TTACAAGGCT	3060
	GCTTTCCACG	AAGGGAGGTC	TGGTGTATCT	CATGGGAGAA	TCTGGGGTGT	CTGTAGTGTC	3120
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40	AGGACACTCT	CGCATACTTT	GCCAAATGAG	GCCTGCTCAG	AGGAGTAGGA	GCTGAAAGAT	3240
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45	GTGGGATGGA	GTTGGGGTAT	AGAAATTAAC	CAGGAAGATG	TTTCCACCAA	GCCTGCTGTG	3540
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50	TCAGACCAGC	AGCAGCAGGA	GGGCTCCCGA	GGGCCTTATG	AGAAAACCTG	TGTGGACATC	3840
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	TCTACCTCCA	TGCTAGCATT	GCTGGTGTTA	GAGAGGAATT	AACCTCCTGG	TCTGTGCCCT	3960
	TCTCTAGAAG	AATATAAGAT	GCTCTCTCTC	CTCACCCCTT	CTCAGCCTCC	TCCCAAGTCT	4020
	TCCTCTTCTG	CACCACCCCC	GAGTCCAAAC	CCACCTCTTG	CCCCAGCATT	CAGGCTGGAA	4080
55	AACACTGATG	TGGACTCAGT	ATGACAACCT	AGATGGGGGA	AGCCAGACAT	GTGAGGACGC	4140
	TGTCCTCCGA	GAGGTGTCCC	CGGCTGTTAG	CCAGCTGTGC	TGTGGTGTCT	TGGGTCTGTC	4200
	ATACCTCTCC	TGCTTCTTGG	TCACACTGGG	AGGCCCACTC	CTGGCTCACC	TCTCCCTCTC	4260
	AGGGACCCAC	GTGGGAGCCT	GGATCCCTGG	ACTGTCTCTG	GCATAGGTTT	CAGGGGCCTC	4320
	CTTTGTTGTC	ATCAGAACCCT	AGAGGAATTC	TTCTCTCTAA	AAATACGTAT	GGCATAACCA	4380
60	TCTGTGCGGG	GCAGTGTCTT	AAGCACTTAG	ACTACATCAG	GGAAGAACAC	AGACCAACATC	4440
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	GCATCCCCCT	GCCTCATGTT	CCTCCCACTT	TCAAAGAAATG	AAGAGCCCCA	TGGGCCCAGC	4680
65	CCCTGCCCTG	GGAACCAAGC	AGCCTTCCAG	ACCTCAGGGG	CTGAGGCAGA	CTATTAGGGC	4740
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	ATTGGCCTCA	CACATGCCTA	GGCCAATGCC	CAAAATAAGG	AGTTCCAAAT	TGGGGCCAAA	4980
70	TGAGGAAGGA	CACAGACTCT	GCCCTGGGAT	CTCCTGTGCT	AGCGGCCAAT	GACAAATCCA	5040
	GTCAATTGGC	ACCAGCCACC	TCTGCAGTGG	GGACCACACT	AGCAGCCCTG	ACTCCACACT	5100
	CCTCTGCGGG	ACCCAAGAGG	CAGTGTGTCT	GTCTGCGTGT	CCACCTTGGA	ATCTGGCTGA	5160
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	TGTGAGGGAT	CTTGGAGCTT	CCCTGTAGCC	CACCTTCCCC	TTGCTTCATG	TTTGTAGAGG	5280
75	AACCTTGTGC	CGGCCAGGCC	CAGTTTCCCT	GTGTGATACA	CTAATGTATT	TGCTTTTTTT	5340
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Seq ID NO: 79 Protein sequence:  
Protein Accession #: CAA98022.1

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85	QSMENWSRIH	PRGSCNTTGA	GSDICFMQKI	KASRSEPDLY	CDPRGTLRKG	TLGSKGQKTT	180
	QNRYSFYSTC	SGQKAIKKCF	VRPPSCASKQ	DPVYIPIPI	ISCKDLSPFHRS	ASSKICSEDI	240
	ECSGLTIIPKA	VQYLSSQDEK	YQAI GAYIYQ	HTCFQDESAK	QQVYQLGGIC	KLVDLLRSPN	300
	QNVQQAAGA	LRNLVFRSTT	NKLETRRRQNG	IREAVSLLRR	TGNAEIQKQL	TGLLWNLSST	360



DELKEELIAD ALPVLADRVI IPFSGWCDGN SNMSREVVDV EVFFNATGCL RNLSSADAGR 420  
 QTMRYNSGLI DSLMAYVQNC VAASRCDDKS VENCMLVHVN LSYRLDAEVP TRYRQLEYNA 480  
 RNAYTEKSSST GCFSNKSDKM MNMNYDCPLP EEBTNPKGSG WLYHSDAIRT YLNLGMKSKK 540  
 5 DATEACAGA LQNLTAQKGL MSSGMSQLIG LKEKGLPQIA RLLQSGNSDV VRSGLSLLSN 600  
 MSRHPLLHRV MGNOVFPEVT RLLTSHTGNT SNSEDILSSA CYTVRNLMAS QPQLAKQYFS 660  
 SSMNNIINL CRSSASPKAA EAARLLLSDM WSSKELQGV L RQQGFDRNML GTLAGANSLR 720  
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 25 TGCTGATCCT GGGCCGCTTC ATCATCGGTG TGTA CTGCGG CCTGACCACA GGCTTCGTGC 600  
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Seq ID NO: 81 Protein sequence:  
 Protein Accession #: NP\_006507.1

1 11 21 31 41 51  
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 GNKDLWPLLL SIIFIPALLQ CIVLPFCPEP PRFLLINRNE ENRAKSVLKK LRGTADVTHD 240  
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 75 AGVQPPVYAT IGSGIVNTAF TVVSLFVVER AGRRTLHLIG LAGMAGCAIL MTIALALLEQ 360  
 LPWMSYLSIV AIFGFVAFPE VGPPIPWFI VAELEFSQGR PAIAVAGFS NWTNSNFIVGM 420  
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Seq ID NO: 82 DNA sequence  
 Nucleic Acid Accession #: BC001291  
 Coding sequence: 44-541

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 85 GCTGCTGGTC GTGGCCCTAC CGCGGGTGTG GACAGACGCC AACCTGACTG CGAGACAACG 120



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 20 ACTTAGGCCA AGTAGAGAGC ATCAGGTAA ATGGCGTTCA TTTCTCTGTT AAGATGCAGC 1260  
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Seq ID NO: 83 Protein sequence:  
 Protein Accession #: AAH01291

1 11 21 31 41 51  
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 30 CNLEGGPPINS SVFKEYAGSM GESCGGLWLA ILLLLASIAA GLSLSL

Seq ID NO: 84 DNA sequence  
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 Coding sequence: 229-2726

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	TGAGAGAAAA	AGAGAGAGAG	AGAGAAAAAG	ACCATGCTGC	ATACATTCTG	TAATACATAT	3240
5	CATGTACAGT	TTTATTTTAT	AACGTGAGGA	GGAAAAACAG	TCTTTGGATT	AACCCTCTAT	3300
	AGACAGAATA	GATAGCACTG	AAAAAAAATC	TCTATGAGCT	AAATGTCTGT	CTCTAAAGGG	3360
	TTAAATGTAT	CAATTGGAAA	GGAGAAAAAA	AGGCCTTGAA	TTGACAAATT	AAACAGAAAA	3420
	CAGAACAAAT	TTATTCATAT	ATTTCGTTT	AAAATATGAG	TGCCTTGGAT	CTATTAAAAA	3480
10	CACATCGATG	GTTCTTTCTA	CTTGTATATA	ACTTGTAGCT	TAATTCAGCA	TTGGGTGAGG	3540
	TAATAAACCT	TAGGAAC TAG	CATATAATTC	TATATTGTAT	TTCTCACAAAC	AATGGCTACC	3600
	TAAAAAGATG	ACCCATTATG	TCCTAGTTAA	TCATCATTTT	TCCTTTAGTT	TAATTTTATA	3660
	AACAAAAC TG	ATTATACCA G	TATAAAAGCT	ACTTTGCTCC	TGGTGAGAGC	TTAAAAAGAA	3720
	TGGGCTGTTT	TGCCCAAAGT	TTTATTTTTT	TTAAACAATG	ATTAAATTGA	ATGTGTAATG	3780
15	TGCAAAAGCC	CTGGAACGCA	ATTAAATACA	CTAGTAAGGA	GTTCAATTTA	TGAAGATATT	3840
	TGCTTTAATA	ATGTCCTTTT	AAAAAATACT	GCACCAAAAG	AAATAGATCC	AGATCTACTT	3900
	GGTTGTCAAG	TGGACATCA	AATGATAAAC	TTTAAGACCT	TGTATACCAT	ATTGAAAGGA	3960
	AGAGGCTGAC	AATAAGGTTT	GACAGAGGGG	AACAGAAGAA	AATAATATGA	TTTATTAGCA	4020
	CAACGTGGTA	CTATTTTGCCA	TTTAAAACTA	GAACAGGTAT	ATAAGCTAAT	ATTGATACAA	4080
20	TGATGATTAA	CTATGAATTC	TTAAGACTTG	CATTTAAATG	TGACATTCTT	AAAAAAGAA	4140
	GAGAAAGAA	TTTAAGAGTA	GCAGTATATA	TGCTCTGTCT	CCCTAAAAGT	TGTAATTCAT	4200
	TTCTTTTCCA	TACACTGTGT	GCTATTTGTG	TTAACATGGA	AGAGGATTC	TTGTTTTTAT	4260
	TTTATTTTTT	TTAATTTTTT	CTTTTTTATT	AAGCTAGCAT	CTGCCCCAGT	TGGTGTTCAT	4320
	ATAGCACTTG	ACTCTGCTGT	TGATATCTGT	ATCTTTTCTC	TAATCAGAGA	TACAGAGGTT	4380
25	GAGTATAAAA	TAAACCTGCT	CAGATAGGAC	AATTAAGTGC	ACTGTACAAT	TTTCCCAGTT	4440
	TACAGGTCTA	TACTTAAGGG	AAAAGTTGCA	AGAATGCTGA	AAAAAAATTG	AACACAATCT	4500
	CATTGAGGAG	CATTTTTTAA	AAACTAAAAA	AAAAAAACT	TTGCCAGCCA	TTTACTTGAC	4560
	TATTGAGCTT	ACTTACTTGG	ACGCAACATT	GCAAGCGCTG	TGAATGGAAA	CAGAATACAC	4620
	TTAACATAGA	AATGAATGAT	TGCTTTCGCT	TCTACAGTGC	AAGGATTTTT	TTGTACAAAA	4680
30	CTTTTTTAAA	TATAAATGTT	AAGAAAAATT	TTTTTTTAAA	AACACTTCAT	TATGTTTAGG	4740
	GGGGAAC TGC	ATTTTAGGGT	TCCATTGTCT	TGGTGGTGTT	ACAAGACTTG	TTATCCATTT	4800
	AAAAATGGTA	GTGGAAATTC	TATGCCCTGG	ATACACACCG	CTCTTCAGGT	TGTAAAAAAA	4860
	AAAAACATAC	ATTGGGGAAA	GGTTTAAAGT	TATATAGTAC	TTAAATATAG	GAAAATGCAC	4920
	ACTCATGTG	ATTCCATATG	TAAATACAT	TTATGGTCTT	TTTTCTGTAT	TTCTAGAATG	4980
35	GTATTTGAAT	TAAATGTTCA	TCTAGTGTTA	GGCACTATAG	TATTTATATT	GAAGCTTGTA	5040
	TTTTTAACTG	TGCTTGTTC	TCTTAAAGG	TATCAATGTA	CCTTTTTTGG	TAGTGGAAAA	5100
	AAAAAAGACA	GGCTGCCACA	GTATATTTTT	TTAATTTGGC	AGGATAATAT	AGTGCAAAAT	5160
	ATTTGTATGC	TTCAAAAAAA	AAAAAAGAG	AGAAACAAAA	AAGTGTGACA	TTACAGATGA	5220
	GAAGCCATAT	AATGGCGGTT	TGGGGGAGCC	TGCTAGAATG	TCACATGGAT	GGCTGTCATA	5280
40	GGGGTTGTAC	ATATCCCTTT	TTGTTCCTTT	TTCTTGCTGC	CATACGTGAT	GCAGTACTGC	5340
	AAGCTAATAA	CGTTGGTTTG	TTATGTAGTG	TGCTTTTTGT	CCCTTTCTCT	CTATCACCTT	5400
	ACATTCACAG	ATCTTACCTT	CATATGCAGT	AAAAGAAAGA	AAGAAAAAAA	AAGGAAAAAA	5460
	AAAAAAAAC	CAATGTTTTG	CAGTTTTTTT	CATTGCCAAA	AACTAAATGG	TGCTTTATAT	5520
	TTAGATTGGA	AAGAAATTTCA	TATGCAAGC	ATATTAAAGA	GAAAGCCCGC	TTTAGTCAAT	5580
45	ACTTTTTTGT	AAATGGCAAT	GCAGAAATAT	TTGTTATTTG	CCTTTTCTAT	TCCTGTAATG	5640
	AAAGCTGTTT	GTCGTAACCT	GAAATTTTAT	CTTTTACTAT	GGGAGTCACT	ATTTATATT	5700
	GCTTATGTGC	CCTGTTCAAA	ACAGAGGCAC	TTAATTTGAT	CTTTTATTTT	TCTTTGTTTT	5760
	TATTTTTTTT	TTTATTTAGA	TGACCAAGG	TCATTACAAC	CTGGCTTTTT	ATTTGATTTG	5820
	TTTCTGGTCT	TTGTTAAGTT	CTATTGGAAA	AACCACTGTC	TGTGTTTTTT	TGGCAGTTGT	5880
50	CTGCATTAAC	CTGTTTCATAC	ACCCATTTTG	TCCCTTTATT	GAAAAAATAA	AAAAAATTAA	5940

Seq ID NO: 85 Protein sequence:  
Protein Accession #: NP\_075044.1

55	1	11	21	31	41	51	
	MSRRKQKQKP	HLKSKREFSPE	PLEAILTDDE	PDHGFLGAPE	GDHDLTTCGQ	QCMNFPLGDI	60
	LIFIEHKRKQ	CNGLSLCLEKA	VDKPPSPSP	EMKKASNPVE	VGIQVTPEDD	DCLSTSSSRI	120
60	CPKQEHIAAD	LLHWRGLSSP	RSAGHALIPT	PGMSAEYAPQ	GICKDEPSSY	TCTTCKQPFT	180
	SAWFLQLQHA	NTHGLRLIYE	SEHGSPLTPR	VGIPSGLGAE	CPSPQPLHLGI	HIADNPNFNL	240
	LRIPIGSVSR	ASGLAEGRFP	PTPLFSFPFP	RHLDLPHRIE	RLGAEEMALA	THFPSAFDRV	300
	LRLNPMAMEP	FAMDFSRRLR	ELAGNTSSPP	LSPGRPSPMQ	RLQPFQPGS	KPFPLATPPL	360
	PPLQSAAPPP	QPPVKSKSCE	FCGKTFKFQS	NLVVHRRSHT	GEKPYKCNLC	DHACTQASKL	420
65	KRHKMTHMHK	SSPMTVKSDE	GLSTASSPEP	GTSDLVGSAS	SALKSVVAKF	KSENDPNLIP	480
	ENGDEEEED	DEEBEEEEEE	EEBELTESER	VDYGFGLSLE	AARHHENSSR	GAUVGVGDES	540
	RALPDVMQGM	VLSSMQHFSE	AFHQVLGEKH	KRGHLAEAE	HRDTCDEDSV	AGESDRIDDG	600
	TVNRCGCSFG	ESASGGLSKK	LLLGSPSSLS	PFSKRIKLEK	EPDLPPATMP	NTENVYSQWL	660
	AGYAASRLQK	DPFLSFGDSR	QSPFASSESH	SENGSLRFS	TPPGLDGGI	SGRSCTGSGG	720
70	STPHISGFGT	GRPSSKEGRR	SDTCEYCGKV	FKNCSNLT VH	RRSHTGERPY	KCELCNYACA	780
	QSSKLTRHMK	THGVQGVKDV	KCEICKMPFS	VYSTLEKHMK	KWHSRDLN	DIKTE	

Seq ID NO: 86 DNA sequence  
Nucleic Acid Accession #: XM\_035292.2  
Coding sequence: 53-1576

75	1	11	21	31	41	51	
80	GCTCGCTGGG	ACGCGGCTCC	CGGGTGTCCC	AGGCCCGGCC	GGTGCGCAGA	GCATGGCGGG	60
	TGCGGGCCCC	AAGCGGCGCG	CGCTAGCGGC	GCGGCGCGCC	GAGGAGAAGG	AAGAGGCGCG	120
	GGAGAAGATG	CTGCCCCCA	AGAGCGCGGA	CGGCTCGGCG	CCGGCAGGCG	AGGGCGAGGG	180
	CGTGACCTCG	CAGCGGAACA	TCACGCTGCT	CAACGGCGTG	GCCATCATCG	TGGGGACCAT	240
	TATCGGCTCG	GAGCATCTCG	TGACGCCAC	GGCGGTGCTC	AAGGAGGCAG	GCTCGCGGG	300
85	GCTGGCGCTG	TGTTGTGGGG	CCGCGTGGCG	CGTCTTCTCC	ATCGTGGGCG	CGCTCTGCTA	360
	CGCGGAGCTC	GGCACCAATC	TCTCCAAATC	GGGCGGCGAC	TACGCTTACA	TGCTGGAGGT	420
	CTACGGCTCG	CTGCCCCGCT	TCCTCAAGCT	CTGGATCGAG	CTGCTCATCA	TCCGGCCTTC	480
	ATCGCAGTAC	ATCGTGCGCC	TGGTCTTCGC	CACCTACCTG	CTCAAGCCGC	TCTTCCCCAC	540



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CTGCCCCGGTG CCCGAGGAGG CAGCCAAGCT CGTGGCCTGC CTCTGCGTGC TGCTGCTCAC 600
GGCCGTGAAC TGCTACAGCG TGAAGGCGCG CACCCGGGTC CAGGATGCCT TTGCCGCCGC 660
CAAGCTCCTG GCCTTGCCCC TGATCATCCT GCTGGGCTTC GTCCAGATCG GGAAGGGTGA 720
TGTTGTCCAAT CTAGATCCCA ACTTCTCATT TGAAGGCACC AAAGTGGATG TGGGGAACAT 780
5 TGTTGCTGGCA TTATACAGCG GCCTCTTTGC CTATGGAGGA TGAATTACT TGAATTTCGT 840
CACAGAGGAA ATGATCAACC CCTACAGAAA CCTGCCCTG GCCATCATCA TCTCCCTGCC 900
CATCGTGACG CTGGTGACG TGCTGACCAA CCTGGCCTAC TTCACCACCC TGTCACCCGA 960
GCAGATGCTG TCCTCCGAGG CCGTGGCCGT GGACTTCGGG AACTATCACC TGGGCGTCAT 1020
10 GTCTGGATC ATCCCCGTCT TCCTGGGCTC GTCTGCTTC GGCTCCGTCA ATGGGTCCCT 1080
GTTACATCC TCCAGGCTCT TCTTCGTGGG GTCCCGGGAA GGCCACCTGC CCTCCATCCT 1140
CTCCATGATC CACCCACAGC TCCTCACCCC CGTGCCGTCC CTGCTGTTC CGTGTGTGAT 1200
GACGCTGCTC TACGCTTCT CCAAGGACAT CTTCTCCGTC ATCAACTTCT TCAGCTTCTT 1260
CAACTGGCTC TGGTGGCCC TGGCCATCAT CGGCATGATC TGGCTGCGCC ACAGAAAGCC 1320
15 TGAGCTTGAG CGGCCCATCA AGGTGAACCT GGCCTGCGCT GTGTTCTTCA TCCTGGCCTG 1380
CCTCTTCTG ATCGCCGTCT CCTTCTGGAA GACACCCGTG GAGTGTGGCA TCGGCTTCAC 1440
CATCATCTC AGCGGGCTGC CCGTCTACTT CTTGGGGTTC TGGTGGAAAA ACAAGCCCAA 1500
GTGGCTCCTC CAGGGCATCT TCTCCACGAC CGTCTGTGT CAGAAGCTCA TGCAGTGGT 1560
CCCCAGGAG ACATAGCCAG GAGGCCGAGT GGCTGCCGGA GGAGCATGC

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Seq ID NO: 87 Protein sequence:  
Protein Accession #: XP\_035292.2

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1      11      21      31      41      51
|      |      |      |      |      |
25 MAGAGPKRRA LAAPAAEKE EAREKMLAAK SADGSAPAGE GEGVTLQRNI TLLNGVAIIV 60
   GTIIGSGIFV TPTGVLKEAG SPGLALVWVA ACVFSIVGA LCYAEIGTTI SKSGGDYAYM 120
   LEVYGSILPAF LKLWIELLII RPSSQYIVAL VFATYLLKPL FPCTCPVEEA AKLVACLCLV 180
   LLTAVNCYSV KAATRVQDAF AAKLLALAL IILLGFVQIG KGDVSNLDPN FSEFGTKLDV 240
30 GNIVLALYSY LFAYGWNLYL NFVTEEMINP YRNLPLAIII SLPIVTLVYV LTNLAYFTTL 300
   STEQMLSSSEA VAVDFGNYHL GVMWIIIPVF VGLSCFSGVN GSLFTSSRLF FVGSREGHLP 360
   SILSMIHPQL LTPVPLVFT CVMTLLYAFS KDIFSVINFF SFPNWLVAL AIIGMIWLRH 420
   RKPELERPIK VNIALVPFFI LACFLIAVS FWKTPVECGI GFTIILSGLP VYFFGVWWKN 480
   KPKWLLQGIF STTVLCQKLM QVVPQET

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Seq ID NO: 88 DNA sequence  
Nucleic Acid Accession #: NM\_005268.1  
Coding sequence: 168-989

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1      11      21      31      41      51
|      |      |      |      |      |
40 TAAAAAGCAA AAGAATTGCG GGCCGCGTCG ACACGGGCTT CCCCAGAAAC CTTCCTCGCT 60
   TCTGGATATG AAATTCGAAG TGCTTGCTGA GTCTATTGTC CGGCTGCTGG GAGCCAGGAG 120
45 AGCCCTGAGG AGTAGTCACT CAGTAGCAGC TGACGCGTGG GTCCACCATG AACTGGAGTA 180
   TCTTTGAGGG ACTCCTGAGT GGGGTCAACA AGTACTCCAC AGCCTTTGGG CGCATCTGGC 240
   TGTCTCTGGT CTTCATCTTC CGCGTGTGCG TGTACCTGGT GACGGCCGAG CGTGTGTGGA 300
   GTGATGACCA CAAGGACTTC GACTGCAATA CTGCGCAGCC CGGCTGCTCC AACGTCTGCT 360
   TTGATGAGTT CTTCCCTGTG TCCCATGTGC GCCTCTGGGC CCTGCAGCTT ATCCTGGTGA 420
50 CATGCCCTC ACTGCTCGTG GTCATGCACG TGGCCTACCG GGAGGTTTCA GAGAAGAGGC 480
   ACCGAGAAGC CCATGGGGAG AACAGTGGGC GCCTCTACCT GAACCCCGGC AAGAAGCGGG 540
   GTGGGCTCTG GTGGACATAT GTCTGCAGCC TAGTGTTCAA GCGGAGCGTG GACATCGCCT 600
   TTCTCTATGT GTTCCACTCA TTCTACCCCA AATATATCCT CCTCTCTGTG GTCAAAGTGC 660
   ACGCAGATCC ATGTCCCAAT ATAGTGGACT GCTTCATCTC CAAGCCCTCA GAGAAGAACA 720
55 TTTTCAACCT CTTATGGTG GCCACAGCTG CCATCTGCAT CCTGCTCAAC CTCGTGGAGC 780
   TCATCTACCT GGTGAGCAAG AGATGCCACG AGTGCCCTGGC AGCAAGGAAA GCTCAAGCCA 840
   TGTGCACAGG TCATCACCCC CACGGTACCA CCTCTTCTTG CAAACAAGAC GACCTCCTTT 900
   CGGGTGACCT CATCTTCTG GGCTCAGACA GTCATCCTCC TCTCTTACCA GACCGCCCCC 960
   GAGACCATGT GAAGAAACC ATCTTGTGAG GGGCTGCTCG GACTGCTCTG GCAGGTTGGG 1020
60 CCTGGATGGG GAGGCTCTAG CATCTCTCAT AGGTGCAACC TGAGAGTGGG GGAGCTAAGC 1080
   CATGAGGTAG GGGCAGGCAA GAGAGAGGAT TCAGACGCTC TGGGAGCCAG TTCCTAGTCC 1140
   TCAACTCCAG CCACCTGCCC CAGCTCGACG GCACTGGGCC AGTCCCCCT CTGCTCTGCA 1200
   GCTCGGTTTC CTTTCTAGA ATGGAATAG TGAGGGCCAA TGC

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Seq ID NO: 89 Protein sequence:  
Protein Accession #: NP\_005259.1

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1      11      21      31      41      51
|      |      |      |      |      |
70 MNWSIFEGLL SGVNKYSTAF GRWLSLVFI FRVLVYLVT A ERVWSDDHKD FDCNTRQPGC 60
   SNVCFDEFFP VSHVRLWALQ LILVTCPSLL VVMHVAYREV QEKRHREAHG ENSGRLYLNP 120
   GKKRGGWLWT YVCSLVFKAS VDIAPLYVFH SFYPKYILPP VVKCHADPCP NIVDCFISKP 180
   SEKNIFTLFM VATAAICILL NLVELIYLV KRCHECLAAR KAQAMCTGHH PHGTTSSCKQ 240
   DDLLSGDLIF LGSDSHPPLL PDRPRDHVKK TIL

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Seq ID NO: 90 DNA sequence  
Nucleic Acid Accession #: NM\_002391.1  
Coding sequence: 26-457

```

1      11      21      31      41      51
|      |      |      |      |      |
80 CGGGCGAAGC AGCGCGGGCA GCGAGATGCA GCACCGAGGC TTCCTCTCTC TCACCTCCTC 60
   CGCCTGCTG CGCTCACCT CCGCGGTGCG CAAAAAGAAA GATAAGGTGA AGAAGGGCGG 120
   CCCGGGAGC GAGTGCGCTG AGTGGGCTG GGGGCCCTGC ACCCCAGCA GCAAGGATTG 180
85 CGGCTGGGT TTTCCGAGG GCACCTGCGG GGGCCAGACC CAGCGCATCC GGTGAGGGT 240
   GCCCTGCAAC TGAAGAAGG AGTTTGGAGC GCACTGCAAG TACAAGTTTG AGAACTGGGG 300
   TCGTGTGAT GGGGCGACAG GCACCAAGT CCGCAAGGC ACCCTGAAGA AGGCGCGCTA 360

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CAATGCTCAG TGCCAGGAGA CCATCCGCGT CACCAAGCCC TGCACCCCA AGACCAAAGC 420  
 AAAGGCCAAA GCCAAGAAAG GGAAGGGAAA GGACTAGACG CCAAGCCTGG ATGCCAAGGA 480  
 GCCCTGGTGG TCACATGGGG CCTGGCCACG CCCTCCCTCT CCCAGGCCCG AGATGTGACC 540  
 CACCAGTGCC TTCTGTCTGC TCGTTCAGCT TAATCAATCA TGCCCTGCCT TGTCCCTCTC 600  
 ACTCCCCAGC CCCACCCCTA AGTGCCCAAA GTGGGGAGGG ACAAGGGATT CTGGGAAGCT 660  
 TGAGCCTCCC CCAAAGCAAT GTGAGTCCCA GAGCCCGCTT TTGTTCTTCC CCACAATTCC 720  
 ATTACTAAGA AACACATCAA ATAAACTGAC TTTTTCCTCC CAATAAAAGC TCTTCTTTT 780  
 TAATAT

Seq ID NO: 91 Protein sequence:  
 Protein Accession #: NP\_002382.1

1 11 21 31 41 51  
 | | | | |  
 MQHRGFLLLT LLALLALTSA VAKKKDKVKK GPGSECAEW AWGPCTPSSK DCGVGFREGT 60  
 CGAQTORIRC RVPCNWKKEF GADCKYKFEN WGACDGGTGT KVRQGTLLKA RYNAQCQETI 120  
 RVTKPCTPKT KAKAKAKKKG KGD

Seq ID NO: 92 DNA sequence  
 Nucleic Acid Accession #: NM\_005130.1  
 Coding sequence: 98-802

1 11 21 31 41 51  
 | | | | |  
 CTCTACCTGA CACAGCTGCA GCCTGCAATT CACTCCCACT GCCTGGGATT GCCTGGATC 60  
 CGTGTGCTCA GAACAAGGTG AACGCCCAGC TGCAGCCATG AAGATCTGTA GCCTCACCCCT 120  
 GCTCTCCTTC CTCCTACTGG CTGCTCAGGT GCTCCTGGTG GAGGGGAAAA AAAAAGTGAA 180  
 GAATGGACTT CACAGCAAGG TGGTCTCAGA ACAAAGGAC ACTCTGGGCA ACACCCAGAT 240  
 TAAGCAGAAA AGCAGGCCCG GGAACAAAGG CAAGTTTGTG ACCAAAGACC AAGCCAACTG 300  
 CAGATGGGCT GCTACTGAGC AGGAGGAGGG CATCTCTCTC AAGGTTGAGT GCCTCAATT 360  
 GGACCATGAA TTTTCTGTGT TCTTTGCTGG CAATCCAACC TCATGCCTAA AGCTCAAGGA 420  
 TGAGAGAGTC TATTGGAAC AAGTTGCCCG GAATCTGCGC TCACAGAAAG ACATCTGTAG 480  
 ATATTCCAAG ACAGCTGTGA AAACCAGAGT GTGCAGAAAG GATTTTCCAG AATCCAGTCT 540  
 TAAGCTAGTC AGCTCCAATC TATTTGGGAA CACAAAGCCC AGGAAGGAGA AAACAGAGAT 600  
 GTCCCCCAGG GAGCACATCA AGGGCAAAGA GACCACCCCT TCTAGCCTAG CAGTGACCCA 660  
 GACCATGGCC ACCAAAGCTC CCGAGTGTGT GGAGGACCCA GATATGGCAA ACCAGAGGAA 720  
 GACTGCCCTG GAGTTCTGTG GAGAGACTTG GAGCTCTCTC TGCACATICT TCCTCAGCAT 780  
 AGTCAGGAC ACCTCATGCT AATGAGGTCA AAAGAGAAGC GGTTCCTTTA AGAGATGTCA 840  
 TGTGTAAGT CCCTCTGTAT ACTTTAAAGC TCTCTACAGT CCCCCAAAAA TATGAACCTT 900  
 TGTGCTTAGT GAGTGCAACG AAATATTAA ACAAGTTTGT TATTTTGTG TTTTGTGTT 960  
 TGGAATTGCT CTTATTTTTC TTGGATGCGA TGTTCAGAGG CTGTTTCTCT CAGCATGTAT 1020  
 TTCCATGGCC CACACAGTGA TGTGTTGAG CAGCGAAGAG TCTTTGAGCT GAATGAGCCA 1080  
 GAGTGATAAT TTCAGTGCAA CGAAGTTTCT GCTGAATTAA TGGTAATAAA ACTCTGGGTG 1140  
 TTTTTCAAAA AAAAAAAAAA AAA

Seq ID NO: 93 Protein sequence:  
 Protein Accession #: NP\_005121.1

1 11 21 31 41 51  
 | | | | |  
 MKICSLTLLS FLLLLAAQVLL VEGKKKVKNG LHSKVVSEQK DTLGNTQIKQ KSRPGNKGKF 60  
 VTQDQANCRW AATQEEEGIS LKVECTQLDH EFSVCFAGNP TSCLKLKDER VYWKQVARNL 120  
 RSQKIDICRY S KTAVKTRVCR KDFPESLKL VSSTLFGNTK PRKEKTEMSP REHIKKGKETT 180  
 PSSLAVTQTM ATKAPCEVED PDMANQRKTA LEFCGETWSS LCTFFLSIVQ DTSC

Seq ID NO: 94 DNA sequence  
 Nucleic Acid Accession #: NM\_012101  
 Coding sequence: 125-1891

1 11 21 31 41 51  
 | | | | |  
 CTCCTCAGAG GTGTGTCTCT AGTCTCTGTG GTTGCCCTGCC CCACTCCCTG CCGAGAGGCC 60  
 TGCCAGAAAG GTACCTATC CTGAACCCCA GCAAGCCTGA AACAGCTCAG CCAAGCACCC 120  
 TGCATGGGAA GCTGCAGATG CCTCCAGGAG CAACGGGTGCG AGCCCAAGAG CCAAGGATGC 180  
 CCGGAGCCCG TCGGGCCCCA GTGCGAGCCT GGAGAATGGC ACCAAGGCTG ACGGCAAGGA 240  
 TGCCAAGACC ACCAACGGGC ACGGCGGGGA GGCAGCTGAG GGCAAGAGCC TGGGCAGCGC 300  
 CCTGAAGCCA GGGGAAGGTA GGAGCGCCCT GTTCGCGGGC AATGAGTGGC GGCAGCCCAT 360  
 CATCCAGTTT GTCGAGTCCG GGGACGACAA GAACTCCAAC TACTTCAGCA TGGACTCTAT 420  
 GGAAGGCAAG AGGTGCGCGT ACGCAGGGCT CCAGCTGGGG GCTGCCAAGA AGCCACCCGT 480  
 TACCTTTGCC GAAAGGGCGG ACGTGCAGCA GTCCATTTC TCGGAGTCCC GGAAGCCCAT 540  
 GGTGTCCATC ATGGAGCCCG GGGAGACCCG GCGGAACAGC TACCCCGGG CCGACACGGG 600  
 CCTTTTTCAT CGGTCCAAGT CCGGCTCCGA GGAGGTGCTG TCGCACTCCT GCATCGGCAA 660  
 CAAGCAGAGC GCGGTCAAGT CCTGCCTGGT GTGCCAGGCC TCCTTCTGCG AGCTGCATCT 720  
 CAAGCCCAAC CTGAGGGGCG CCGCCTTCCG AGACCAACAG CTGCTCGAGC CCATCCGGGA 780  
 CTTTGGAGCC CGCAAGTGTG COGTGCATGG CAAGACGATG GAGCTCTTCT GCCAGACCCA 840  
 CCAGACCTGC ATCTGCTACC TTTGCATGTT CCAGGAGCAC AAGAATCATA GCACCGTGAC 900  
 AGTGGAGGAG GCCAAGGCGG AGAAGGAGAC GGAGCTGTCA CTGCAAAAGG AGCAGCTGCA 960  
 GCTCAAGATC ATTGAGATTG AGGATGAAGC TGAGAAGTGG CAGAAGGAGA AGGACCCCAT 1020  
 CAAGAGCTTC ACCACCAATG AGAAGGCCAT CCTGGAGCAG AACTTCCGGG ACCTGGTGCG 1080  
 GGACCTGGAG AAGCAAAAGG AGGAAGTGA GGTGCGCTG GAGCAGCGGG AGCAGGATGC 1140  
 TGTGGACCAA GTCAAGGTGA TCATGGATGC TCTGGATGAG AGAGCCAAGG TGTGTCATGA 1200  
 GGACAAGCAG ACCCGGAGC AGCTGCATAG CATCAGCGAC TCTGTGTGT TCTGTCAGGA 1260  
 ATTTGGTGCA TTGATGAGCA ATTACTCTCT CCCCCACCC CTGCCCACCT ATCATGTCTT 1320  
 GCTGGAGGGG GAGGGCCTGG GAGGCTCACT AGGCAACTTC AAGGACGACC TGCTCAATGT 1380  
 ATGCATGCGC CACGTTGAGA AGATGTGCAA GCGGACCTG AGCCGTAAC TCAATTGAGG 1440  
 GAACCACATG GAGAACGGTG GTGACCATCG CTATGTGAAC AACTACACGA ACAGCTTCGG 1500



	GGGTGAGTGG	AGTGCACCGG	ACACCATGAA	GAGATACTCC	ATGTACCTGA	CACCCAAAGG	1560
	TGGGGTCCGG	ACATCATACC	AGCCCTCGTC	TCCTGGCCGC	TTCAACCAAGG	AGACCACCCA	1620
	GAAGAATTTC	AACAATCTCT	ATGGGACCAA	AGGTAACCTAC	ACCTCCCGGG	TCTGGGAGTA	1680
5	CTCCTCCAGC	ATTGAGAACT	CTGACAAATGA	CCTGCCCGTC	GTCCAAGGCA	GCTCCTCCTT	1740
	CTCCCTGAAA	GGCTATCCCT	CCCTCATGCG	GAGCCAAAGC	CCCAAGGCC	AGCCCCAGAC	1800
	TTGGAAATCT	GGCAAGCAGA	CTATGCTGTC	TCACTACCGG	CCATTCTACG	TCAACAAAGG	1860
	CAACGGGATT	GGGTCCAACG	AAGCCCATAG	AGCTCCTGGC	GGAAAGGAACG	AGGCGCCACA	1920
	CCCCTGCTCT	TCCTCCTGAC	CCTGCTGCTC	TTGCCCTTCTA	AGCTACTGTG	CTTGCTCTGGG	1980
10	TGGGAGGGAG	CCTGGTCTCTG	CACCTGCCCT	CTGCAGCCCT	CTGCCAGCCT	CTTGGGGGCA	2040
	GTTCGGGCT	CTCCGACTTC	CCCCTGCGC	ACACTCCATT	CAGACTCCTT	TCCTGCCTTG	2100
	TGACCTCAGA	TGGTACCCAT	CATTCTGTG	CTCAGAGGCC	AACCCATCAC	AGGGGTGAGA	2160
	TAGGTTGGGG	CCTGCCCTAA	CCGCCAGCC	TCCTCCTCTC	GGGCTGGATC	TGGGGGCTAG	2220
	CAGTGAGTAC	CCGCATGGTA	TCAGCCTGCC	TCTCCCGCCC	ACGCCCTGCT	GTCTCCAGGC	2280
	CTATAGACGT	TTCTCTCCAA	GGCCCTATCC	CCCAATGTTG	TCAGCAGATG	CCTGGACAGC	2340
15	ACAGCCACCC	ATCTCCCAAT	CACATGGCCC	ACCTCCTGCT	TCCAGAGGA	CTGGCCCTAC	2400
	GTGCTCTCTC	TGTCCTTACC	TATCAATGCC	CAGCATGGCA	GAACCTGCAG	TGGCCAAGGG	2460
	CTGCAGATGG	AAACCTCTCA	GTGTCTTGAC	ATCACCTTAC	CCAGGCGGTG	GGTCTCCACC	2520
	ACAGCCACTT	TGAGTCTGTG	GTCCCTGGAG	GGTGGCTTCT	CCTGACTGGC	AGGATGACCT	2580
20	TAGCCAAGAT	ATTCTCTGTG	TCCTCTGCT	GAGATAAAGA	ATTCCTTAA	CATGATATAA	2640
	TCCACCCATG	CAATAGCTA	CTGGCCAGC	TACCATTAC	CATTGCTCTA	CAGAATTTCA	2700
	TTCACTCTAC	ACTTTGGCAT	TCCTCTGGC	GATGGAGTGT	GGCTGGGCTG	ACCGCAAAG	2760
	GTGCTTACA	CACCTGCCCC	ACCCTCAGCC	GTGCCCCAT	CAGAGGCTGC	CTCCTCCTTC	2820
	TGATTACCCC	CCATGTGCA	TATCAGGGTG	CTCAAGGAT	GGAGAGGAGA	CAAAACCAGG	2880
25	AGCAGCACAG	TGGGGACATC	TCCGTCTCA	ACAGCCCCAG	GCCTATGGGG	GCTCTGGAAG	2940
	GATGGGCCAG	CTTGCAGGGG	TTGGGGAGGG	AGACATCCAG	CTTGGGCTTT	CCCCTTGGGA	3000
	ATAAACCAAT	GGTCTGTC					

Seq ID NO: 95 Protein sequence:  
Protein Accession #: NP\_036233.1

	1	11	21	31	41	51	
	MEAADASRSN	GSSPEARDAR	SPSGPSPGSL	NGTKADGKDA	KTTNGHGGEA	AEGKSLGSAL	60
35	KPGEGRSALF	AGNEWRRPII	QFVESGDDKN	SNYFSMSDME	GKRSPYAGLQ	LGAAKPPVT	120
	FAEKGDVRKS	IFSESRRPTV	SIMEPGETRR	NSYPRADTGL	FSRSKSGSEE	VLCDSCIGNK	180
	QKAVKSCLV	QASFCLEHLK	PHLEGAAPRD	HQLLEPIRDF	EARKCPVHGK	TMELFCQTDQ	240
	TCICYLQMFQ	EHKNHSTVT	EEAKAEKETE	LSLQKEQLQL	KIIEIEDEAE	KWQKEKDRIK	300
40	SFTTNEKAIL	EQNFRDLVRD	LEKQKEEVRA	ALBQREQDAV	DQVKVIMDAL	DERAKVLHED	360
	KQTRQLHSI	SDSVLFLQEF	GALMSNYSLP	PPLPTVHVL	EGEGLGQSLG	NFKDDLNLVC	420
	MRHVEKMKCA	DLSRNFIERN	HMENGGDHRY	VNNYTNSEFG	EWASAPDTMKR	YSMYLTPKGG	480
	VRTSYQSPSP	GRPTKETTTQK	NFNPLYGTGK	NYTSRVWEYS	SSIQNSDNDL	PVVQSSSFS	540
	LKGYPSLMRS	QSPKAQPQTW	KSGKQTMLSH	YRPFYVNKGN	GIGSNEAP		

Seq ID NO: 96 DNA sequence  
Nucleic Acid Accession #: NM\_080668.1  
Coding sequence: 83-841

	1	11	21	31	41	51	
50	GGCAGGAGGG	CAGCGAGTGG	CCTTCCCGGT	TGGCGCGCGC	CCGGGGCGGC	GGCGCTGGAG	60
	GAGCTCGAGA	CGGAGCCTAG	TTATGTCTGG	GAGGCGAACG	CGGTCCGGAG	GAGCCGCTCA	120
	GCGCTCCGGG	CCAAGGGCCC	CATCTCCTAC	TAAGCCTCTG	CGGAGGTCCC	AGCGGAAATC	180
55	AGGCTCTGAA	CTCCCGAGCA	TCCTCCCTGA	AATCTGGCCG	AAGACACCCA	GTGCGGCTGC	240
	AGTCAGAAAG	CCCATCGTCT	TAAAGAGGAT	CGTGGCCCAT	GCTGTAGAGG	TCCAGCTGT	300
	CCAATCACCT	CGCAGGAGCC	CTAGGATTTT	CTTTTCTTGG	GAGAAAGAAA	ACGAGCCCCC	360
	TGGCAGGGAG	CTTACTAAGG	AGGACCTTTT	CAAGACACAC	AGCGTCCCTG	CCACCCCCAC	420
	CAGCACTCCT	GTGCCGAACC	CTGAGGCCGA	GTCAGCTICC	AAGGAAGGAG	AGCTGGACGC	480
60	CAGAGACTTG	GAAATGTCTA	AGAAAGTCAG	GCGTTCCTAC	AGCCGGCTGG	AGACCCCTGGG	540
	CTCTGCCTCT	ACCTCCACCC	CAGGCCGCCG	GTCCTGCTTT	GGCTTCGAGG	GGCTGTGGGG	600
	GGCAGAAGAC	TTGTCCGGAG	TCTCGCCAGT	GGTGTGCTCC	AAACTCACCC	AGGTCCCCAG	660
	GGTTTGTGCA	AAGCCCTGGG	CCCCAGACAT	GACTCTCCCT	GGAATCTCCC	CACCACCCGA	720
	GAAACAGAAA	CGTAAGAGAA	AGAAAATGCC	AGAGATCTTG	AAAACGGAGC	TGGATGAGTG	780
65	GGCTGCGGCC	ATGAATGCCG	AGTTTGAAGC	TGCTGAGCAG	TTTGATCTCC	TGGTTGAATG	840
	AGATGCAGTG	GGGGGTGCAC	CTGGCCAGAC	TCTCCCTCCT	GTCCTGTACA	TAGCCACCTC	900
	CCTGTGGAGA	GGACACTTAG	GGTCCCTTCC	CCTGGTCTTG	TTACCTGTGT	GTGTGCTGGT	960
	GCTGCGCATG	AGGACTGTCT	GCCTTTGAGG	GCTTGGGCAG	CAGCGGCAGC	CATCTTGGTT	1020
	TTAGGAAATG	GGGCCGCTG	GCCAGCCAC	TCACTGGTGT	CCTGTCTCTT	GTCTCTCTGT	1080
70	CCTTCCTATC	TCCCCAAGT	ACCATAGCCA	GTTTCCAGAT	GGGCCACAGA	CTGGGGAGGA	1140
	GAATCAGTGG	CCCAGCCAGA	AGTTAAAGGG	CTGAGGGTTG	AGGTGAGAGG	CACCTCTGCT	1200
	CTTGTGGGGA	GGGGTGGCTG	CTTGGAAATA	GGCCAGGGG	CTCTGCCAGC	CTCGGCTCT	1260
	CCCTCTGAG	TTGCCTTCTG	TTGGTGGCTT	TCTTCTTGAA	CCCACTGTG	TAAAGAGGTT	1320
	TTCACTTCCG	TGGGTTTCCC	CTTTGATTCT	GTAATAGTCT	CCAGAGAGAA	TTCTGTGGCT	1380
	GAGGGCAATT	CTGTCTTGGA	GGAAGAAGCT	GGACATTGAG	CCTGTGGAGT	CTGAGTTTGG	1440
75	AAGGATGTAG	GGAGCCTTAG	TTGGGTCTCA	GACCATAAGT	GTGTACTACA	CAGAAGCTGT	1500
	GTTTCTAGT	TCTGTCTGTC	TGTTGAGATG	TTGGTAAAT	GCCAGGTTGA	TAGGGCGCTG	1560
	GCTGCTTGA	GCAAAGGGTG	CATTTCAGGG	TGTGGCCACC	AGGTGCTGTG	AGTTTCTGTG	1620
	GCTCATGGCC	TCTGGGCTGG	TCCCTTGCAC	AGGGCCACG	CTGGAGTCTT	ACCACTCTGC	1680
80	TGCAGGGGGT	GAAGTGGGCC	CCTCTTGTCA	CCCATACCCA	TTTCTTACAA	AATAAGTTAC	1740
	ACCGAGTCTA	CTTGGCCCTA	GAAGAGAAAG	TGAAGAGTCT	CCAGACCTAC	TAGCATTTTG	1800
	CAACTATGCT	TGTAAAGTCC	TCGGAAAGTT	TCCTCGCGTA	CCAGACAGCG	GCGGGGGCTG	1860
	ATAGCAATTT	TAGTTTGTGG	CCTCCCTATC	CTCTCACATG	AGAACACTGC	CTGGATGCAT	1920
	CTCATGATCT	CTGGAGAATT	TCCCATCTT	TCTCTTCTTT	CCATCGTGTG	GATTCAATAG	1980
	TTTGGATTGG	AAGGCTGCC	TGCCCCGAC	TCTCTGCGG	CACCCCTGGC	CATTGTACCT	2040
85	TTTGTATGTT	AGAAGTTCGT	GGAAGTAGAC	GCTGAGGTGT	GCAGAGGAGC	TGGTGGATAA	2100
	CAGAGAATGC	CAGGGAAGAT	GAGTGCTGGG	TCAGGGTACT	TGGATGAAAC	GGTGCAGGCC	2160
	AGGGGGGCC	TAATAAAACC	CTCTGCCAGG	TCTGGGAGTC	CCAGGCCATC	TGCTCAACGC	2220



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